



AN 94148842 EMBASE
DN 1994148842
TI Parenteral formulation development of renin inhibitor Abbott-72517.
AU Gupta S.L.; Patel J.P.; Jones D.L.; Partipilo R.W.
CS Clinical Center Pharmacy Department, NIH, Bldg 10, 9000 Rockville Pike, Bethesda, MD 20892, United States
SO PDA Journal of Pharmaceutical Science and Technology, (1994) 48/2 (86-91).
ISSN: 0279-7976 CODEN: JPHTEU
CY United States
DT Journal; Article
FS 027 Biophysics, Bioengineering and Medical Instrumentation
030 Pharmacology
037 Drug Literature Index
LA English
SL English
AB Abbott-72517 is an inhibitor of human renin and is being investigated for the treatment of hypertension. It is an orally bioavailable candidate which is being developed for oral as well as **intravenous** use. The preclinical development of this molecule involved studies to evaluate irritation at the site of injection in an animal model. Several formulation variables such as drug concentration, types of buffer (citrate or acetate), addition of **cosolvent (ethanol)** to enhance drug solubility, and tonicity modifiers such as glycerin or mannitol were evaluated. Additionally, in vitro formulation- whole blood hemolysis and plasma precipitation studies were conducted. Based on these studies, a liquid formulation containing 1.2 mg/mL Abbott-72517·HCl as base, 0.01M citrate buffer, pH 3.7, in 0.45% sodium chloride containing 2.5% mannitol was recommended for preclinical studies. Various processing and administration parameters were evaluated including filter qualification and compatibility of the drug with typical infusion fluids and administration sets. The liquid formulation was further characterized for physical and chemical stability. It was shown that it has acceptable stability at ambient temperature. Based on the accelerated temperature storage results, T90 at 25°C is > 1 year for the ready-to-use liquid formulation. Additionally, a lyophilized version of the liquid formulation was evaluated.

RESERVED. on STN

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ANSWER 116 OF 42399 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS

RESERVED. on STN

AN 94120900 EMBASE

DN 1994120900

TI Acute **intravenous** toxicity of dimethyl sulfoxide, polyethylene glycol 400, dimethylformamide, absolute **ethanol**, and benzyl alcohol in inbred mouse strains.

AU Montaguti P.; Melloni E.; Cavalletti E.

CS Via della Libertà km. 0.750, I-20052 Monza, Italy

SO Arzneimittel-Forschung/Drug Research, (1994) 44/4 (566-570).
ISSN: 0004-4172 CODEN: ARZNAD

CY Germany

DT Journal; Article

FS 052 Toxicology

LA English

SL English; German

AB Acute **intravenous** toxicity of some **solvents**, i.e. dimethyl sulfoxide (DMSO), polyethylene glycol 400 (PEG 400), dimethylformamide (DMF), absolute **ethanol** (EtOH) and benzyl alcohol (BeOH), was determined in three inbred (CD2F1, B6D2F1 and C57BL/6N) mouse strains used in many preclinical tests, mainly in oncology and toxicology. Haemolytic and precipitation potential tests in vitro were performed to assess the blood compatibility of the investigated **solvents** and its relationship with the observed symptoms. The single tested **solvents** did not show any major differences in acute toxicity in the three tested strains with the exclusion of DMSO (less toxic in CD2F1) and BeOH and EtOH (less toxic in B6D2F1). The tested dose ranges in the three strains (in ml/kg) were 1.0-5.66 for DMSO, 2.0-8.0 for PEG 400, 1.0-4.0 for DMF, 0.75-4.24 for EtOH, 0.025-0.4 for BeOH. The lowest tested dose was a safe dose and the highest one was the dose causing mortality in no more than half the animals in each group. The in vitro results suggest avoiding the use of BeOH (which also is more toxic than the other **solvents** in the in vivo test) and DMSO and using PEG 400, EtOH and DMF even though the latter induced a body weight decrease in the B6D2F1 mouse strain. As a general conclusion, dilution of these **solvents** in water is suggested to ameliorate their blood compatibility and the use of doses not higher than the lowest dose tested in this study is recommended.

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AN 94120900 EMBASE

DN 1994120900

TI Acute **intravenous** toxicity of dimethyl sulfoxide, polyethylene glycol 400, dimethylformamide, absolute **ethanol**, and benzyl alcohol in inbred mouse strains.

AU Montaguti P.; Melloni E.; Cavalletti E.

CS Via della Liberta km. 0.750, I-20052 Monza, Italy

SO Arzneimittel-Forschung/Drug Research, (1994) 44/4 (566-570).
ISSN: 0004-4172 CODEN: ARZNAD

CY Germany

DT Journal; Article

FS 052 Toxicology

LA English

SL English; German

AB Acute **intravenous** toxicity of some **solvents**, i.e. dimethyl sulfoxide (DMSO), polyethylene glycol 400 (PEG 400), dimethylformamide (DMF), absolute **ethanol** (EtOH) and benzyl alcohol (BeOH), was determined in three inbred (CD2F1, B6D2F1 and C57BL/6N) mouse strains used in many preclinical tests, mainly in oncology and toxicology. Haemolytic and precipitation potential tests in vitro were performed to assess the blood compatibility of the investigated **solvents** and its relationship with the observed symptoms. The single tested **solvents** did not show any major differences in acute toxicity in the three tested strains with the exclusion of DMSO (less toxic in CD2F1) and BeOH and EtOH (less toxic in B6D2F1). The tested dose ranges in the three strains (in ml/kg) were 1.0-5.66 for DMSO, 2.0-8.0 for PEG 400, 1.0-4.0 for DMF, 0.75-4.24 for EtOH, 0.025-0.4 for BeOH. The lowest tested dose was a safe dose and the highest one was the dose causing mortality in no more than half the animals in each group. The in vitro results suggest avoiding the use of BeOH (which also is more toxic than the other **solvents** in the in vivo test) and DMSO and using PEG 400, EtOH and DMF even though the latter induced a body weight decrease in the B6D2F1 mouse strain. As a general conclusion, dilution of these **solvents** in water is suggested to ameliorate their blood compatibility and the use of doses not higher than the lowest dose tested in this study is recommended.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 07:39:07 ; Search time 2183 Seconds
(without alignments)
7418.913 Million cell updates/sec

Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GGTTGACCTTATCCTCTCT.....CAGATGATGACCGGGTGC 1000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:*

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4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	328	32.8	337	17	AQ356083 CITBI-E1-
C 2	306.8	30.7	667	17	AG155188 Pan trogl
C 3	295	29.5	713	17	AG011265 Homo sapi
C 4	294.2	29.4	3001	11	BC018568 Homo sapi
C 5	292	29.2	986	14	BQ710535 AGENCOURT
C 6	290.4	29.0	1060	13	BM469250 AGENCOURT

7	290	543	17	AQ514325	AQ514325 HS_5194_B
8	289	542	17	AQ426757	AQ426757 CITBI-E1-
C 9	287.4	705	17	AQ115225	AQ115225 RPII1-56
C 10	287.2	695	17	AG113036	AG113036 Pan trogl
C 11	286.6	691	17	AG012294	AG012294 Homo sapi
C 12	285.8	545	12	BG110480	BG110480 602278903
C 13	285.4	470	9	AI679871	AI679871 tu65g12.x
C 14	284.8	568	17	AQ484455	AQ484455 RPII-11-2
C 15	284	895	14	BQ437946	BQ437946 AGENCOURT
C 16	283	780	10	BE340631	BE340631 601067276
C 17	282.2	595	17	AQ424714	AQ424714 CITBI-E1-
C 18	281.2	416	9	AI679871	AI679871 tu65g12.x
C 19	280.8	802	12	BG204346	BG204346 RS23748
C 20	280	465	9	AA601230	AA601230 nc14f04.s
C 21	279.6	646	9	AL044489	AL044489 DKFZP434I
C 22	278.8	575	17	B60004	B60004 CIT-HSP-347
C 23	278.2	689	14	BM990649	BM990649 UI-H-DIO-
C 24	277.6	749	14	BQ435700	BQ435700 AGENCOURT
C 25	276	710	17	AG014826	AG014826 Homo sapi
C 26	275.8	583	17	AQ379630	AQ379630 RPII1-16
C 27	275.6	649	14	BQ005009	BQ005009 UI-H-EIO-
C 28	275.4	447	10	AM243793	AM243793 xo56e06.x
C 29	275	738	12	BG575092	BG575092 602598209
C 30	274.8	759	12	BF674628	BF674628 6021378A9
C 31	274	1875	11	BC009270	BC009270 Homo sapi
C 32	273.4	741	17	BH021064	BH021064 HSC 00332
C 33	273	545	17	AQ505381	AQ505381 RPII-11-3
C 34	273	794	12	BG742810	BG742810 602632558
C 35	272.4	496	9	AI694178	AI694178 WC83g06.x
C 36	272.2	550	10	AW821097	AW821097 PM2-ST030
C 37	272	652	10	BE144300	BE144300 MKO-HT016
C 38	271.8	562	9	AU156861	AU156861 AU156861
C 39	271.8	602	10	AM965008	AM965008 EST377081
C 40	271.6	497	9	AL589495	AL589495 DKFZP451G
C 41	271.2	642	14	BM998857	BM998857 UI-H-DIO-
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C 43	269.8	670	17	AG111511	AG111511 Pan trogl
C 44	269.2	500	9	AI204309	AI204309 qe76a11.x
C 45	268.4	417	9	AA487475	AA487475 ab23c04.s

ALIGNMENTS

RESULT 1

AQ356083/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CITBI-E1-2534J20.TF CITBI-E1 Homo sapiens genomic clone 2534J20,
DNA sequence.
GI:4183256

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
Use of PAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITBI-E1-2534J20.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeettig@ig.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

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Seq primer: M13-21
Class: BAC ends.
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    /sex="male"
    /cell_type="sperm"
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    Caltech Human BAC Library D"
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Best Local Similarity 98.5%; Pred. No. 2.9e-32;
Matches 331; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 353 A A A T T A G C C A G G T G T G T G C A C A G C C T G A G T C C C A G C T A C T T G G G A G G C T G A G G G 412
Db 337 A G A A T T A G C C A G G T G T G T G C A C A G C C G C T G A G T C C C A G C T A C T T G G G A G G C T G A G A G C 278
QY 413 G A G A A T C C T T G A C C C A G T A G C A G G T T G C A G T G A G C C G A G A T A A G A T C A C T G C A 472
Db 277 C A G A A T C C T T G A C C C A G T A G C A G G T T G C A G T G A G C C G A G A T A A G A T C A C T G C A 218
QY 473 C T C C A G C C T G G T G A C A G A G A G A C T C C C T C T C A G A A A T A A A A T A A A A T A A A A 532
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QY 533 T A A A T A A A T A A A T A A A T A A A A T T C T A A A G G G C T G G C A T T T G C T A G C A C T T A T A T 592
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QY 593 G C C C A A T A A G T A T A T C A A T A T C C C A C C C T A C C A G T G C T G A A A T T A G T T C 652
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RESULT 2
AG155188/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-019G22.TJ, genomic survey
ACCESSION
AG155188
VERSION
AG155188.1 GI:16684866
KEYWORDS
GSS.
SOURCE
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC library clone:RP43-019G22.TJ.
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
Unpublished
2 (bases 1 to 667)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpbes@gsc.riken.go.jp URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance

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of clone tracking errors.

PRIMERS

Sequencing: TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1..667

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ORIGIN

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Matches 411; Conservative 0; Mismatches 93; Indels 9; Gaps 4;

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Db 515 T C T A C T A A A A A T A C A A A A A T T G T T G G C G T A G T T G G G C G C T T G T A A T C C C A G C A C T 456

QY 126 T T A G A G S T C R A G A G G G T G A T C A C T T G A G G T C A G G A G T T T T G A G A C C A G C C T G G C C A A 185

Db 455 T T G G G A G C C A G G G G G T G G A T C A C T G A G G T C A G G A G - T T C A A G A C C A G C C T G G C C A A 397

QY 186 C A C G G T G A A A C C C C A T C T C T A C T A A A A A T T A A A A A T T A G C T T G G G T G G G T G G G T C A C A C 245

Db 396 C A T G G C A A A C C T C C C C T C T A C T A A A A A T T A C A A A T T A G C C A G C A T G T G G T C A C A C 337

QY 246 C T G T A T C C C A G C A C T T T G G A G G C T G A G A G G S T G G A T C A C C T G A G T C A G G A G T T C A A 305

Db 336 C T G T A T C C C A G C A C T T T G G A G G C T G A T G C G G T G A T C A C C T G A G T C A G G A G T T C A A 277

QY 306 G G C C A C C T G G C C A C A C T T G T G A A C C A G C G T C T C T A C T A A A A A T A C A A A A T T A G C C A G G 365

Db 276 G A C C A C C T G G C C A C A C A T T G T G A A C C C A T C T C T A T T A A A A T A C A A A A T T G T T G G 217

QY 366 T G T G - G T G C A C A G C C C T G T A G T C C C A C T A C T T G G A G G C T G A G C G G A G A T C G C T T 424

Db 216 T C T T A G T G C A G G T G C C T G T A T C A T G C T A C T T T G G A G G C T G A G G C A G G A A T C A C T G 157

QY 425 G A C C C A G T A G C A G A G T T G C A G T G A G C C G A G A T A A G A G T C A C T G C A C T C C A G C C T G G G 484

Db 156 G A A C C C A G G C A G A G G T T G C A G T G A G A T C A - T G C C A C T G C A C T C C A T C C T G G G 98

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RESULT 3

AG011265

LOCUS

DEFINITION

Homo sapiens genomic DNA, 713 bp DNA linear GSS 07-FBB-1999

survey sequence.

ACCESSION

AG011265

VERSION

AG011265.1 GI:3370908

KEYWORDS

GSS.

SOURCE

Homo sapiens DNA, clone:S594SPN2Nh.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 713)

Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.

TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE 2 (bases 1 to 713)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,
Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
FEATURES Location/Qualifiers
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1. .713

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Matches 363; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

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QY 122 CACTTTAGAGGTGGAAGAGGTGATCAGTTCAGGTTCAGAGGTTTTCAGACCAAGCTCG 181
DB 106 CACTTTGGGAAGCCAAAGTGGAGGATCACCTGAGGTTCAGGAG-TTCAGACCAAGCTCG 164
QY 182 CCACACCGGTGAACCCCATCTCTACTATAAATAAATAAATAGCTNGGGTGGCGTGC 241
DB 165 CCAACATGGTGAACCCCATCTTTTACTATAAATAAATAAATGGCCGGCGCAGTGC 224
QY 242 ACACCTGTAAATCCAGCATTGGGAGGTGAGAGCGGTGGATCAGTTCAGGTTCAGGAGT 301
DB 225 ACACCTGTAAATCCAGCATTGGGAGGTGAGAGCGGTGGATCAGTTCAGGTTCAGGAGT 284
QY 302 TCAGGCCAGCTGGGCACATGGTGAACACGCTCTCTACTATAAATAAATAAATAATAGC 361
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QY 362 CAGGTGTGTGGTGCACAGCGCTGTAGTCCAGCTACTTGGAGGTGAGCGGAGGAATCG 421
DB 345 TGAGGTGTATGTTGATGCTGTATCCAGCAGTTCGGAGGTGAGCGGAGGAATCG 404
QY 422 CTGAACCCAGTAGGAGGTGTCAGTTCAGTTCAGCGGAGATAGTCACTGCCAGCT 481
DB 405 CTGAACCCAGGAGGAGGTGTCAGTTCAGTTCAGCGGAGATAGTTCAGCTTCAGCT 464
QY 482 GGGTGCACAGCAGACTCCCTCTCAGAAATAAATAAATAA 522
DB 465 GGGGACACAGCAGACTCTGCTCAAAAAAAAAAAAAA 505

RESULT 4
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LOCUS Homo sapiens, clone IMAGE:3446135, mRNA.
DEFINITION BC018568
ACCESSION BC018568
VERSION BC018568.1 GI:17235741
KEYWORDS HTC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

REMARK
COMMENT

USA NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalona@bcm.tmc.edu.
Villalona, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Gibbs,R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 19 Row: k Column: 5
This clone has the following problem: no 5' EST match.

FEATURES
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/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
BASE COUNT 715 a 688 c 693 g 905 t
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Best Local Similarity 80.58; Pred. No. 9.9e-29;
Matches 380; Conservative 0; Mismatches 89; Indels 3; Gaps 3;

QY 52 AGCTGTAGATTTGTTGTAATAAATAAATTAATGAATAGCTAGCGCGGTGGCTCAGCGCT 111
DB 474 ATCTGTCACAGAAATTTAAAGACAGATCATAAGAACACAGCTGGCGGTGGCTCAGCGCT 415
QY 112 GTAATCCAGCACTTTAGAGGTGGAAGAGGTGGATCAGTTCAGTTCAGAGTTTGGAG 171
DB 414 GTCATCCAGCACTTTGTGAGCGCAGAGCGGCGAGATCAGTTCAGTTCAGGAG-TTTGAA 356
QY 172 ACCAGCTGGCCACACCGGTGAACCCCATCTCTACTATAAATAAATAAATAATAGCTNGSGT 231
DB 355 ACCAGCTGGCAACATGTTGTAACCCCATCTCTACTATAAATAAATAAATAATAGCAGGT 296
QY 232 GCGTGGCTCACACCTGTATCCAGCACTTTGGAGGTGAGAGCGGTGGATCAGCTGA 291
DB 295 GCAGTGGCTTACGCTGTATCCAGCACTTTGTGAGCGCGAGGGCGGAGATCAGCTGA 236
QY 292 AGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGTGAACCCAGCTCTCTACTATAAATAC 351
DB 235 GGTCAAGAGTTTGAACACCGCTGGACACATGTTGTAACCCCATCTCTACTATAAATAC 176
QY 352 AAAAAATCCAGGTGTTGGTGGCACACCGCTGTAGTCCAGCTACT-TGGGAGGTGAGG 410
DB 175 AAAAAATAGCTGGGTGTTGGTGGTACCTGTAGTCCAGCTACTTCGGGAGGTGAGG 116
QY 411 CGGAAGATTCGCTGAACCCAGTTCAGGAGGTTCAGTTCAGGCGGAGATAGAGTCACTG 470
DB 115 CACGAGATTCGCTGAACCCAGGAGGTGAGGTGTAGTGAAGCCAAATCA-TGCCACCG 57
QY 471 CACTCCAGCTGGGTGACAGAGCAAGACTCCCTCTCAGAAAAATAAATAA 522
DB 56 CACTCCAGCTGGGTGACAGACAGCAAGCTCCATCTCAAAAAAAAAAAAAA 5

RESULT 5
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LOCUS BQ710535
DEFINITION AGNC007_8352291 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277543

5', mRNA sequence.
BQ710535
BQ710535.1 GI:21849434
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: b column: 08
High quality sequence stop: 599.
Location/Qualifiers
1. 986
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site: 1; XhoI; Site: 2;
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 284 a 231 c 243 g 225 t 3 others
ORIGIN
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Best Local Similarity 82.0%; Pred. No. 4.2e-28;
Matches 396; Conservative 0; Mismatches 81; Indels 6; Gaps 5;
QY 54 CTGCTAGATTGTTGTAATAAATTAATGATAGCTAGCGCGGTGCTCAGCCCTGT 113
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Db 205 CTCTGCTTGTCTTCTAGCAGAGTTATTAAAGGCCAGCAGCTGGCCACGCTGT 264
QY 114 AATCCAGCACTTTAAGGTCGAAGAGGTGGATCACTTGAAGTCAAGGAGTTTGAGAC 173
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Db 265 AATCCAGCACTTTGGAGGCCGAGGTGGTGGATCCTTGAAGTCAAGGAGTTTGAGAC 173
QY 174 CAGCTGGCCACAGCGTGAACCCATCTCTACTTAAATAAATAAATAATAGCTTGGGTG 232
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Db 324 CAGCTGGCCACAGCGTGGAAACCCGCTCTCTACTTAAATAAATAAATAATAGCTTGGGTG 232
QY 233 CGTGGCTCACACCTGTAAATCCAGCACTTTGGAGGCTGAGAGGCTGGATCACTGTAA 292
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Db 384 CGTGGCTCA-CCTTGTATCCAGCACTTTGGAGGCTGAGAGGCTGGATCACTGTAA 292
QY 293 GTAGAGGTTCAAGGCCAGCGCTGGCAACATGGTGAACACAGCTCTCTACTTAAATAAATA 352
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Db 441 GTAGAGGTTCAAGGCTGGTGGACAGCGCTGTAGTCCAGCTACTTGGAGGCTGGAGGG 412
QY 353 AAAATTAGCAGGTTGGTGGACAGCGCTGTAGTCCAGCTACTTGGAGGCTGGAGGG 412
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Db 501 AAAATTAGCAGGTTGGTGGACAGCGCTGTAGTCCAGCTACTTGGAGGCTGGAGGG 412
QY 413 GAAGATTCGTTGAACCCAGTAGGACAGAGTTGCAGTACGCGCAGATTAAGTCACTGCA 472
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Db 561 GGAGATTCGTTGAACCCAGTAGGACAGAGTTGCAGTACGCGCAGATTAAGTCACTGCA 472

QY 473 CTCAGCCTGGTGCAGAGCAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAA 532
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Db 620 CTCAGCCTGGTGCATAGAGGAGACTCTGTCTCAAAATAAATAAATAAATAAATAA 679
QY 533 TAA 535
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Db 680 AAA 682
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BM469250
LOCUS
DEFINITION BM469250 1060 bp mRNA linear EST 05-FEB-2002
AGENCOURT_644645 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5585187
5', mRNA sequence.
ACCESSION BM469250
VERSION BM469250.1 GI:18518292
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1060)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2351 row: b column: 04
High quality sequence stop: 659.
Location/Qualifiers
1. 1060
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 294 a 229 c 283 g 254 t
ORIGIN
Query Match 29.0%; Score 290.4; DB 13; Length 1060;
Best Local Similarity 84.1%; Pred. No. 6.3e-28;
Matches 375; Conservative 0; Mismatches 66; Indels 5; Gaps 4;
QY 72 AAAATTAAATGGAATAGGTAGGCGGTGGCTCAGCTGTATATCCAGCACTTAA 131
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Db 205 AAAATAGTCTCAGTAGGCTGGCGGTGGCTCAGCTGTATATCCAGCACTTAA 264
QY 132 GGTCAAGAGGGTGGATCACTTGAAGTCAAGGCTTTTGAAGACAGCTGCGCCACACGGT 191
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Db 265 GSCCGAGCAGCGGATCACCTGAGGTGAGGAG-TTCAAGACAGCTGCGCCACACGGT 323
QY 192 GAACCCCATCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAA 251
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Db 324 GAACCCCATCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAA 382
QY 252 TCCAGCACTTTGGAGGCTGAGAGGCTGGATCACTTGAAGTCAAGTCAAGGCGCAG 311
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Db 383 TCCAGCACTTTGGAGGCTGAGAGGCTGGATCACTTGAAGTCAAGTCAAGGCGCAG 440
QY 312 CTTGGCAACATGGTGAACACCGCTCTCTACTTAAATAAATAAATAAATAAATAA 371

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Db 441 CCTGACCAATGGTGAACCCCTGCTCTACTAAAAATACAAAAATAGCCGGGTGTGT 500
QY 372 GGCACAGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGGGAGGAATCGCTTGACCCA 431
Db 501 GGTGGGCGCTCTAATCCAGCTACTCGGAGGCTGAGGGGAGGAATTCCTTGAACGG 560
QY 432 GTAGGAGAGTTCAGTGGAGCCGATAGAGTCACTGACCTCCAGCCTGGGTGACAGA 491
Db 561 GGAGCGGAGGTTCAGTGAACAGGAT-CGGCCACTGACCTCCAGCCTGGGCGACAGA 619
QY 492 GCAGACTCCCTCTCAGAAAAATAAAA 517
Db 620 GCGAGACTCCGCTCAGAAAAATAAAA 645

RESULT 7
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LOCUS HS_5194_B2_H07_T7A_RPC1-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate-770 Col=14 Row=P, DNA sequence.
ACCESSION A0514325
VERSION A0514325.1 GI:4746616
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 543)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPC1-11. For BAC
library availability, please contact Pieter de Jong
(pierder@u.washington.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 770 row: P column: 14
Seq primer: T7
Class: BAC ends
High quality sequence stop: 543.
FEATURES
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/db_xref="taxon:9606"
/clone="Plate=770 Col=14 Row=P"
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/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRII. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 145 a 123 c 152 g 113 t 10 others
ORIGIN

Query Match 29.0%; Score 290; DB 17; Length 543;
Best Local Similarity 77.6%; Pred. No. 1.2e-27;
Matches 384; Conservative 0; Mismatches 107; Indels 4; Gaps 3;
QY 40 CGTAAATGAAGCTCCTAGATTGCTTAAATAATTAATGGATAGGCTAGGCGGG 99

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Db 22 CTTGNATGATGCANTTCGGGAATCTCTGATAGATTNTANAGGTGGAGCCAGGTGCGG 81
QY 100 TGGCTCAGCCTGTGTAATCCAGCAGCTTTAGAGAGTGAAGAGGTGGATCATTGAGTGC 159
Db 82 TGGCTCAGCAGTGTATTCCTGACCTCTGGGATGCTGAGGTGGGTGGGACACCTGAGGTT 141
QY 160 AGAGTTTGGAGCCAGCCTGGCCAAACACAGGTGAAACCCCACTCTCTACTAAAAATAAAA 219
Db 142 AGGAG--TTGAGAGACCAAGCTGGCCCAACATGGTGAACCTCTCTCTACTTAANAATACAAA 200
QY 220 ATTACTNGGCTGGGTGGCTCAGACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGG 279
Db 201 AAATTCGAGGATGATGGCTATGCTCTGTAATCCAGCGCTTTGGGAGCTGAGCCANG 260
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Db 261 AGGATCAC--GAGTCTCATGAGTTTGACACAGCCTGGCCCAATATGGTGAACACCGGCTC 318
QY 340 TACTAAAAATACAAAAATTAAGCCAGGTGGTGGCACACAGCCTCTAGTCCAGGCTACTTG 399
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Db 379 GGAGGCTGAGGCGGAGAGAGATATCTTGAACCTGCAAGGACAGAGTTCAGTGGAGCCGAGAT 438
QY 460 AAGAGTCACTGACCTCCAGCCTGGGTGACAGAGCAAGACTCCCTCTCTCAAAAAATAAATA 519
Db 439 -CGTGCCACTTGCCTCCAGCCTGGGACAGAGACAGACTCTGTCTCTCATTAACAAACAAC 497
QY 520 AATATAAATAAATA 534
Db 498 AAACCAAGAAAAATA 512

RESULT 8
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LOCUS CITBI-EI-2572B9, TF CITBI-EI Homo sapiens genomic clone 2572B9, DNA
DEFINITION sequence.
ACCESSION A0426757
VERSION A0426757.1 GI:4499437
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 542)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbest@igrr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
Location/Qualifiers
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/db_xref="taxon:9606"
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone="2572B9"
/clone_lib="CITBI-EI"
/sex="male"

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JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 695)
 AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Toki, Y., Watanabe, H. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail: chimpbes@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library PTB. This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: M13Rev

LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI

FEATURES
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 Matches 378; Conservative 0; Mismatches 114; Indels 3; Gaps 2;

QY 88 GCTAGGCGCGGCTCAGCGCTGTATCCAGCACCTTTAGAGGTCGAGAGGGTGA 147
 DB 610 GGCAGGCAGACGTCCCTCATGCTATTATCCACCACCTTTGGAGGCTGAGCAAGGA 551
 QY 148 TCACCTTGAGGTCAGGAGTTTTCAGACAGCCTGCGCCACACGCTGAACCCCATCTCTAC 207
 DB 550 TTGCTTGAGCCAGGAGTTAAGACAGCCCGGCTAAGCTAGTGAACCTTATCTCTAC 491
 QY 208 TAAATAAATAATAGCTNGGTCGGTGGCTCACACCTGTATCCAGCACCTTTGGA 267
 DB 490 - -AAAAACAAAATAGGCGCAGGCATGGTGGCTCACACCTGTATGCGACCTTTGCGAG 433
 QY 268 GGTGAGAGGGTGGATCACCTGAGTTCAGAGTTCAGGCGCCAGCTGGGCAACATGGTG 327
 DB 432 GGTGAGGAGGTTGAGTACCTGAGGTCGAGGTCGAGACCGCTGGCCACATGGTG 373
 QY 328 AAACCATCTCTACTATAAATAACAAAATAGCCAGTGTGGTGGCACAGCGCTGTAGT 387
 DB 372 AAACCTGTCTCTACTATAAATAACAAAATAGCCAGGCTGGTGGCGAGCGCCTGTAA 313
 QY 388 CCAGCTACTTGGAGGCTGAGGCGGGAAGATCGTTGAACCCAGTAGGAGGAGTTGCA 447
 DB 312 CCCAGCTACTCAGAGGCTGAGGCGGAGAGATTGCTTGAACCCAGGAGCGGAGATTGCA 253
 QY 448 GTGAGCGAGATAAGAGTCACTGCATCCAGCTGGGTGAGCAGCAGCAAGCTCCCTCA 507
 DB 252 GTGAGCGAGAT-AGCTCCACTGTGCTCCAGCTGAGCGAGAGTGACACTCCATCTCA 194
 QY 508 GAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 567
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 QY 568 CTGGCATTTGGCTA 582
 DB 133 TAGGTCAAGCATA 119

RESULT 11
 AG012294/c

LOCUS AG012294
 DEFINITION Homo sapiens genomic DNA, 21q region, clone: PQ245P17N48, genomic
 survey sequence.
 ACCESSION AG012294 AG005230
 VERSION AG012294.1 GI:3413563
 KEYWORDS GSS.
 SOURCE Homo sapiens DNA, clone: PQ245P17N48.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 691)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
 TITLE Homo sapiens genomic DNA, chromosome 21q
 JOURNAL Published only in Database (1998)
 REFERENCE 2 (bases 1 to 691)
 AUTHORS Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-1998) Masahira Hattori, Kitasato University,
 Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1,
 Sagamihara 228, Japan (E-mail: hattori@hgc.ims.u-tokyo.ac.jp,
 Tel: 0427-78-9732, Fax: 0427-78-9561)
 COMMENT On Feb 5, 1999 this sequence version replaced gi:2879965.
 AG005230; Submitted (13-Feb-1998).

FEATURES
 Location/Qualifiers

1..691
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 /db_xref="taxon:9606"
 /chromosome="21"
 /map="21q"

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 Best Local Similarity 77.6%; Pred. No. 2.6e-27;
 Matches 394; Conservative 0; Mismatches 109; Indels 5; Gaps 4;

QY 42 TAAATCAAAAGCTGCTAGATTGTTGTAATAAATAATTAATGAATAGGTAGGCGCGGTG 101
 DB 515 TGAATTAATGATTTAATAATCAGTTTAAAAACAAAACAAACAGACTGGCACAGTT 456
 QY 102 GTCAGCGCTTAATCCAGCACCTTTAGAGGTCGAGAGGTTGGATCACTTCTAGTCTCT 161
 DB 455 GTCAGCGCTGTAATCTCAGCACTTTGGAGCGCGAGTGGGTGATNCCTGAAGTCAG 396
 QY 162 CAGTTTGAAGACCGCTGGCCACACGCTGGAACCCCTCTCTACTAAAAATA-AAAAA 220
 DB 395 GAG-TTCAAGACACCGCTGGCCACACATGGTGAACCCCTCTCTACTAAAAATAA 337
 QY 221 TTAGCTNGGTCGCGTGGCTCACACCTGTATCCAGCACCTTTGGAGGCTGAGACGGGT 280
 DB 336 GTAGCCAGCGCAGGTGGCTCACACCTGTATCCAGCTGTGCTTTGGAGGCTGAGCGGT 277
 QY 281 GGATCACTTGAAGTCAGAGTTTCAAGCGCCAGCTGGGCAACATGTGTAACACCTCTCT 340
 DB 276 GGATCACTTGAAGTCAGAGTTGGAGACCGCTGGCCACACATGTGTAACACCTCTCT 217
 QY 341 ACTAAAAATACAAAATATAGCCAGGTGTTGGCACACGCTGTAGTCCAGCTTACTTGG 400
 DB 216 ACCAAAAATACAAAATAGCCAG--ACCCAGCTGCATGCGCTGTATCCAGCTACTCAG 159
 QY 401 GAGGCTGAGCGGGAAGATCGGCTGAACCCAGTAGGACAGGTTGCGAGCGCGAGATA 460
 DB 158 GAGGCTGAGCGGAGGAGATCGGCTGTATCCGGAGGTTGGAGGTTGCACTGAGCGGATC 99
 QY 461 AGAGTCACCTCCAGCTCGGTCAGAGCAAGCACTCCCTCTCAGAAAAATAAATAA 520
 DB 98 A-CGACACTGCCTCCAGCCTGGGTGACAGAGTGAAGCTGCTCAAAAAATAAATAA 40
 QY 521 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 548
 DB 39 AAACAAANACANGNCTGAGCTGAAT 12

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RESULT 12
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DEFINITION 602278903F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4366465 5',
ACCESSION  BG110480
VERSION     BG110480.1 GI:12603986
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 545)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10017 row: f column: 02
            High quality sequence stop: 545.
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                /lab_host="DH10B (phage-resistant)"
                /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
                Average insert size 1.533 kb. Library enriched for
                full-length clones and constructed by Life Technologies.
                Note: this is a NIH_MGC Library."
            BASE COUNT  169 a 122 c 135 g 119 t
            ORIGIN
            Query Match      28.6%; Score 285.8; DB 12; Length 545;
            Best Local Similarity 81.1%; Pred. No. 3.9e-27;
            Matches 368; Conservative 0; Mismatches 83; Indels 3; Gaps 3;

QY 79 AATGCATAGGTAGCGCGGTGGCTCAGCCCTGTAATCCAGCAGCTTTAGAGAGTCGAA 138
Db 93 AATGTCCTGAGTCAGCGCTGGTGGTGCATCTAATCCAGCAGCTTTGGAGCGCGAG 152
QY 139 GAGGTGGATCACTTAGCTCAGGAGTTTGTAGACACCGCTGGCCACACCGTGAACCC 198
Db 153 GCATGTGGATCACTTAGCTCAGG -GGTTGAACACCGCTGGCCACACATGTTGAACCC 211
QY 199 CATCTCTACTAAATAAATAAATAGCTNGGTGGGTGGCTCACACCTGTAAATCCAGC 258
Db 212 CATCTCTACTAAATAAATAAATAGCTNGGTGGGTGGCTCACACCTGTAAATCCAGC 271
QY 259 ACTTTGGAGGCTGAGACGGGTGGATCACTTGAAGTCAGGAGTTTCAAGCCAGCGCTGGC 318
Db 272 ACTTTGAGAGACCGAGGAGGAGCAGATCACTGAGTCAGGAGTTTGAACACCGCTGGCC 331
QY 319 AACATGTGTAACACCGCTCTCTACTAAATAAATAAATAGCCAGGTGTGGTGACAC 378
Db 332 AACATGTGTAACACCGCTCTCTACTAAATAAATAAATAGCCAGGTGTGGTGACAC 391
QY 379 GCTGTAGTCCACGCTACTTTGGAGGCTGAGCGGAAGATCGCTGAACCCAGTAGGCA 438
Db 392 ACCTGTAAATCCAGCTACTCAGGAGGCTGAGCGAGAGAAATCACTTTGAACCCAGGAG 451
QY 439 GAGGTTCAGTCAGCGGAGATAGAGTCACTCCAGCTGGGTGCAC -AGAGCAAGA 497

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Db 452 GAGTTGAGTGACCGAGAT-TGAGCCACTACACTCCAGCTGGGCAACAAGAGCGAGA 510
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Db 511 CTCCTCTCAAAAAAATAAATAAATAAATAAATAA 544

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DEFINITION tu62q12.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2255686 3',
ACCESSION  AI679294
VERSION     AI679294.1 GI:4889476
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 470)
AUTHORS    Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT     Tumor Gene Index
            Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing Arrayed by: Greg Lennon, Ph.D.
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
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                /lab_host="DH10B"
                /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
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            Query Match      28.5%; Score 285.4; DB 9; Length 470;
            Best Local Similarity 80.1%; Pred. No. 4.8e-27;
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QY 60 GATTGTTCTTAAATAAATAAATTAATGGAATAGGTAGCGCGGTGGCTCAGCCTGTAATCCC 119
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Db 386 AGCAGCTTTGAGAGCGCGAGGCGAGCATCACTTGTAGCTCAGGAG-TTCCAGACCGCCT 328
QY 180 GGGCAACACCGTGAACACCCCATCTCTACTAAATAAATAAATAAATAGCTNGGTGGTGGC 239
Db 327 GAACAATATGTTAAACCCCATCTCTACTAAATAAATAAATAAATAGCCAGCGCTGGTGGC 268
QY 240 TCACACCTGTAAATCCAGCAGCTTTGGAGGCTGAGACGGGTGGATCACCTGAAGTCAGGA 299
Db 267 GGGCACCTGTAATCCAGCAGCTTTGGAGGCGCGAGTGGGCGACATCACTGAGGTGGGGA 208

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QY 360 GCCAGGTGTGGTGGCAGACAGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGCGGAGAAAT 419
Db 147 GCCAGGTGTGGTGGCGGGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGCGGAGAAAT 88
QY 420 CCCTTGAACCCAGCTAGGCGAGAGGTTCAGTGGAGCGGAGATAGAGTCACTGCATCTCCAGC 479
Db 87 CCCTTGAACCCAGGAGATGGAGTTGCAGTGGAGCGGAGATCA-CGCCACTGCATCTCCGC 29
QY 480 CTGGGTGACAGACAGAGACTCCCTCTCA 507
Db 28 CTGGACGACAGAGGAGACTGTATCTCA 1

RESULT 14
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DEFINITION
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ACCESSION
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VERSION
    GSS.
KEYWORDS
    human.
ORGANISM
    Homo sapiens
REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
    Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
    J.C.
TITLE
    Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
    Map Building
JOURNAL
    Unpublished (1997)
COMMENT
    Other_GSSs: RPCI-11-243K18.TJ
    Contact: Shaying Zhao, William Nierman, Mark Adams
    Department of Eukaryotic Genomics
    The Institute for Genomic Research
    9712 Medical Center Dr., Rockville, MD 20850
    Tel: 301 838 0200
    Fax: 301 838 0208
    Email: hbeetigr.org
    Clones are derived from the human BAC library RPCI-11. For BAC
    library availability, please contact Pieter de Jong
    (pieter@dejong.med.buhalo.edu). Clones may be purchased from
    BACPAC Resources (http://bacpac.med.buhalo.edu/ordering) or from
    Research Genet cs (info@resgen.com). BAC end search page:
    http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
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    Class: BAC ends.
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        /sex="Male"
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ORIGIN

Query Match
    Best Local Similarity 28.5%; Score 284.8; DB 17; Length 568;
    Matches 359; Conservative 0; Mismatches 88; Indels 2; Gaps 2;

QY 78 AAATGGGAATAGCTAGCGCGGTGGCTGACCGCTGTATCCAGCACTTTAGAAAGTCA 137
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QY 138 AGAGGTGGATCACTTGGAGTTCAGGAGTTTTCAGACAGCGCTGGCCACACAGGTGAACC 197
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QY 198 CCATCTCTACTATAAATAAATAAATTTAGCTNGGTTGGTGGTGCCTACACCTGTATATCCAG 257
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QY 258 CACTTTGGAGGCTGAGACGGGTGGATCACCTGAAGTTCAGGAGTTCAGGCGGAGCGCTGGG 317
Db 361 CACTTTGGAGGCGCAAGCGGAGGACATCACTGAGGTTCAGGAGTTCGAAACCCAGCGCTGC 302
QY 318 CACATGTGTGAACACAGCTCTCTACTATAAATAAATAAATTTAGCAGGTGTGGTGACACA 377
Db 301 CACGTGTGTGAATCCCTCTCTACTATAAATAAATAAATTTAGCTGGTGTGGTGGCGG 242
QY 378 CGCTGTAGTCCAGCTACTTGGAGGCTGAGGCGGAGAAATTCGCTTGAACCCAGTGGC 437
Db 241 TGCTGTATCCAGCTACTTGGAGGCTGAGGAGGAGTTCGCTGAAACCCAGGAGGC 182
QY 438 AGAGTTCAGTGGAGCGGAGATAGTCACTGCCTCCAGCGCTGGTGGAGACAGCAAGA 497
Db 181 GGAGGTGCAGTGGAGCGCAAGA-CGCGATCACTGCCTCCAGCTGGGTGGTGGAGTGA 123
QY 498 CTCCTCTCTCAAAAAATAAATAAATAAATAA 526
Db 122 CTCCTCTCAAAAAATAAATAAATAAATAA 94

RESULT 15
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ACCESSION
    BO437946
VERSION
    BO437946.1 GI:21177022
KEYWORDS
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SOURCE
    human.
ORGANISM
    Homo sapiens
REFERENCE
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
    NIH-MGC http://mgi.nci.nih.gov/.
TITLE
    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
    Unpublished (1999)
COMMENT
    Contact: Robert Strausberg, Ph.D.
    Email: cgabbs-r@mail.nih.gov
    Tissue Procurement: ATCC/DCTD/DTF
    cDNA Library Preparation: Life Technologies, Inc.
    DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
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    High quality sequence stop: 641.
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BASE COUNT
    246 a 200 c 258 g 190 t 1 others
ORIGIN

Query Match
    28.4%; Score 284; DB 14; Length 895;

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 06:08:16 ; Search time 292 Seconds
(Without alignments)
7712.323 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGTGACCTTATCTCTCT.....CAGATGATGACCGCGTGC 1000

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99.9	99.9	1000	AA227732	Human DNA marker C
2	320.2	32.0	7017	AA227732	Human musculoskele
3	320.2	32.0	20522	AA227732	Human musculoskele
4	320.2	32.0	92638	AA227732	Human osteoblast d
5	307	30.7	17424	AA227732	Ovary cancer relat
6	306.8	30.7	2007	AA227732	Human immune/haema
7	306.8	30.7	2007	AA227732	Human immune/haema
8	306.8	30.7	22680	AA227732	Human immune/haema
9	306.8	30.7	22680	AA227732	Human immune/haema

C 10	306.8	30.7	22680	22	AAK73344	Human immune/haema
C 11	306.8	30.7	22680	22	AAK73625	Human immune/haema
C 12	306.8	30.7	22680	22	AAK73847	Human immune/haema
C 13	306.8	30.7	22680	22	AAK73934	Human immune/haema
C 14	306.8	30.7	22680	22	AAK78350	Human immune/haema
C 15	306.4	30.6	4243	22	ABAL6762	Human nervous syst
C 16	305.6	30.6	15682	22	AAK89506	Human digestive sy
C 17	305.6	30.6	81800	24	ABK84756	Human cDNA differe
C 18	304.4	30.4	13919	24	ABK86218	DNA encoding AIP-1
C 19	304.4	30.4	13919	24	ABK85220	AIP-1/FLASH promot
C 20	304.4	30.4	13919	24	ABK88221	AIP-1/FLASH promot
C 21	304.4	30.4	21404	24	ABK86229	Ovary cancer relat
C 22	301.4	30.1	17424	24	ABL68122	Kidney cancer relat
C 23	301.2	30.1	49634	24	ABL68647	Human transporter
C 24	300.6	30.1	32816	24	ABK49701	Human immune/haema
C 25	299.6	30.0	52616	22	AAK70459	Human immune/haema
C 26	299.6	30.0	52616	22	AAK78930	Human immune/haema
C 27	298	29.8	12221	22	AAK71585	DNA encoding novel
C 28	297.2	29.7	24533	22	AAK71589	Human immune/haema
C 29	296.6	29.7	37314	22	AAK71358	DNA encoding Aldeh
C 30	296.6	29.7	46765	24	AAK59306	Human osteoblast d
C 31	296.6	29.7	172570	24	ABO88207	Human reproductive
C 32	296.4	29.6	5281	22	AAK05101	Human testicular a
C 33	296.4	29.6	5281	23	ABL97994	Human reproductive
C 34	296.4	29.6	5284	22	AAK05100	Human testicular a
C 35	296.4	29.6	5284	23	ABL97993	Human cDNA differe
C 36	296	29.6	12263	24	ABK84514	Human proto-oncoge
C 37	296	29.6	15297	24	ABK84501	Human secreted pro
C 38	295	29.5	1166	22	AAH19172	Human immune/haema
C 39	295	29.5	21596	22	AAK71582	Human immune/haema
C 40	294.8	29.5	30393	22	AAK67239	Human immune/haema
C 41	294.4	29.4	19490	22	AAK70177	Human nervous syst
C 42	294.2	29.4	32249	22	ABAL7155	Gene #3429 used to
C 43	293.8	29.4	99014	24	ABN96931	Human immune/haema
C 44	293.6	29.4	48045	22	AAK84730	Human immune/haema
C 45	293.6	29.4	48045	22	AAK85984	Human immune/haema

ALIGNMENTS

RESULT 1
AAZ27732
ID AAZ27732 standard; DNA; 1000 BP.

XX AAZ27732;

XX 23-DEC-1999 (first entry)

XX Human DNA marker clone S132.

XX Tandem repeat sequence: DNA isolation; intermediate tandem repeat;
XX IIR sequence: pentanucleotide tandem repeat; stutter artifact;
XX DNA typing; DNA profiling; linkage analysis; criminal justice;
XX paternity testing; animal lineage analysis; microsatellite loci;
XX polymorphism detection; ds.

XX Homo sapiens.

XX WO9940194-A1.

XX 12-AUG-1999.

XX 04-FEB-1999; 99WO-0502345.

XX 04-FEB-1998; 98US-0018584.

XX (PROM-) PROMEGA CORP.

XX Schumm JW, Bacher JW;

XX WPI; 1999-590696/50.

PT Isolating DNA containing intermediate tandem repeat sequences, useful
 XX in DNA profiling -

PS Claim 22; Page 78; 11pp; English.

CC This sequence represents a human DNA marker clone used in the method of
 CC the invention. The method is for isolating a fragment of DNA containing
 CC an intermediate tandem repeat (ITR) sequence using hybridization
 CC selection, and comprises: (a) providing several DNA fragments, at least
 CC one of which contains an ITR sequence, a region of the DNA fragment which
 CC contains at least one repeat unit consisting of a sequence of five, six
 CC or seven bases repeated in tandem at least two times; (b) providing a
 CC stationary support having at least one oligonucleotide associated with
 CC it, where the oligonucleotide includes a sequence of nucleotides which is
 CC complementary to a portion of the ITR sequence; and (c) combining the DNA
 CC fragments with the support under conditions where the DNA fragments
 CC including the DNA fragment containing the ITR sequence hybridize to the
 CC pentanucleotide tandem repeat sequences as well as to detect target ITR
 CC DNA sequences having a low incidence of stutter artifacts (no more than
 CC 2.4%). The method is useful in DNA profiling for linkage analysis,
 CC criminal justice, paternity testing and other forensic and medical uses.
 CC DNA typing is also useful for confirming the lineage of horses, dogs and
 CC other prize animals. The invention overcomes problems related to the use
 CC of microsatellite loci in DNA profiling. The method can detect
 CC polymorphisms with a low incidence of stutter artifacts, which has
 CC previously been a problem in interpreting allelic content of loci. The
 CC development of markers based on larger repeat units, enables easier
 CC separation of the fragments on electrophoretic gels. This allows the
 CC simultaneous analysis of more loci.

SQ Sequence 1000 BP; 302 A; 240 C; 231 G; 226 T; 1 other;

Query Match 99.9%; Score 999; DB 20; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 4.7e-196;
 Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db |||||||
 QY 1 GGTGTGACCTTATCCTCTCTGAACCTCAGTTTCTCATCCGTAATAAAGAACTGCTAG 60
 Db |||||||
 QY 61 ATTGTTGTAATAAATAAATGAATAGCTAGGCGGCTGCCTCAGCGCTGTAATCCCA 120
 Db |||||||
 QY 61 ATTGTTGTAATAAATAAATGAATAGCTAGGCGGCTGCCTCAGCGCTGTAATCCCA 120
 QY 121 GCATTTAGAGGTGAAGAGGTGGATCACTTGAGTGCAGGATTTGAGACACAGCTG 180
 Db |||||||
 QY 121 GCATTTAGAGGTGAAGAGGTGGATCACTTGAGTGCAGGATTTGAGACACAGCTG 180
 QY 181 GCCACACGCTGAACCCGCTCTCTACTAAAAATAAAAAATTAGCTNGGCTGCGTGGCT 240
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 QY 181 GCCACACGCTGAACCCGCTCTCTACTAAAAATAAAAAATTAGCTNGGCTGCGTGGCT 240
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 QY 301 TTCAGGCCAGCCTGGGCAACATGGTGAACCCAGCTCTCTACTAAAAATAAAAAATTAG 360
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 QY 361 CCAGGTGTGGTGGACAGGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGGGAAGATC 420
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 Db |||||||
 QY 421 GCTTGAACCCAGTAGGAGAGGTTCAGTGAAGCGGAGATAAGATCACTGCTCCAGCC 480
 QY 481 TGGGTGACAGCAGCAAGACTCCCTCTCAGAAAAATAAAAAATAAATAAATAAATAA 540
 Db |||||||
 QY 481 TGGGTGACAGCAGCAAGACTCCCTCTCAGAAAAATAAAAAATAAATAAATAAATAA 540

QY 541 AATAAATAAATAAATAAATTTCTAAAGGGCTGGCATTGGCTAGCATTATATATGCCAATA 600
 Db |||||||
 QY 541 AATAAATAAATAAATAAATTTCTAAAGGGCTGGCATTGGCTAGCATTATATATGCCAATA 600
 QY 601 AGTAATAGCTATCAATATATCCCAACCCCTACCACTGGTGTGAAATTTAGTTTCTTTTGTG 660
 Db |||||||
 QY 601 AGTAATAGCTATCAATATATCCCAACCCCTACCACTGGTGTGAAATTTAGTTTCTTTTGTG 660
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 Db |||||||
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 QY 721 GGCAATAGTTGGGTCTCAGTGAACATPGTGTAGTGAATGAGCAAAATGCAAGGATCTCC 780
 Db |||||||
 QY 721 GGCAATAGTTGGGTCTCAGTGAACATPGTGTAGTGAATGAGCAAAATGCAAGGATCTCC 780
 QY 781 AGGCCATCTGGAGCCCTCCCAAGGGGTGAGTTCGGTCCCACTCCGACCCCACTCTGCTCAAT 840
 Db |||||||
 QY 781 AGGCCATCTGGAGCCCTCCCAAGGGGTGAGTTCGGTCCCACTCCGACCCCACTCTGCTCAAT 840
 QY 841 GGCCACTGAAAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTGCTGACTCAC 900
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 QY 841 GGCCACTGAAAGGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTGCTGACTCAC 900
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 QY 901 TGCTGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
 QY 961 CAGGACTGCAAGGAGCCGAGCAAGATGATGACCGGCTGC 1000
 Db |||||||
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RESULT 2

AAL37408/c

ID AAL37408 standard; DNA; 7017 BP.

AC AAL37408;

DT 08-JAN-2002 (first entry)

DE Human musculoskeletal system related polynucleotide SEQ ID NO 3773.
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
 KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system; ds.

OS Homo sapiens.

XX WO2000155367-Al.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01338.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0214886.

XX 30-JUN-2000; 2000US-0215135.

XX 07-JUL-2000; 2000US-0216647.

XX 11-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
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PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
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PR 08-SEP-2000; 2000US-0231413.
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PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
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PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
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PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
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PR 01-NOV-2000; 2000US-0244617.

PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
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PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0250390.
PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451937/48.

Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -

Example 2; SEQ ID NO 3773; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (AB03087-AB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,

KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
 KW osteoporosis; osteopathic; ss.
 XX Homo sapiens.
 XX WC200250301-A2.
 XX PD 27-JUN-2002.
 XX PF 18-DEC-2001; 2001WO-US48276.
 XX PR 18-DEC-2000; 2000US-255882P.
 XX PR 24-APR-2001; 2001US-285691P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PA (PROC) PROCTER & GAMBLE CO.
 XX XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
 PI Mertz L;
 XX DR WPI; 2002-557663/59.
 XX XX
 XX PT Use of genes and their expression profiles associated with osteoblast
 PT differentiation for screening modulators bone formation, for diagnosing
 PT or treating e.g. osteoporosis, or as markers for the differentiation
 PT process -
 XX PS Claim 1; SEQ ID NO 3; 78pp + Sequence Listing; English.
 XX CC The invention relates to genes and their expression profiles are used
 CC for;
 CC (a) screening modulators of precursor stem cell differentiation into
 CC osteoblasts, or bone tissue deposition;
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
 CC osteoblast formation or osteoporosis; or
 CC (c) treating or monitoring treatment of the conditions cited in (b), or
 CC monitoring the progression of bone tissue deposition.
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
 CC drug-induced abnormalities in bone formation or bone loss, conditions
 CC that involve altered bone metabolism (e.g. idiopathic juvenile
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,
 CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
 CC osteoblast differentiation associated cDNA marker of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 92638 BP; 21460 A; 24572 C; 25235 G; 21371 T; 0 other;
 Query Match 32.0%; Score 320.2; DB 24; Length 92638;
 Best Local Similarity 84.6%; Pred. No. 1.5e-56;
 Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;
 QY 86 TAGCTAGGCGGTGGCTGAGCTGCTGATCCAGCAGCTTTGAGAGTTCGAGAGGGTG 145
 Db 69545 TGGGCGACACGGGTGGCTGACCTGTTATCCAGCAGCTTTGAGAGCGGCGGTG 69604
 QY 146 GATCACTTGAGGTGAGGTTTGTGAGCAGCCTGCGCAACACGGTGAACCCGATCTCT 205
 Db 69605 GATCACTTGAGAGAGAG-TTCGAGACACGCTGGCCAAACATGGTGAACCTGCTCT 69663
 QY 206 ACTAAATATAAATAGCTNGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
 Db 69664 ACTAAATATAAATAGCTNGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 69723
 QY 266 GAGGCTGAGAGGGTGCATCAGCTTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 325
 Db 69724 GAGGCGAAGGGGGGAGATCA--TGAGGTCAAGATGAGACCATCTGGTACATGG 69781
 QY 326 TGAACACGCTCTCTACTATAAATAACAAAAATAGCAGGTGCTGGGACACGCTGTA 385
 Db 69782 TGAACACGCTCTCTACTATAAATAACAAAAATAGCAGGTGCTGGGACACGCTGTA 69841

QY 386 GTCCAGCTACTTGGAGGCTGAGCGGAGAGATCGCTTGAACCCAGTAGCAGAGTTG 445
 Db 69842 GTCCAGCTACTTGGAGGCTGAGCGGAGAGATAGCTGAACCCAGGAGGAGTTG 69901
 QY 446 CAGTGAGCGGAGATAGAGTCACTGCTCCAGCTGGGTGACAGAGCAAGACTTCCCTCT 505
 Db 69902 CAGTGAGCGGAGATCA-CGACACTGCTCCAGCTGGGCAACAGAGGAGATCCGCTCT 69960
 QY 506 CAGAAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
 Db 69961 CA-AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 70019
 RESULT 5
 ABL68122/c
 ID ABL68122 standard; DNA; 174424 BP.
 XX
 XX ABL68122;
 XX
 XX 15-MAY-2002 (first entry)
 XX
 XX Ovary cancer related gene sequence SEQ ID NO:6459.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
 KW gene; ds.
 XX
 XX Homo sapiens.
 XX
 XX WO200194629-A2.
 XX
 XX 13-DEC-2001.
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 XX 30-MAY-2001; 2001WO-US10838.
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 XX 05-JUN-2000; 2000US-209473P.
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 XX 25-SEP-2000; 2000US-234924P.
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 XX 26-SEP-2000; 2000US-235638P.
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 XX 28-SEP-2000; 2000US-236032P.
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 XX 28-SEP-2000; 2000US-236033P.
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 XX 28-SEP-2000; 2000US-236034P.
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 XX 28-SEP-2000; 2000US-236109P.
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 XX 29-SEP-2000; 2000US-236111P.
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 XX 29-SEP-2000; 2000US-236842P.
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 XX 29-SEP-2000; 2000US-236891P.
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 XX 02-OCT-2000; 2000US-237172P.
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 XX 02-OCT-2000; 2000US-237173P.
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 XX 02-OCT-2000; 2000US-237278P.
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 XX 02-OCT-2000; 2000US-237294P.
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 XX 02-OCT-2000; 2000US-237295P.
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 XX 03-OCT-2000; 2000US-237316P.
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 XX 03-OCT-2000; 2000US-237425P.

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PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX (AVAL-) AVALON PHARM.
XX
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX Claim 1; SEQ ID 6459; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity. Determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
XX Sequence 174424 BP; 39582 A; 48304 C; 48535 G; 38003 T; 0 other;
Query Match 30.7%; Score 307; DB 24; Length 174424;
Best Local Similarity 83.1%; Pred. No. 8.2e-54;
Matches 409; Conservative 0; Mismatches 76; Indels 7; Gaps 5;
QY 76 TTAATGGAATAGCTAGCGGGTGGCTCAGCGTGTAAATCCAGCACTTTAGAGGTC 135
Db 132168 TAAATAAAAGAGCTAGCGGCGAGTGGCTCACACCTATAATCTTAGCACTTTGGAGGCC 132109
QY 136 GAAGAGGTGGATCACTTGAAGTCAGGAGTTTGGAGACCGGCTGGCGCAACAGGTGAAA 195
Db 132108 GAGGAGGTGGATCACTTGAAGTCAGGAGTTTGGAGACCGGCTGGCGCAACAGGTGAAA 132050
QY 196 CCCATCTCTACTAAATAT-AAAAATAGCTNGGCGGTGGCTCACACCTGTAAT 252
Db 132049 CCCGCTCTTACAAAATAACAAAAATAGGCGGCGAGGTGGCTCACACCTGTAAT 131990
QY 253 CCCAGCACTTTGGAGGCTGAGACGGTGGATCACTGAAGTCAGGAGTTCAAGCGCAGC 312
Db 131989 CCCAGCACTTTGGAGGCGAGCGGGTGGATCACTTGAAGTCAGGAGTTCCAGCACT 131930
QY 313 CTGGGCAACATGGTGAACACCACTCTCTACTATAAA-ATACAAAAATAGGCGGTGGT 371
Db 131929 CTGGGCAACATGGTGAACACCTCTCTACTATAAAATACAAAAATAGGCGGTGGT 131870
QY 372 GGCACAGCGCTGATCCAGCTACTTTGGAGGCTGAGCGGGAAGATCGCTTCAACCCA 431
Db 131869 GGCACAGCGCTGATCCAGCTACTTTGGAGGCTGAGCGGGAAGATCGCTTGAACCCA 131810
QY 432 GTAGGAGAGTTGCACTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGA 491
Db 131809 GGAGGAGAGTTGCACTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTGACAGA 131751
QY 492 GCAAGACTCCCTCTCAG-AAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 550
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Db 131750 GTGAGACTTCATCTCAGAAAAACAAACAAACAAACAAACAAACAAACAAACAA 131691
QY 551 AATAAAATCTTA 562
Db 131690 AACAAAAAATTA 131679
RESULT 6
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XX AAK73932 standard; DNA; 2007 BP.
XX AC AAK73932;
XX DT 07-NOV-2001 (first entry)
XX DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:28744.
XX KW Human; immune; haematopoietic; Immune/haematopoietic antigen; cancer;
XX KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX PN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01354.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
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XX PR 30-JUN-2000; 2000US-0215135.
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XX PR 07-JUL-2000; 2000US-0216880.
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XX PR 01-SEP-2000; 2000US-0229344.
XX PR 01-SEP-2000; 2000US-0229345.
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XX PR 06-SEP-2000; 2000US-0230437.
XX PR 06-SEP-2000; 2000US-0230438.
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PR	08-NOV-2000;	2000US-0246475.
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PR	08-NOV-2000;	2000US-0246526.
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PR	08-NOV-2000;	2000US-0246528.
PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249214.
PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
PR	17-NOV-2000;	2000US-0249217.
PR	17-NOV-2000;	2000US-0249218.
PR	17-NOV-2000;	2000US-0249219.

PR	17-NOV-2000;	2000US-0249245.
PR	17-NOV-2000;	2000US-0249264.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	17-NOV-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251868.
PR	08-DEC-2000;	2000US-0251869.
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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPT; 2001-483426/52.	
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
XX		
PS	Disclosure; SEQ ID NO 28744; 3071pp + Sequence Listing; English.	
XX		
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
CC	amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients' own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting	
CC	the nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat immune/hematopoietic-related diseases, especially	
CC	cancers and cancer metastases of hematopoietic-derived cells. AAK64703	
CC	to AAK87694 represent human immune/hematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAK82169	
CC	represent sequences used in the exemplification of the present invention.	
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ID AAK73933 standard; DNA; 2007 BP.
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XX XX
DT 07-NOV-2001 (first entry)
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28745.
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
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PN WO200157182-A2.
XX XX
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XX XX
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 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 XX
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 21120; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;

Query Match 30.7%; Score 306.8; DB 22; Length 22680;
 Best Local Similarity 84.3%; Pred. No. 7.3e-54;
 Matches 380; Conservative 0; Mismatches 68; Indels 3; Gaps 3;
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RESULT 9
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DT 06-NOV-2001 (first entry)
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28146.
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
PN WC200157182-A2.
PD 09-AUG-2001.
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XX 17-JAN-2001; 2001WO-US01354.
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PA (HUMA-) HUMAN GENOME SCI INC.
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PI Rosen CA, Barash SC, Ruben SM;
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XX WPI; 2001-483426/52.
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PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis.
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PS Disclosure; SEQ ID NO 28146; 3071pp + Sequence Listing; English.
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CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.

XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;
Query Match 30.7%; Score 306.8; DB 22; Length 22680;
Best Local Similarity 84.3%; Pred. No. 7.3e-54;
Matches 380; Conservative 0; Mismatches 68; Indels 3; Gaps 3;
QY 86 TAGCTAGGCGGCTGCTACGCTGTATATCCAGCACCTTTAGAGGTGCAAGAGGGTG 145
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DB 9074 TAGCTGGGCGGGTGGCTACGCTGTATATCTAGCACCTTTGGAGAGTGAGGAGGCA 9015
QY 146 GATCACTTGAGGTGAGAGTTTGGACAGCGCTGGCCAAACGCGTGAACCCCATCTCT 205
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 9014 GATCACTTGAGGTGAGAGT-TGAGACCGAGCTGGCCAAACGCGTGAACCCCATCTCT 8956
QY 206 ACTAAATATAAAATTAGCTNGGCGGTGGCTCACACCTGTATATCCAGCACCTTTGG 265
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 8955 ACTAAATATAAAATTAGCCAGGTGGCGTGCATGCTATATATCCAGCACCTTTGG 8896
QY 266 GAGGCTGAGCGGCTGATCACCCTGAAGTCAGAGGTTTCAAGCCAGCGCTGGCAACATGG 325
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DB 8895 GAGGCTGAGGTGGGT-GATCACTTGAGGTGAGAGTTAGGCCAGCTGGCCAAACATGA 8837
QY 326 TGAACACCGCTCTCTACTATAAATACAAAATTAGCCAGGTGTGGTGGCAGCGCTGTA 385
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DB 8836 TGAACCGCGCTCTCTACTATAAATATAAATTAGCGGGCGTGTGGCAGCGCTGTA 8777
QY 386 GTCCAGCTACTTGGGAGGCTGAGCGGAAGATTCCTTGAACCCAGTATAGGAGGTTG 445
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DB 8776 ATCCGCGCTACTCAGGAGGCTGAGCGAGGAGATCGCTTGAAGCTGGGAGGCGAGTTG 8717
QY 446 CAGTGAGCGGAGATAAGTCACTCACTCCAGCTGGGTGGTGACAGACAGATCCCTCT 505
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DB 8716 CGGTGAGCGGAGATCA-TGCCACTGCACTCCAGCTCGGCGACACACAACTATCT 8658
QY 506 CAGAAATATAAATAAATAAATAAATAAATAA 536
DB 8657 CAAATAAATAAATAAATAAATAAATAAAGA 8627
RESULT 10
AAK73344/c
ID AAK73344 standard; DNA; 22680 BP.
XX
AC AAK73344;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28156.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
XX
XX W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.
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 PR 14-AUG-2000; 2000US-0225757.
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 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
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 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
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PR 20-OCT-2000; 2000US-0241809.
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 PR 08-NOV-2000; 2000US-0246532.
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 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -

XX Disclosure; SEQ ID NO 28156; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)

PD	09-AUG-2001.	
XX		
PF	17-JAN-2001; 2001WO-US01354.	
XX		
PR	31-JAN-2000; 2000US-0179065.	
PR	04-FEB-2000; 2000US-0180628.	
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PR	02-MAR-2000; 2000US-0186350.	
PR	16-MAR-2000; 2000US-0189874.	
PR	17-MAR-2000; 2000US-0190076.	
PR	18-APR-2000; 2000US-0198123.	
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PR	28-JUN-2000; 2000US-0214886.	
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PR	08-NOV	

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PR 27-SEP-2000; 2000US-0235836.
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PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
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PR 20-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241787.
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PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis
XX
PS Disclosure; SEQ ID NO 28746; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 22680 BP; 4444 A; 6635 C; 7046 G; 4555 T; 0 other;
Query Match 30.7%; Score 306.8; DB 22; Length 22680;
Best Local Similarity 84.3%; Pred. No. 7.3e-54;
Matches 380; Conservative 0; Mismatches 68; Indels 3; Gaps 3;
QY 86 TAGGCTAGGCGGGTGGCTCAGCGCTGTATCCAGACACTTAGAAGGTGCAAGAGGTG 145
Db 9074 TAGGCTGGGCGGGTGGCTCAGCGCTGTATCCAGACACTTAGAAGGTGCAAGAGGTG 145
QY 146 GATCAGTTGAGTTCAGGAGTTTTCAGACAGCGCTGGCCACACGGTGAACCCATCTCT 205
Db 9014 GATCAGTTGAGTTCAGGAGTTTTCAGACAGCGCTGGCCACACGGTGAACCCATCTCT 205
QY 206 ACTAAAAATAAAAAATTAGCTNGGCTGCGGTGCTCACACCTGTATCCAGCAGCTTGG 265
Db 8955 ACTAAAAATAAAAAATTAGGCGGTGGCTGCGGTGCTCATGCTATATCCAGCAGCTTGG 265
QY 266 GAGGCTGAGCGGGTGGATCACCTGAAGTCAGGAGTTCAAGGCGGAGCTGGGCAACATGG 325
Db 8895 GAGGCTGAGTGGGT -GATCATTTGAGTTCAGGAGTTAGAGGCCACTTGGCCACATGA 8837
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Db 8836 TGAACCCAGCTCTCTACTTAAATAACAAAATTAGCAGGTGTGTGGCACACGCCCTGTA 385
QY 386 GTCCCGACTACTTGGGCGGTGAGCGGGAAGATCGCTTGAACCCAGTAGGAGGTTG 445
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Db 8716 CGGTGAGCGGAGATCA -TGCCACTGCCTCCAGCTCGGCGGACACAGCAAACTCTATCT 8658
QY 506 CAGAAATATAAATAAATAAATAAATAA 536
Db 8657 CAAAAAAGAAAAAAGAAAAAAGAGAGAAGA 8627

RESULT 14

AAK78350/c
 ID AAK78350 standard; DNA; 24680 BP.
 XX AC AAK78350;
 XX DT 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33162.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.
 XX PN WO200157182-A2.
 XX PD 09-AUG-2001.
 XX PF 17-JAN-2001; 2001WO-US01354.
 XX PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
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 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -
XX
XX Disclosure; SEQ ID NO 33162; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent, the
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
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XX Matches 380; Conservative 0; Mismatches 68; Indels 3; Gaps 3;
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XX AC ABAL6762;
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XX DT 23-JAN-2002 (first entry)
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XX DE Human nervous system related polynucleotide SEQ ID NO 9093.
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XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischlicking; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiatherogenic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX
XX PN WO200159063-A2.
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XX PD 16-AUG-2001.
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XX PF 17-JAN-2001; 2001WO-US01334.
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XX PR 31-JAN-2000; 2000US-0179065.
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XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-541565/60.
DR
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
XX Disclosure; SEQ ID NO 9093; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 79.9%; Pred. No. 7.5e-54;
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 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

HS496C20 69964 bp DNA linear PRI 12-DEC-1999
 Human DNA sequence from clone RP3-496C20 on chromosome 22 Contains
 STSs, GSSs and two putative CpG islands, complete sequence.
 Z83847
 HTG: CpG island.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 69964)
 Clark G.
 Direct Submission
 Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Sep 8, 1998 this sequence version replaced gi:3413284.
 This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated human repeat sequence elements (e.g. Alu). Where the
 sequence is ambiguous, there is an annotation using the 'unsure'
 feature key.

This sequence was generated from part of bacterial clone contigs of
 human chromosome 22, constructed by the Sanger Centre Chromosome 22
 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr22
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/projects/C.elegans/wormpep
 from the library RPCI-3 constructed at the Roswell Park Cancer
 Institute by the group of Pieter de Jong. For further details see
 http://bacpac.med.buffalo.edu/
 VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-496C20 The true
 left end of clone RP3-340K22 is at 21972 in this sequence. The true
 right end of clone RP1-140N12 is at 41206 in this sequence. The
 start of this sequence overlaps with sequence Z82206 The end of
 this sequence overlaps with sequence AL022238.

FEATURES

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 /db_xref="taxon:9606"
 /chromosome="22"
 /clone="RP3-496C20"
 /clone_lib="RPCI-3"
 24..186
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 169..311
 /note="MIR repeat: matches 71..211 of consensus"
 551..600
 /note="L2 repeat: matches 2626..2696 of consensus"
 2394..2462
 /note="MIR repeat: matches 21..192 of consensus"
 3226..3535

misc_feature
 repeat_region
 repeat_region
 repeat_region
 repeat_region
 repeat_region

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repeat_region /note="AluJb repeat: matches 5. .312 of consensus"
repeat_region /note="MIR repeat: matches 35. .236 of consensus"
misc_feature /note="L2 repeat: matches 2701. .2748 of consensus"
repeat_region /note="match: GSS: Em:AQ356083"
repeat_region /note="AluSx repeat: matches 1. .312 of consensus"
repeat_region /note="AluSg/x repeat: matches 1. .135 of consensus"
repeat_region /note="MIR repeat: matches 70. .146 of consensus"
repeat_region /note="AluSx repeat: matches 1. .297 of consensus"
misc_feature complement(8207. .8891)
repeat_region /note="match: GSS: Em:AQ344529"
repeat_region /note="MIR repeat: matches 80. .191 of consensus"
misc_feature /note="264 copies 2 mer cc 58 conserved"
misc_feature /note="forced join; gap estimated as 1kb by restriction
digest data"
repeat_region complement(9187. .9189)
repeat_region /note="forced join. Gap estimated as 1kb by restriction
digest data."
repeat_region /note="25 copies 5 mer ctct 62 conserved"
repeat_region /note="MIR repeat: matches 76. .255 of consensus"
repeat_region /note="MER5A repeat: matches 57. .150 of consensus"
repeat_region /note="MER5A repeat: matches 57. .185 of consensus"
repeat_region /note="L2 repeat: matches 1865. .2127 of consensus"
repeat_region /note="AluSx repeat: matches 28. .305 of consensus"
repeat_region /note="L1M4 repeat: matches 5393. .5854 of consensus"
repeat_region /note="AluSg repeat: matches 1. .310 of consensus"
repeat_region /note="L1M4 repeat: matches 5340. .5393 of consensus"
repeat_region /note="AluSx repeat: matches 2. .304 of consensus"
repeat_region /note="AluY repeat: matches 1. .306 of consensus"
repeat_region /note="L1M4 repeat: matches 5352. .5341 of consensus"
repeat_region /note="L1M4 repeat: matches 3784. .5097 of consensus"
repeat_region /note="L1 repeat: matches 3186. .3382 of consensus"
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repeat_region /note="MER91A repeat: matches 114. .193 of consensus"
repeat_region /note="LTR23 repeat: matches 210. .437 of consensus"
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repeat_region /note="AluSg repeat: matches 1. .313 of consensus"
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repeat_region /note="MIR repeat: matches 207. .245 of consensus"

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repeat_region /note="MIR repeat: matches 29. .261 of consensus"
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repeat_region /note="AluSg/x repeat: matches 134. .302 of consensus"
repeat_region 20465. .20747
repeat_region /note="AluSg repeat: matches 1. .296 of consensus"
repeat_region 22217. .22508
repeat_region /note="AluSx repeat: matches 14. .305 of consensus"
repeat_region 22764. .22848
repeat_region /note="MIR repeat: matches 164. .249 of consensus"
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misc_feature /note="Cpg island"
repeat_region 23946. .24063
repeat_region /note="MIR repeat: matches 21. .140 of consensus"
repeat_region 25053. .25142
repeat_region /note="MIR repeat: matches 21. .119 of consensus"
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repeat_region 26997. .27304
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repeat_region 27326. .27595
repeat_region /note="AluSx repeat: matches 37. .311 of consensus"
repeat_region 28098. .28406
repeat_region /note="AluSg repeat: matches 1. .311 of consensus"
repeat_region 28847. .29128
repeat_region /note="L2 repeat: matches 2362. .2745 of consensus"
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repeat_region 30940. .30989
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repeat_region 30990. .31054
repeat_region /note="MER41A repeat: matches 400. .464 of consensus"
misc_feature 31120. .31339
repeat_region /note="match: STS: Em:G03731; match: STS: Em:G03731"
repeat_region 34416. .34721
repeat_region /note="AluY repeat: matches 1. .310 of consensus"
repeat_region 34776. .34821
repeat_region /note="L2 repeat: matches 2688. .2733 of consensus"
repeat_region 34944. .35243
repeat_region /note="AluSx repeat: matches 1. .300 of consensus"
repeat_region 35351. .35551
repeat_region /note="MER20 repeat: matches 1. .204 of consensus"
repeat_region 36460. .36544
repeat_region /note="L2 repeat: matches 2665. .2749 of consensus"
repeat_region 37480. .37620
repeat_region /note="MIR repeat: matches 4. .150 of consensus"
repeat_region 37861. .38188
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misc_feature complement(38024. .38419)
misc_feature /note="match: STS: Em:G28177; match: STS: Em:R54672"
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repeat_region 38802. .38948

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Query Match 98.8%; Score 988; DB 9; Length 69964;
Best Local Similarity 99.9%; Pred. No. 6.5e-248;
Matches 999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGTGTGACCTTATCTCTGAACCTCAGTTCTTCATCCGTAATAAATAAAGCTGCTAG 60
DB 6683 GGTGTGACCTTATCTCTGAACCTCAGTTCTTCATCCGTAATAAATAAAGCTGCTAG 6624
QY 61 ATTGTTGTAATAAATAAATAAATGAATGAGTAGCGGTGGCTCACCCCTGTAATCCCA 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 138459)

Birren,B., Linton,L., Nusbaum,C. and Lander,E. (2004) The Human Genome Project: Initial sequencing and assembly of human chromosome 8. *Nature* 431: 1411-1416.

2 (bases 1 to 138459)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barina,N., Bastien,V., Boguslavsky,I., Boukigalier,B., Brown,A., Camarata,J., Campiano,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodgson,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,D., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., Larocque,K., Lamazares,R., Landers,T., Lehotzky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Melidrim,J., Meneus,L., Mihova,T., Milenga,V., Murphy,T., Taylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P., Sounez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 11, 2001 this sequence version replaced gi:13270664.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information -----

Center project name: L12790

Center clone name: 254_K_5

----- Summary Statistics -----

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 133567 bases at least Q40

Consensus quality: 135811 bases at least Q30

Consensus quality: 136678 bases at least Q20

Insert size: 139000; agarose-fp

Insert size: 137359; sum-of-contigs

Quality coverage: 6.5 in Q20 bases; agarose-fp

Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 1411: contig of 1411 bp in length

* 1412 1511: gap of 100 bp

* 1512 2165: contig of 654 bp in length

* 2166 2265: gap of 100 bp

* 2266 3074: contig of 809 bp in length

* 3075 3174: gap of 100 bp

* 3175 4763: contig of 1589 bp in length

* 4764 4863: gap of 100 bp

* 4864 6161: contig of 1298 bp in length

* 6162 6261: gap of 100 bp

[illegible]

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* 6262 8601: contig of 2340 bp in length
* 8602 8701: gap of 100 bp
* 8702 13139: contig of 4438 bp in length
* 13140 13239: gap of 100 bp
* 13240 17613: contig of 4374 bp in length
* 17614 17713: gap of 100 bp
* 17714 30894: contig of 13181 bp in length
* 30895 30994: gap of 100 bp
* 30995 40051: contig of 9057 bp in length
* 40052 40151: gap of 100 bp
* 40152 95859: contig of 55708 bp in length
* 95860 95959: gap of 100 bp
* 95960 138459: contig of 42500 bp in length.
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            /chromosome="8"
            /map="8"
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            /clone_lib="RPC1-11 Human Male BAC"
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                vector_side:left"
                1512..2165
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                        3175..4763
                            /note="assembly_fragment"
                            4864..6161
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                                6262..8601
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                                                        95960..138459
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BASE COUNT 38140 a 31260 c 30041 g 37914 t 1104 others
ORIGIN

Query Match 95.6%; Score 956.4; DB 2; Length 138459;
Best Local Similarity 97.8%; Pred. No. 1.3e-239;
Matches 998; Conservative 0; Mismatches 1; Indels 21; Gaps 2;

QY 1 GGGTGACCTTATCCTCTGAACTCAGTTTCTCATCCGTAAATGAAAGCTCTAG 60
D 138459
Db 33521 GGGTGACCTTATCCTCTGAACTCAGTTTCTCATCCGTAAATGAAAGCTCTAG 33580
QY 61 ATTGTTGTAATAAATAAATGGAATAGGCTAGCGCGGTGCTCAGCTGTAATCCCA 120
D 33581 ATTGTTGTAATAAATAAATGGAATAGGCTAGCGCGGTGCTCAGCTGTAATCCCA 33640
QY 121 GCACCTTAGAGGTCGAAGAGGTGGATCATTGAGGTGAGGTTTGTAGACAGCCTG 180
D 33641 GCACCTTAGAGGTCGAAGAGGTGGATCATTGAGGTGAGGTTTGTAGACAGCCTG 33700
QY 181 GCCACACGGTGAACCCCATCTCTACTTAAATAAATAAATAGCTNGGTGGGTGGCT 240
D 33701 GCCACACGGTGAACCCCATCTCTACTTAAATAAATAAATAGCT-GGGTGGGTGGCT 33759
QY 241 CACACCTGTAATCCAGCACTTTGGAGGCTGAGAGGGTGGATCAGCTGAAGTCAGG 300

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Db 33760 CACACCTGTAATCCAGCACTTTGGAGGCTGAGACGGGTGGATCACCTGAAGTCAGGAG 33819
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D 33820 TTCAGGCCAGCTGGGCAACATGGTGAACACAGTCTCTACTTAAATAAATAAATAAATAAATAG 33879
QY 361 CAGGTGTGGTGGCACACGCTGTAGTCCAGCTTACTTGGAGGCTGAGGCGGAAGAATC 420
D 33880 CAGGTGTGGTGGCACACGCTGTAGTCCAGCTTACTTGGAGGCTGAGGCGGAAGAATC 33939
QY 421 GCTTGAACCCAGTAGGACAGGTTGACGTGAGCCGAGATAAGTCACTGACTCCAGCC 480
D 33940 GCTTGAACCCAGTAGGACAGGTTGACGTGAGCCGAGATAAGTCACTGACTCCAGCC 33999
QY 481 TGGGTGACAGCAGCAAGCTCCCTCTCAGAAA-----ATAAATAA 520
D 34000 TGGGTGACAGCAGCAAGCTCCCTCTCAGAAAATAAATAAATAAATAAATAAATAAATAA 34059
QY 521 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 580
D 34060 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 34119
QY 581 TAGCACTTATATGCCCAATAAGTATCAATATCCCCGCCCTTACCACTGTGCTG 640
D 34120 TAGCACTTATATGCCCAATAAGTATCAATATCCCCGCCCTTACCACTGTGCTG 34179
QY 641 AATATTAGTTCTTTTGTACCCGCCCTTACCACTTAAAGCAGAAATCTCACCGTACTCC 700
D 34180 AATATTAGTTCTTTTGTACCCGCCCTTACCACTTAAAGCAGAAATCTCACCGTACTCC 34239
QY 701 TCTGTAAATTTCTGTCTGTCGACATAGTTGGTCTCAGTGAACATAGTGAGTGAATG 760
D 34240 TCTGTAAATTTCTGTCTGTCGACATAGTTGGTCTCAGTGAACATAGTGAGTGAATG 34299
QY 761 AGCAATGCAAGGAATCTCCAGGCAATCTGGAGGCCCTCCAGCGGGTGAAGTTCGCGAA 820
D 34300 AGCAATGCAAGGAATCTCCAGGCAATCTGGAGGCCCTCCAGCGGGTGAAGTTCGCGAA 34359
QY 821 ACTCATAGTCTGCTCTCAATAGGCCCACTGAAAGGTAGAGAGTTCTGGGTCCCACTCCGC 880
D 34360 ACTCATAGTCTGCTCTCAATAGGCCCACTGAAAGGTAGAGAGTTCTGGGTCCCACTCCGC 34419
QY 881 ACCCCCATCTCTGACTCCTGCTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 940
D 34420 ACCCCCATCTCTGACTCCTGCTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 34479
QY 941 GAGCTCCCACTGCTTGGCAGGCTGCAAGGAGCCAGCAGAAATGATGACCGCGTGC 1000
D 34480 GAGCTCCCACTGCTTGGCAGGCTGCAAGGAGCCAGCAGAAATGATGACCGCGTGC 34539

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RESULT 4
AC104363 62102 bp DNA linear HTG 08-DEC-2001
LOCUS Homo sapiens chromosome 18 clone RP11-42N11 map 18, LOW-PASS
SEQUENCE SAMPLING.
AC104363
VERSION AC104363.1 GI:17426352
KEYWORDS HTG; HTGS-PHASE0.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62102)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Allen,N.,
TITLE Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhaltier,B.,
JOURNAL Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
REFERENCE Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
2 (bases 1 to 62102)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Allen,N.,
TITLE Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhaltier,B.,
JOURNAL Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
REFERENCE Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
2 (bases 1 to 62102)
AUTHORS

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Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Hearford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (08-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIAR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L22094
Center clone name: 42_N_11

* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be generic-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 665: contig of 665 bp in length
* 666 765: gap of 100 bp
* 766 1454: contig of 689 bp in length
* 1455 1554: gap of 100 bp
* 1555 2232: contig of 678 bp in length
* 2233 2332: gap of 100 bp
* 2333 3028: contig of 696 bp in length
* 3029 3128: gap of 100 bp
* 3129 3753: contig of 625 bp in length
* 3754 3853: gap of 100 bp
* 3854 4459: contig of 606 bp in length
* 4460 4559: gap of 100 bp
* 4560 5225: contig of 666 bp in length
* 5226 5325: gap of 100 bp
* 5326 5979: contig of 654 bp in length
* 5980 6079: gap of 100 bp
* 6080 6752: contig of 673 bp in length
* 6753 6852: gap of 100 bp
* 6853 7526: contig of 674 bp in length
* 7527 7626: gap of 100 bp
* 7627 8307: contig of 681 bp in length
* 8308 8407: gap of 100 bp
* 8408 9090: contig of 683 bp in length
* 9091 9190: gap of 100 bp
* 9191 9880: contig of 690 bp in length
* 9881 9980: gap of 100 bp
* 9981 10667: contig of 687 bp in length
* 10668 10767: gap of 100 bp
* 10768 11436: contig of 669 bp in length

* 11437 11536: gap of 100 bp
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* 12158 12257: gap of 100 bp
* 12258 12913: contig of 656 bp in length
* 12914 13013: gap of 100 bp
* 13014 13667: contig of 654 bp in length
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* 13768 14429: contig of 662 bp in length
* 14430 14529: gap of 100 bp
* 14530 15189: contig of 660 bp in length
* 15190 15289: gap of 100 bp
* 15290 15950: contig of 661 bp in length
* 15951 16050: gap of 100 bp
* 16051 16724: contig of 674 bp in length
* 16725 16824: gap of 100 bp
* 16825 17505: contig of 681 bp in length
* 17506 17605: gap of 100 bp
* 17606 18290: contig of 685 bp in length
* 18291 18390: gap of 100 bp
* 18391 19050: contig of 660 bp in length
* 19051 19150: gap of 100 bp
* 19151 19807: contig of 657 bp in length
* 19808 19907: gap of 100 bp
* 19908 20568: contig of 661 bp in length
* 20569 20668: gap of 100 bp
* 20669 21322: contig of 654 bp in length
* 21323 21422: gap of 100 bp
* 21423 22079: contig of 657 bp in length
* 22080 22179: gap of 100 bp
* 22180 22852: contig of 673 bp in length
* 22853 22952: gap of 100 bp
* 22953 23621: contig of 669 bp in length
* 23622 23721: gap of 100 bp
* 23722 24386: contig of 665 bp in length
* 24387 24486: gap of 100 bp
* 24487 25174: contig of 688 bp in length
* 25175 25274: gap of 100 bp
* 25275 25957: contig of 683 bp in length
* 25958 26057: gap of 100 bp
* 26058 26729: contig of 672 bp in length
* 26730 26829: gap of 100 bp
* 26830 27478: contig of 649 bp in length
* 27479 27578: gap of 100 bp
* 27579 28237: contig of 659 bp in length
* 28238 28337: gap of 100 bp
* 28338 29002: contig of 665 bp in length
* 29003 29102: gap of 100 bp
* 29103 29764: contig of 662 bp in length
* 29765 29864: gap of 100 bp
* 29865 30544: contig of 680 bp in length
* 30545 30644: gap of 100 bp
* 30645 31330: contig of 686 bp in length
* 31331 31430: gap of 100 bp
* 31431 32107: contig of 677 bp in length
* 32108 32207: gap of 100 bp
* 32208 32887: contig of 680 bp in length
* 32888 32987: gap of 100 bp
* 32988 33679: contig of 692 bp in length
* 33680 33779: gap of 100 bp
* 33780 34451: contig of 672 bp in length
* 34452 34551: gap of 100 bp
* 34552 35216: contig of 665 bp in length
* 35217 35316: gap of 100 bp
* 35317 35978: contig of 662 bp in length
* 35979 36078: gap of 100 bp
* 36079 36731: contig of 653 bp in length
* 36732 36831: gap of 100 bp
* 36832 37486: contig of 655 bp in length
* 37487 37586: gap of 100 bp
* 37587 38249: contig of 663 bp in length
* 38250 38349: gap of 100 bp
* 38350 39032: contig of 683 bp in length
* 39033 39132: gap of 100 bp

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* 39133 39815: contig of 683 bp in length
* 39816 39915: gap of 100 bp
* 39916 40576: contig of 661 bp in length
* 40577 40676: gap of 100 bp
* 40677 41356: contig of 680 bp in length
* 41357 41456: gap of 100 bp
* 41457 42141: contig of 685 bp in length
* 42142 42241: gap of 100 bp
* 42242 42899: contig of 658 bp in length
* 42900 42999: gap of 100 bp
* 43000 43650: contig of 651 bp in length
* 43651 43750: gap of 100 bp
* 43751 44412: contig of 662 bp in length
* 44413 44512: gap of 100 bp
* 44513 45169: contig of 657 bp in length
* 45170 45269: gap of 100 bp
* 45270 45925: contig of 656 bp in length
* 45926 46025: gap of 100 bp
* 46026 46695: contig of 670 bp in length
* 46696 46795: gap of 100 bp
* 46796 47481: contig of 686 bp in length
* 47482 47581: gap of 100 bp
* 47582 48185: contig of 604 bp in length
* 48186 48285: gap of 100 bp
* 48286 48964: contig of 679 bp in length
* 48965 49064: gap of 100 bp
* 49065 49751: contig of 687 bp in length
* 49752 49851: gap of 100 bp
* 49852 50518: contig of 667 bp in length
* 50519 50618: gap of 100 bp
* 50619 51290: contig of 672 bp in length
* 51291 51390: gap of 100 bp
* 51391 52048: contig of 658 bp in length
* 52049 52148: gap of 100 bp
* 52149 52826: contig of 678 bp in length

Query Match
Best Local Similarity 32.7%; Score 327.4; DB 2; Length 62102;
Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 672 GACTTAAGCAGAAATTCACCGTACTCTCTGTAAATTTCTGTTCTGTCACATAGTT 731
DB 55292 GACTTAAGCAGAAATTCACCGTACTCTCTGTAAATTTCTGTTCTGTCACATAGTT 55351

QY 732 GGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCCAGGCCATCTGG 791
DB 55352 GGGTCTCAGTGAACATGGTGAATGAGCAAAATGCAAGGAATCCAGGCCATCTGG 55411

QY 792 GAGCCCTCCAGCGGGTGGTTCGGGAACTCATAGTCTGTCTTCAATGGCCACTGAA 851
DB 55412 GAGCCCTCCAGCGGGTGGTTCGGGAACTCATAGTCTGTCTTCAATGGCCACTGAA 851

QY 852 AGGTAGAGTTCTGGTGTCCACCTCCGACCCCATCTCTGACTCACTGCTGAAAAAT 911
DB 55472 AGGTAGAGTTCTGGTGTCCACCTCCGACCCCATCTCTGACTCACTGCTGAAAAAT 911

QY 912 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 971
DB 55532 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 971

QY 972 GGAGCCAGCAGAAATGATGACCGGGTGC 1000
DB 55592 GGAGCCAGCAGAAATGATGACCGGGTGC 55620

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RESULT 5
AC092921_2/c
WPCOMMENT
Sequence split into 5 fragments
Fragment Name      LOCUS AC092921 Accession AC092921
AC092921_0        Begin      End
AC092921_1        1      110000
AC092921_2        100001 210000
AC092921_2        200001 310000

```

```

AC092921_3      300001 410000
AC092921_4      400001 460778
Continuation (3 of 5) of AC092921 from base 200001 (AC092921 Homo sapiens chromosome
Query Match      32.6%; Score 326.2; DB 2; Length 110000;
Best Local Similarity 81.5%; Pred. No. 1.3e-74;
Matches 401; Conservative 0; Mismatches 89; Indels 2; Gaps 2;

QY 70 AAAAAATTAATGAATAGCTAGGCGGGTGGCTACGCGCTGTATCCAGCAGCATTAG 129
DB 60535 AAAAGAGATAAGCAATCTCTCTGGCGTGGTGTCTACGCTGTATCCAGCAGCATTGG 60476

QY 130 AAGGTGCGAGAGGGTGCATCAGTTCAGGTAGGAGTTTGTAGCAGCAGCTGGCCACACG 189
DB 60475 GAGCGCGAGGATGTGATCAGTTCAGGTAGGAG-TTCGAGACAGCAGCTGGCCACACG 60417

QY 190 GTGAACACCCCATCTCTACTAAAAATAAAAAATTAAGCTNGGTGGTGGCTCACACTGT 249
DB 60416 GTGAACACCTCTCTCTACTAAGANATCAAAAAATTAAGCGGGGGTGGTGGCTCACACTGT 60357

QY 250 AATCCAGCAGCTTTGGGAGGCTGAGACGGGTGGATCACCTGAAGTCAGGAGTTCAAGGCC 309
DB 60356 AATCCAGCAGCTTTGGGAGGCTGAGACGGGTGGATCACCTGAGTTCAGGAGTTTCAGACC 60297

QY 310 AGCCTGGGCAACATGGTGAACCCAGCTCTCTACTAAAAATAAATAAATAAATAAATAA 369
DB 60296 AGCCTGGGCAACATGGTGAACCCAGCTCTCTACTAAAAATAAATAAATAAATAAATAA 60237

QY 370 GTGGCACACGCTGTAGTCCAGCTTACTTGGGAGGCTGAGGCGGGAAGCAATTCGTTCAACC 429
DB 60236 GTGAAGCATGCGTGTAAATCCAGCTTACTTGGGAGGCTGAGGCGGGAAGCAATTCGTTCAACC 60177

QY 430 CAGTAGGAGAGGTTGCGAGTGGAGGAGTAAGAGTCACTGCTCAGCTCCAGCTGGGTGACA 489
DB 60176 TGGGAGGAGAGGTTTTCAGTGGAGTGGATCA-TGTCATTCAGCTACAGCTGGGCGACA 60118

QY 490 GAGCAAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 549
DB 60117 GAGCAACACTCCCACTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 60058

QY 550 AAATAAATAATCT 561
DB 60057 TAAGATACGCT 60046

RESULT 6
HS424J12/c
LOCUS
DEFINITION
Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
ACCESSION
Z82207.3 GI:12331276
VERSION
HTG; HTGS_PHASE1; HTGS_CANCELLED.
KEYWORDS
human.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 201197)
AUTHORS
Direct Submission
TITLE
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
JOURNAL
requests: clonerquest@sanger.ac.uk
On Jan 22, 2001 this sequence version replaced gi:10045116.
COMMENT
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dJ424J12
----- Summary Statistics
Assembly program: XGAP4; version 4.5

```

```

Sequencing vector: M13; M77815; 74% of reads
Sequencing vector: plasmid; L08752; 25% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator ABI; 96% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 198047 bases at least Q20
Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence,
* as soon as it is available and the accession number will
* be preserved.

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* 1 4154: contig of 4154 bp in length
4155 4254: gap of 100 bp
4255 18703: contig of 14449 bp in length
18704 18803: gap of 100 bp
18804 20941: contig of 2138 bp in length
20942 21041: gap of 100 bp
21042 34907: contig of 13866 bp in length
34908 35012: gap of 105 bp
35013 37508: contig of 2496 bp in length
37509 37608: gap of 100 bp
37609 52739: contig of 15131 bp in length
52740 52839: gap of 100 bp
52840 56933: contig of 4094 bp in length
56934 57033: gap of 100 bp
57034 88245: contig of 31212 bp in length
88246 88346: gap of 101 bp
88347 93386: contig of 5040 bp in length
93387 93486: gap of 100 bp
93487 123956: contig of 30470 bp in length
123957 124056: gap of 100 bp
124057 147917: contig of 23861 bp in length
147918 148017: gap of 100 bp
148018 176236: contig of 28219 bp in length
176237 176336: gap of 100 bp
176337 187128: contig of 10792 bp in length
187129 187228: gap of 100 bp
187229 190824: contig of 3596 bp in length
190825 190939: gap of 135 bp
190940 201197: contig of 10238 bp in length.

FEATURES	
source	

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/db_xref="taxon:9606"
/chromosome="X"
/clone=FP3-424J12"
/clone_lib="RPCI-3"
  1..41154
/note="assembly fragment:02486
fragment_chain:1"
4255..16703
/note="assembly fragment:04764
fragment_chain:1"
18804..20941
/note="assembly fragment:03282
fragment_chain:2"
21042..34907
/note="assembly fragment:03624
fragment_chain:2"
35008..37508
/note="assembly fragment:00340"
37609..52739
/note="assembly fragment:00671.0"
52840..56933

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	/note="assembly_fragment:01287.0"	
misc_feature	57034...88245	
	/note="assembly_fragment:01294"	
misc_feature	88346...93386	
	/note="assembly_fragment:01608"	
misc_feature	93487...123956	
	/note="assembly_fragment:03234"	
misc_feature	124057...147917	
	/note="assembly_fragment:04074"	
misc_feature	148018...176236	
	/note="assembly_fragment:04816"	
misc_feature	176337...187128	
	/note="assembly_fragment:05488"	
misc_feature	187229...190824	
	/note="assembly_fragment:05572.0"	
misc_feature	190925...201197	
	/note="assembly_fragment:03867 clone_end:T7 vector_side:right"	
BASE COUNT	55207 a 43266 c 43712 g 57504 t 1508 others	
ORIGIN		
Query Match	32.5%; Score 325.2; DB 2; Length 201197;	
Best Local Similarity	81.7%; Pred. No. 2.6e-74;	
Matches 411; Conservative 0; Mismatches 89; Indels 3; Gaps 3		
QY	69 AAAAAAATAATGGAATAGGTAGCGCGTGGCTCAGCCCTGTAATCCAGCACTTTA 128	
Db	106056 AAAGAAGAAATGACCCCTGGCTGGTGCGTGCAGCCCTATATCCAGCACTTTG 105997	
QY	129 GAAGTCGAAGAGGTGGATCACTTGAGTCAGGAGTTTGAGACGACGCTGCCAACAC 188	
Db	105996 GGAGGCCAAGCGGGTTCGATCACTGAGTCAGGAG-TTCGAGACCAGCTGACCAACAT 105938	
QY	189 GGTGAACCCCATCTACTAAAATAAAAAATTACTNGGTGGTGCGCTCACACCTG 248	
Db	105937 GGTGAACCCCGTCTCTCTATAAAATACAAAAT-GACCTGGCACGTTGGCTCAGCTG 105879	
QY	249 TAATCCCAGCACTTTGGAGGCTTGAGCGGTTGATCACTCAAGTCAGGAGTTCAGGCG 308	
Db	105878 TAATCCCAGCACTTTGGAGGCTTGAGTGGTGGATCACTTGAGTCAGGAGTTCAGAC 105819	
QY	309 CAGCCTGGGCACATGTTGAACCACTCTCTACTAAAATACAAAATTACCCAGGTGT 368	
Db	105818 CAGCCTGTTCAATGTGTGAACCCCGTCTCTACTAAAATACAAAAGTAGCCAGCGGT 105759	
QY	369 GTGGCACACGCGCTGTAGTCCCACTACTTGGAGGCTGAGCGGAGATCGCTGAAC 428	
Db	105758 GTGGCAGGCTCCTGTAGTCCCACTACTCGGAGGCTGAGACTGGAATTTGCTTGAAC 105699	
QY	429 CCAGTAGGCAGAGTTCCAGTGAGCCGAGATAGATCACTGCACTCCAGCCTGGGTGAC 488	
Db	105698 CCAGGAGGCGGAGGTTCCAGCAGCGCCGAGATCA-TGCCACTGCACTCCAGCTGGGTGAC 105640	
QY	489 AGAGCAAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAAT 548	
Db	105639 AGAGCGAGACTCCGCTCTCAAAAAAAAAAAAAAAAAAAAAAAGAAATGGACAAAAC 105580	
QY	549 AAAATAAAATCTTAAAGGGCTG 571	
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RESULT 7	AC110871	97110 bp	DNA	linear	PRI 30-MAY-2002
LOCUS	AC110871				
DEFINITION	Homo sapiens 3 BAC Rp11-639B4 (Roswell Park Cancer Institute Human BAC Library) complete sequence.				
ACCESSION	AC110871				
VERSION	AC110871.6	GI:21263157			
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE AUTHORS

1 (bases 1 to 97110)
Muzly,D.M., Adams,C., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alsbrooks,S.L., Anaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbacia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brivia,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleaveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabsi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louiseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabort,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,Y., Villalon,B., Vinson,R., Wang,O., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 97110)
Worley,K.C.

Direct Submission
Submitted (16-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 97110)
Worley,K.C.

Direct Submission
Submitted (09-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

4 (bases 1 to 97110)
Worley,K.C.

Direct Submission
Submitted (30-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 30, 2002 this sequence version replaced gi:20452973.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect <1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES	QUALSTAT-REPORT	
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repeat_region	/clone="RP11-639B4"	complement(139..266)
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repeat_region	/rpt_family="AT-rich"	1903..2215
	/rpt_family="AluSx"	4975..5004
repeat_region	/rpt_family="AT-rich"	5256..5568
	/rpt_family="AluSg"	5369..5597
repeat_region	/rpt_family="AluSg"	5598..5632
	/rpt_family="AluSg"	7245..7737
repeat_region	/rpt_family="L2"	7717..7844
	/rpt_family="MIR"	10274..10308
repeat_region	/rpt_family="AT-rich"	11121..11398
	complement(11424..11534)	/rpt_family="MLT1J"
repeat_region	/rpt_family="MLT1J"	11574..13164
	/rpt_family="MER52A"	complement(13394..13428)
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	/rpt_family="MER52A"	14476..14531
repeat_region	/rpt_family="polypurine"	14645..14734
	/rpt_family="MIR"	15617..15959
repeat_region	/rpt_family="MER58B"	16501..16526

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17332..17385
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17825..18125
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19143..19448
repeat_region /rpt_family="Alusg"
19737..20018
repeat_region /rpt_family="Alusx"
20019..20045
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complement(20464..20512)
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21922..22002
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22209..22366
repeat_region /rpt_family="L2"
complement(22563..22810)
repeat_region /rpt_family="MIR"
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23583..23843
repeat_region /rpt_family="AlusP"
24087..24327
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24584..24588
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26741..26778
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28690..28739
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28740..28793
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Query Match 32.5%; Score 324.8; DB 9; Length 97110;
Best Local Similarity 83.1%; Pred. No. 3e-74;
Matches 393; Conservative 0; Mismatches 78; Indels 2; Gaps 2;

QY 70 AAAAAATTAAATGAATAGCTAGCGGGTGGCTACGCCCTGTAATCCAGCATTGTAG 129
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Db 62866 AAGAGATAAGCAATCTCTGGCGGTGGTGGCTACGCCCTGTAATCCAGCATTGTG 62925
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 130 AAGTGTGAAGAGGTGGATCATTGAGTCTAGGAGTTTGGAGACCAAGCTGGCCACAGG 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62926 GAGCGCGAGGATGTGATCACTGAGTCTAGGAGTTTGGAGACCAAGCTGGCCACAGG 62984
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 190 GTGAACCCCATCTCTACTAAATAAATAAAATTTAGCTNGGGTGGCTGGCTACACCTGT 249
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62985 GTGAACCCCATCTCTACTAAATAAATAAAATTTAGCTNGGGTGGCTGGCTACACCTGT 63044
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 250 AATCCAGCATTGGGAGGCTGAGCGGTGGATCACTGAAGTCTAGGAGTTCAAGGCC 309
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63045 AATCCAGCATTGGGAGGCTGAGCGGTGGATCACTGAAGTCTAGGAGTTCAAGGCC 63104
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 310 AGCTGGGCAACATGGTGAACACAGCTCTCTACTAAATAAATAAAATTTAGCAGGTGTG 369
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63105 AGCTGGGCAACATGGTGAACACAGCTCTCTACTAAATAAATAAAATTTAGCAGGTGTG 63164
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 370 GTGGCACAGCTGTAGTCCCGAGCTACTTGGAGGCTGAGCGGGAAGATCGCTTGAACC 429
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 63165 GTGAAGCATGCTGTAAATCCAGCTACTCAGGAGCGTGGAGGAGAGATCGCTTGAACC 63224
QY 430 CAGTAGCAGAGGTTGGAGTGGAGCCGAGATAAGAGTCACTGCACCTCCAGCTGGGTGACA 489
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63225 TGGGAGCGAGAGGTTTCAGTGAAGTGAATCA-TGTCTTGCACCTACAGCTGGCGACA 63283
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 490 GAGCAAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAA 542
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63284 GAGCAACACTCCACTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 63336
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 8
AC004596 92638 bp DNA linear PRI 02-FEB-1999
LOCUS Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.
AC004596
AC004596 AC004596.1 GI:4210521
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
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REFERENCE
AUTHORS Birren, B., Fasnacht, K., McKernan, K., Nusbaum, C., Richardson, P.,
Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,
Benn, J., Boatman, C., Boutwell, C., Brown, A., Byrne, S., Cantu, C.,
Castle, A., Cerny, J., Cooke, P., Daly, M. J., Depayre, E., Devon, K.,
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Hagos, B., Harris, K., Horton, L., Howland, J. C., Hui, L., Jacotot, L.,
Kann, L., Linton, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A.,
Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J.,
Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Pavlin, B.,
Peterson, K., Riley, R., Roberts, D., Rollins, G., Rossello, R., Roy, A.,
Shyam, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C.,
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Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y.,
Ye, W. J., Zhao, J. and Zody, M.
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Direct Submission
Submitted (19-APR-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 92638)
```

```
REFERENCE
AUTHORS Birren, B., Fasnacht, K., McKernan, K., Nusbaum, C., Richardson, P.,
Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R.,
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Ye, W. J., Zhao, J. and Zody, M.
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Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;
QY 86 TAGGCTAGGCGGGTGGCTCAGCGCTGATCCAGCACTTAGAGGTCGAGAGGGTG 145

Db 69545 TGGGCCACGCGGTGGCTCACACTGTTATCCAGCACTTTGGAAGCGCGAGCGGGTG 69604
QY 146 GATCACTTGAGGTCTAGAGTTTGGAGCAGAGCTGGCCAAACAGCGTGAACACCCCACTCTCT 205
Db 69605 GATCACTGAAGACAAGAG-TTCGAGACAGAGCTGGCCAAACAGTGTGAACCTCTCTCT 69663
QY 206 ACTAAATATAAATTAAGCTNGGTCGGGTGGCTCACACCTGTATCCAGCACTTTGG 265
Db 69664 ACTAAATATAAATTAAGCTNGGTCGGGTGGCTCACACCTGTATCCAGCACTTTGG 69723
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Db 69782 TGAACACCACTCTCTACTATAAATAAATAGCAGGTGGTGGGACACGCGCTGTA 69841
QY 386 GTCCCAAGCTACTTGGGAGGCTGAGGCGGGAAGATCGCTGAACCCAGTACAGGAGTTG 445
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Db 69902 CAGTGAGCGGAGATCA-CGACACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCCTCT 69960
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RESULT 9
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LOCUS Human DNA sequence from clone Rp13-163c4 on chromosome X, complete
DEFINITION sequence.
ACCESSION AL591583
VERSION AL591583.14 GI:20338452
KEYWORDS HFG.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Howden, P.
JOURNAL Direct Submission

COMMENT
Submitted (25-APR-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
On Apr 29, 2002 this sequence version replaced gi:16973107.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred/quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX

Rp13-163c4 is from the library RPI-13.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBac3.6.
FEATURES
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/clone_lib="RPI-13.1"
BASE COUNT 18850 a 16494 c 16633 g 18716 t
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Best Local Similarity 82.4%; Pred. No. 5.8e-73;
Matches 402; Conservative 0; Mismatches 83; Indels 3; Gaps 3;
QY 69 AAAAAATTAATAGGCTAGGCGGCTGGCTCAGCGCTGTATCCAGCACTTTA 128
Db 32038 AAAAGAAAGATGAGCCCTGGCTGGGTGGCTCAGCGCTATAATCCAGCACTTTG 31979
QY 129 GAGGTGCAAGAGGTTGATCTACTTAAATAAATAAATAAATAAATAAATAAATAA 188
Db 31978 GGAGGCCAAGCGGCTGCATCACTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTG 31920
QY 189 GGTGAACCCCATCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAA 248
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QY 249 TAATCCAGCACTTTGGGAGGCTGAGAGCGGTGGATGATCAGCTCAGGAGTTCAAGGC 308
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QY 429 CCAGTAGCAGAGGTTGAGTGGGAGGCTGAGCGGAGATAGAGTCACTGCACTCCAGCTGGGTGAC 488
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QY 489 AGAGCAGAGCTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAA 548
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QY 549 AAAATAAA 556
Db 31561 CAAACAAA 31554

RESULT 10
AL161908
LOCUS Human DNA sequence from clone Rp11-123K19 on chromosome 9 Contains
DEFINITION part of a novel gene, part of a putative novel gene and CpG
islands, complete sequence.
ACCESSION AL161908
VERSION AL161908.13 GI:14148791
KEYWORDS HFG; CpG island.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Tracey, A.
JOURNAL Direct Submission

COMMENT
Submitted (04-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

COMMENT humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On May 18, 2001 this sequence version replaced gi:1387277.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em., EMBL; SW,
 SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr9>
 RP11-123K19 is from the library RP11-11.1 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-123K19 it may be shorter because we sequence overlapping
 sections only once, except for a short overlap.
 The true left end of clone RP11-123K19 is at 1 in this sequence.
 The true left end of clone RP11-489N22 is at 106117 in this
 sequence.

FEATURES

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repeat_region	776..945
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repeat_region	1561..1654
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repeat_region	2201..2480
	/note="AluJb repeat: matches 1..293 of consensus"
repeat_region	2481..2780
	/note="AluSp repeat: matches 1..301 of consensus"
repeat_region	2871..3156
	/note="AluX repeat: matches 9..294 of consensus"
repeat_region	3234..3518
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repeat_region	6203..6506
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misc_feature	7754..8091
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repeat_region	7837..7930
	/note="MIR repeat: matches 73..191 of consensus"
repeat_region	8066..8127
	/note="31 copies 2 mer cc 74% conserved"
repeat_region	8303..8549
	/note="L2 repeat: matches 2483..2736 of consensus"
repeat_region	8611..8756
	/note="MIR repeat: matches 60..192 of consensus"
repeat_region	9046..9089
	/note="11 copies 4 mer aatg 81% conserved"
repeat_region	9093..9124
	/note="16 copies 2 mer aa 87% conserved"
repeat_region	9149..9282
	/note="AluSq/X repeat: matches 1..133 of consensus"
repeat_region	9298..10471
	/note="LMC2 repeat: matches 5133..6328 of consensus"
repeat_region	10529..10828
	/note="AluSp repeat: matches 1..301 of consensus"
repeat_region	11333..11557
	/note="L1 repeat: matches 4258..4489 of consensus"
repeat_region	11689..11779
	/note="MIR repeat: matches 59..151 of consensus"
repeat_region	11867..11948
	/note="MIR repeat: matches 174..255 of consensus"
repeat_region	11953..12046
	/note="MER81 repeat: matches 20..113 of consensus"
repeat_region	12060..12136
	/note="MIR repeat: matches 69..151 of consensus"
repeat_region	12687..12861
	/note="MIR repeat: matches 2..185 of consensus"
repeat_region	12862..13016
	/note="MIR repeat: matches 67..236 of consensus"
repeat_region	13134..13323
	/note="MIR repeat: matches 39..249 of consensus"
repeat_region	13729..13954
	/note="L2 repeat: matches 2427..2642 of consensus"
repeat_region	15602..15989
	/note="L2 repeat: matches 2299..2736 of consensus"
repeat_region	16104..16237
	/note="L2 repeat: matches 1966..2096 of consensus"
repeat_region	16699..16855
	/note="LMD2 repeat: matches 5795..5926 of consensus"
repeat_region	16856..17167
	/note="AluX repeat: matches 1..310 of consensus"
repeat_region	17168..17354
	/note="LMD2 repeat: matches 5926..6121 of consensus"
repeat_region	17355..17410
	/note="14 copies 4 mer ctca 76% conserved"
repeat_region	17419..17537
	/note="LMD2 repeat: matches 6138..6258 of consensus"
repeat_region	17541..18049
	/note="MIR repeat: matches 4..501 of consensus"
repeat_region	18052..18487
	/note="HERV repeat: matches 5330..5758 of consensus"
repeat_region	18488..18775
	/note="AluSg repeat: matches 2..289 of consensus"
repeat_region	18776..22675


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/note="HERVL repeat: matches 1356. .5330 of consensus"
22676. .23077
/note="MTIAL repeat: matches 1. .365 of consensus"
23078. .23162
/note="HERVL repeat: matches 1274. .1356 of consensus"
23164. .23475
/note="AlusX repeat: matches 1. .310 of consensus"
23498. .23809
/note="AlusX repeat: matches 1. .311 of consensus"
23810. .23837
/note="14 copies 2 mer at 92% conserved"
23812. .23839
/note="7 copies 4 mer at 92% conserved"
23839. .24114
/note="AluY repeat: matches 24. .291 of consensus"
24127. .24195
/note="Charlies5 repeat: matches 2471. .2551 of consensus"
24196. .24462
/note="AlusQ repeat: matches 1. .263 of consensus"
24468. .25675
/note="HERVL repeat: matches 36. .1276 of consensus"
25676. .25912
/note="AluY repeat: matches 1. .237 of consensus"
25913. .25948
/note="HERVL repeat: matches 2. .36 of consensus"
25974. .26282
/note="AlusX repeat: matches 18. .312 of consensus"
26285. .26544
/note="L1MD2 repeat: matches 6055. .6323 of consensus"
26545. .26623
/note="MABE1 repeat: matches 1. .80 of consensus"
26624. .26638
/note="L1MD2 repeat: matches 6323. .6336 of consensus"
26812. .27045
/note="MER33 repeat: matches 1. .244 of consensus"
27046. .27344
/note="AlusQ repeat: matches 1. .298 of consensus"
27345. .27448

Query Match      31.9%; Score 319.2; DB 9; Length 106216;
Best Local Similarity 80.5%; Pred. No. 8.7e-73;
Matches 397; Conservative 0; Mismatches 94; Indels 2; Gaps 2;

QY 66 TGTAAAAAATAATGATAGGCTAGCGCGTGCCTCAGCCCTGTATCCGACACT 125
DB 29863 TATATATACATATTAAATTCGCCAGTCAGTGGCTCAGACTTGTATGCGACACT 29922
QY 126 TTGAAGGTGCGAGAGGGTGGATCATTGAGTTCAGGAGTTTGTAGACAGCTGGCCAA 185
DB 29923 TTGGGAGACCAAGGCGAGTGGATCAGCTGAGATCAGGAG-TTCAAGCTCAGCTGGCCAA 29981
QY 186 CAGGTGGAACCCATCTCTACTAAATAAATAAATAATAGCTNGGTGGGTGGCTCACAC 245
DB 29982 CATGGTGAACCATGTCTTACTTAAATAAATAAATAAATAGCTGGTGGCTGGCTCACGC 30041
QY 246 CTGTATCCAGCACTTTGGGAGGTGAGACGGGTGATCAGCTCAGTTCAGTTCAGAGTTCAA 305
DB 30042 CTATATCCAGCACTTTGGGAGGCCAGGCGGATGCTTGGAGTTCAGGTCAGAGTTCAA 30101
QY 306 GGCCAGCTGGGCAACATGTTGAACACAGCTCTCTACTAAAAATACAAAAATAGCAGG 365
DB 30102 GACCACTAGCCATCAATGCGGAACCCATCTCTACTAAAAATACAAAAATAGCCAGG 30161
QY 366 TGTGTGGCACAGCCTGTAGTCCAGCTACTTGGAGGCTGAGCGCGGAAGATCGCTTG 425
DB 30162 TGTGTGGCATGTGCTGTAGTCCAGCTACTTGGAGGCTGAGCGGAGGAAGATCACTTG 30221
QY 426 AACCAGTAGAGAGGTTGCGAGTGGCCGAGATAGAGTCACTGCCTCCAGCCCTGGGT 485
DB 30222 AACCAGAGGTGGAGTTGCGAGGAGCCAGAT-TGCACCAGTGCCTGCGAGCTGGGT 30280
QY 486 GCAGAGCAGCACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAA 545
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Db 30281 GACAGAGCAGAGCTCCATCTCAACACATATAAAATATAAATAAATAAATAAATAA 30340
QY 546 AATAAATAAAT 558
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Db 30341 CAAAAAATAAATT 30353

RESULT 11
LOCUS AL161909 137289 bp DNA linear PRI 21-NOV-2001
DEFINITION Human DNA sequence from clone RP11-146N23 on chromosome 9, complete
sequence.
ACCESSION AL161909
VERSION AL161909.20 GI:17048334
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 137289)
AUTHORS Ramsay,H.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 22, 2001 this sequence version replaced gi:16943970.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em, EMBL; SW,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-146N23 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-146N23. It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-146N23 is at 1 in this sequence.
The true left end of clone RP11-513M16 is at 135290 in this
sequence. The true right end of clone RP11-151U10 is at 26774 in
this sequence.
Location/Qualifiers
1. .137289
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-146N23"
/clone_lib="RPCI-11.1"
53293. .53405
/note="Sequence from reads from a short insert library
derived from a single pUC clone. Restriction digest data
confirm the assembly. Sequence from uni-directional dGTP
big dye terminator reads only."
BASE COUNT 37993 a 27666 c 28638 g 42992 t
ORIGIN
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Query Match          31.9%; Score 319; DB 9; Length 137289;
Best Local Similarity 80.9%; Pred. No. 1e-72;
Matches 420; Conservative 0; Mismatches 95; Indels 4; Gaps 4;

QY 57 CTAGATTGTTTAAAAAATTAAATAGGAATAGCTAGGCGGCTGCCTCAGCCCTGTAAT 116
DQ 57 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30365 CTATTATTTATTTCTTATFAAARACTCTAAGCCCGGCTGAGTGGCTGATGCTGTAAT 30424

QY 117 CCACACCTTTAGAGGTGCAAGAGGTGGATGATCATTTGAGGTTCAGAGTCTTTGAGACAG 176
DQ 117 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30425 CCCAGCATTTGGAGCGGAGCGGGGATCACTGAGTGGCGAG-TTTGAGACAG 30483

QY 177 CTTGCGCCAAACAGGTGAACCCCATCTCTACTATAAATAAATAAATTAGTCTGGTGCCT 236
DQ 177 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30484 CTTGACTTAATGAGAACTCCATCTCTACTATAAACAACAATAATTAGCT-GGCTGTGCT 30542

QY 237 GGCTCACACCTGTAATCCAGCATTTGGAGGCTTGAGCGGCTGAGACGGGTGATCACTGAGTCA 296
DQ 237 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30543 GGCACACACCTGTAATCCAGCATTTGGAGGCTTGAGCGGCTGAGACGGGTGATCACTGAGTCA 30602

QY 297 GGAGTTCAAGCCAGCTGGGCAACATGTTGAACACAGCTCTCTACTATAAATAAATAAATAA 356
DQ 297 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30603 GGAGTTTGAGACACAGCTGGGCAACATGTTGAACACAGCTCTCTACTATAAATAAATAAATAA 30662

QY 357 TTAGCCAGGTGCTGGTGGCACAGCTGTAGTCCAGCTACTTGGAGGCTGAGCGGGAAG 416
DQ 357 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30663 TTAGTGGGCTGGTGGCACAGCTGTAGTCCAGCTACTTGGAGGCTGAGCGGGAAG 30722

QY 417 AATCGTTGAACCCAGTGGGCAACATGTTGAACACAGCTCTCTACTATAAATAAATAAATAA 476
DQ 417 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30723 AATCGTTGAACCCAGTGGGCAACATGTTGAACACAGCTCTCTACTATAAATAAATAAATAA 30781

QY 477 AGCTGGGTGACAGACAGCTCCCTCTCAGA-AAATAAATAAATAAATAAATAAATAA 535
DQ 477 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30782 AGCTGGGTGACAGACAGCTCCCTCTCAGA-AAATAAATAAATAAATAAATAAATAAATAA 30841

QY 536 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 574
DQ 536 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DQ 30842 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 30880

RESULT 12
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LOCUS          152192 bp      DNA      linear      HTG 17-JUN-2000
DEFINITION    Mus musculus chromosome 11 clone CT7-549E22 map 11, WORKING DRAFT
SEQUENCE      35 unordered pieces.
AC027410
AC027410.3    GI:8570504
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE        Mus musculus.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 152192)
AUTHORS       Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H.F., Allen,N.,
              Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
              Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,
              Campiano,A., Castle,A., Chepel,Y., Colangelo,M., Collins,S.,
              Collymore,A., Cooke,P., Dekrellano,K., Dewar,K., Diaz,J.S.,
              Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
              Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
              Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
              Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
              Levine,R., Lieu,C., Liu,G., Locke,K., Landers,T., Lehoczy,J.,
              McCarthy,M., McEwan,P., McGurk,A., McKernan,K., Marquis,N.,
              Melgrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenka,V., Morrow,J.,
              Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
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O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severi,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 17, 2000 this sequence version replaced gi:7652038.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

Project Information
Center project name: L7296
Center clone name: 549_E_22

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 137974 bases at least Q40
Consensus quality: 144343 bases at least Q30
Insert size: 134000; agarose-1p
Insert size: 148792; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; agarose-1p
Quality coverage: 3.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 1254: contig of 1254 bp in length
* 1255 1354: gap of 100 bp
* 1355 2472: contig of 1118 bp in length
* 2473 2572: gap of 100 bp
* 2573 2968: contig of 396 bp in length
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* 3069 4814: contig of 1746 bp in length
* 4815 4914: gap of 100 bp
* 4915 6933: contig of 2019 bp in length
* 6934 7033: gap of 100 bp
* 7034 8533: contig of 1500 bp in length
* 8534 8633: gap of 100 bp
* 8634 10357: contig of 1724 bp in length
* 10358 10457: gap of 100 bp
* 10458 12457: contig of 2000 bp in length
* 12458 12557: gap of 100 bp
* 12558 14866: contig of 2309 bp in length
* 14867 14966: gap of 100 bp
* 14967 17009: contig of 2043 bp in length
* 17010 17109: gap of 100 bp
* 17110 19394: contig of 2285 bp in length
* 19395 19494: gap of 100 bp
* 19495 21122: contig of 1628 bp in length
* 21123 21222: gap of 100 bp
* 21223 23617: contig of 2395 bp in length
* 23618 23717: gap of 100 bp
* 23718 26167: contig of 2450 bp in length
* 26168 26267: gap of 100 bp
* 26268 28470: contig of 2203 bp in length
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AC044812.3 GI:8076957
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159367)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 9, clone RP11-146N23
Unpublished
2 (bases 1 to 159367)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bedalov,F., Boguski,M.S., Bouckhagter,B., Brown,A., Burkett,D., Campiliani,A., Castelle,A., Choe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lakocue,K., Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Liu,Q., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGuck,A., McKernan,K., McPheters,R., Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,C., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 25, 2000 this sequence version replaced gi:7884577.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Center code: WIBR
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: I7174
Center clone name: 146.N.23
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 144681 bases at least Q40
Consensus quality: 152151 bases at least Q30
Consensus quality: 154947 bases at least Q20
Insert size: 165000; agarose-1p
Insert size: 156467; sum-of-contigs
Quality coverage: 4.0 in Q20 bases; agarose-1p
Quality coverage: 4.2 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 1066: contig of 1066 bp in length
* 1067 1166: gap of 100 bp
* 2259 2259: contig of 1093 bp in length
* 2260 2359: gap of 100 bp
* 2360 3711: contig of 1352 bp in length
* 3712 3811: gap of 100 bp

3812 5274: contig of 1463 bp in length
5275 5374: gap of 100 bp
5375 6956: contig of 1582 bp in length
6957 7056: gap of 100 bp
7057 8817: contig of 1761 bp in length
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11539 11638: gap of 100 bp
11639 13616: contig of 1978 bp in length
13617 13716: gap of 100 bp
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25693 25792: gap of 100 bp
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38405 41936: contig of 3532 bp in length
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45622 45721: gap of 100 bp
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50511 56294: contig of 5784 bp in length
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56395 65126: contig of 8732 bp in length
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65227 71685: contig of 6459 bp in length
71686 71785: gap of 100 bp
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87045 87144: gap of 100 bp
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104964 112662: contig of 7699 bp in length
112663 112762: gap of 100 bp
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                  /note="assembly_fragment"

Query Match
Best Local Similarity 80.9%; Pred. No. 1e-72; Length 159367;
Matches 420; Conservative 0; Mismatches 95; Indels 4; Gaps 4;

QY 57 CTAGATTGTTTAAATAATTAATGGAATAGCTAGCGCGGTGGTGGTACGCGCTGAAT 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59074 CTAATTAATTAATTTCTTATAAAACTCTAAGCGCGGTGCAGTGGCTGATGCTTGTAT 59133

QY 117 CCAGCAGCTTTAGAGGTCGAGAGGGTGGATCATCTTGAGTCAAGGATTTTGAGACAG 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59134 CCAGCAGCTTTGGAGCGCGCGAGCGCGGATCCCTGAGGTCGGAG-TTTGAGACAG 59192

QY 177 CTGGCCCAACAGGTGAACCCATCTCTACTAAATAATAATAATAATTAAGTGGTGGGT 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59193 CTTGACTACATGGAGAACTCCATCTCTACTAAACACAAAATAGCT-GGGTGGT 59251

QY 237 GGTTCACAGCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCACTGAAGTCA 296
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59252 GGCACACAGCTGTAATCCAGCAGCTTTGGAGGCGCGAGCGGGTGGATTTGAGGTCA 59311

QY 297 GGAGTTCAAGCCAGCTGGGCAACATGGTGAACACAGCTCTCTACTAAATAATAACAAA 356
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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```
Db 59312 GGAGTTTGAGACCGCTGCGCAACATGAGAAACCCCTCTCTACTAAAAACACAGAA 59371
QY 357 TTAGCCAGGTGTGGTGCACACCCCTGTAGTCCAGCTACTTGGAGGCTGAGCGGGAAG 416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59372 TTAGCTGGGCGTGGTGGCAGCATGCTGTAAACCCAGCTACTCTGGAGGCTGAGCGAGAG 59431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 417 AATCGCTTGAAACCCAGTAGCAGAGTTGCGAGTGCAGTGCAGGATAGACTCACTGCACTCC 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59432 AATCGCTTGAAACCCAGTAGCAGAGTTGCGAGTGCAGTGCAGTGCAGTGCAGTGC 59490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 477 AGCCTGGGTCAGAGCAGCACTCCCTCTCAGA-AAATAATAATAATAATAATAATAATAA 535
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59491 AGCCTGGGTCAGAGTGCAGTCTCTCATAGAACAAACAAACAAACAAACAAACAA 59550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 536 AATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59551 ACAAACAAACAAACAAACAAACCCCTCTAATAAGTCTTACA 59589
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RESULT 14

```
AL590805/c
LOCUS              187990 bp      DNA      linear      HTG 21-SEP-2001
DEFINITION        Homo sapiens chromosome 13 clone RP11-550C2, *** SEQUENCING IN
                    PROGRESS ***, 8 unordered pieces.
ACCESSION          AL590805
VERSION            AL590805.6 GI:15591451
KEYWORDS           HTG: HTGS_PHASE1; HTGS_CANCELLED.
SOURCE             human.
ORGANISM           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Burton, J.
Direct Submission
Submitted (20-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Sep 12, 2001 this sequence version replaced gi:14575406.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA550C2
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 186718 bases at least Q40
Consensus quality: 186962 bases at least Q30
Consensus quality: 187136 bases at least Q20
Insert size: 187290; sum-of-contigs
Insert size: 189573; 2.4% error; agarose-fp
Quality coverage: 9.19x in Q20 bases; sum-of-contigs Quality
coverage: 9.08x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved
1 95038: contig of 95038 bp in length
* 95039 95138: gap of 100 bp
* 95139 100980: contig of 5842 bp in length
* 100981 101080: gap of 100 bp
* 101081 109127: contig of 8047 bp in length
* 109128 109227: gap of 100 bp
* 109228 112743: contig of 3516 bp in length
* 112744 112843: gap of 100 bp
```

REFERENCE

AUTHORS
TITLE
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COMMENT

* 112844 157875: contig of 45032 bp in length
 * 157876 157975: gap of 100 bp
 * 157976 171203: contig of 13228 bp in length
 * 171204 171303: gap of 100 bp
 * 171304 178816: contig of 7513 bp in length
 * 178817 178916: gap of 100 bp
 * 178917 187990: contig of 9074 bp in length.

FEATURES

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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="13"
 /clone="RP11-550C2"
 /clone_lib="RPCI-11.2"
 1. .95038
 /note="assembly_fragment:00652
 fragment_chain:1
 clone_end:T7
 vector_side:left"
 misc_feature 95139..100980
 /note="assembly_fragment:03708
 fragment_chain:1"
 101081..109127
 /note="assembly_fragment:03469
 fragment_chain:1"
 109228..112743
 /note="assembly_fragment:02579
 fragment_chain:1"
 112844..1157875
 /note="assembly_fragment:00971
 fragment_chain:1"
 157876..171203
 /note="assembly_fragment:01228
 fragment_chain:1"
 171304..178816
 /note="assembly_fragment:03498
 fragment_chain:1"
 178917..187990
 /note="assembly_fragment:02788
 fragment_chain:1
 clone_end:SP6
 vector_side:right"
 BASE COUNT 57887 a 39342 c 37957 g 52104 t 700 others
 ORIGIN
 Query Match 31.9%; Score 319; DB 2; Length 187990;
 Best Local Similarity 80.9%; Pred. No. 1.1e-72;
 Matches 420; Conservative 0; Mismatches 95; Indels 4; Gaps 4;
 QY 57 CTAGATTGTTGTAATAAATTAATGATAGCTAGGCGCGGTGGCTCAGCGCTGTAAT 116
 Db 123939 CTATTTAATTATTTCTTATAAAACTCTAAGCGCGGTGCAGTGGCTGATGCTGTAAT 123880
 QY 117 CCAGCAGCTTTAGAGGCGTGAAGAGGGTGGATCAGTTGAGGTCAGAGCTTTTGAGACCAAG 176
 Db 123879 CCAGCAGCTTTGGGAGCGCGAGCGCGGATCACCTGAGGTCGGGAG-TTTGAGACCAAG 123821
 QY 177 CTGCGCCACACGCTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTNGGTCGCGT 236
 Db 123820 CTGCTAACATGAGAAATCCATCTCTACTAAAAACACAAATAGCT-GGGTGGGT 123762
 QY 237 GGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAGCGGTGGATCACCCTGAGTCA 296
 Db 123761 GGCACACCTGTAAACCCAGCAGCTTTGGGAGCGCGGAGCGGTGGATCATTGAGGTCA 123702
 QY 297 GGAGTTCAAGGCCAGCCTGGGCAACATGTTGAACACCACTCTCTACTAAAAATACAAAAA 356
 Db 123701 GGAGTTGAGACAGCTGGCCAACTGGGAACACCCCTCTCTACTAAAAACACAAGAA 123642
 QY 357 TTAGCAGGTGTGTGGACACAGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGCGGAG 416
 Db 123641 TTAGCTGGCGGTGTGGACATGCTGTATACCCAGCTACTCTGGAGGCTGAGGCGGAG 123582

QY 417 AATCGCTGAACCCAGTAGGAGAGGTTGCAGTCAGCCGAGATAGAGTCACTGCACTCC 476
 Db 123581 AATCGCTGAACCCAGTAGGAGAGGTTGCAGTCAGTCAGTGAATGAGAT-TGCCCACTGCACTCC 123523
 QY 477 AGCCTGGGTGACAGAGCAGCACTCCCTCTCAGA-AAATAAAATAAAATAAAATAAA 535
 Db 123522 AGCCTGGGCGACAGAGTGAGACTCTCTCTCAGAAACAAACAAACAAACAA 123463
 QY 536 AATAAATAAAATAAAATAAAATTTCTAAAGGGCTGGCA 574
 Db 123462 AACAAACAAACAAACAAACAAACCTCTTAATAGTCTTACA 123424

RESULT 15

AL354795 195290 bp DNA linear PRI 08-SEP-2001
 LOCUS Human DNA sequence from clone RP11-174B4 on chromosome 9q21.2-22.1,
 DEFINITION complete sequence.
 ACCESSION AL354795
 VERSION AL354795
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 195290)
 Direct Submission
 Submitted (08-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

On May 31, 2001 this sequence version replaced gi:14132885.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw.,
 SWISSPROT; Tr: TREMBL; Wp.: WORMPEP; Information on the WORMPEP
 database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr9
 RP11-174B4 is from the library RPCI-11.1 constructed by the group
 of Pletter de Jong. For further details see
 http://www.chori.org/daopac/home.htm
 VECTOR: pBAC63.6

This sequence is the entire insert of clone RP11-174B4 The true
 right end of clone RP11-64C9 is at 58287 in this sequence.

FEATURES

source
 1. .195290
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="9"
 /map="q21.2-22.1"
 /clone="RP11-174B4"
 /clone_lib="RPCI-11.1"
 143978..144033
 misc_feature
 /note="Sequence from uni-directional dGTP big dye
 terminator reads only."
 BASE COUNT 62521 a 40135 c 37586 g 55048 t
 ORIGIN

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Query Match      31.8%; Score 318.4; DB 9; Length 195290;
Best Local Similarity 84.8%; Pred. No. 1.5e-72;
Matches 391; Conservative 0; Mismatches 67; Indels 3; Gaps 3;

QY 84 AATAGGCTAGGCGGGTGGCTCAGCGCTGTATCCGAGCACTTTAGAGGTGGAAGAGGG 143
Db 89288 ATTGGCGGGTSCAGTGGCTCAGCGCTGTATCCGAGCACTTTGGGAGGCCGAGGCGAGG 89347

QY 144 TGGATCAGTTCAGGTCAGGAGTTTGTAGACCGCTGGCCCAACACAGGTGAAACCCCATCT 203
Db 89348 TGGATCAGTTCAGGTCAGGAG-TTCGAGACCGCTGGCCCAACATGATGAACCCCGTCT 89406

QY 204 CTACTAAAAATA-AAAAATTAGCTNGGTCGCGTGGCTCAGCGCTGTATCCAGCACTT 262
Db 89407 CTACTAAAAATACAAAAATTAGGCTGGGTGCAGTGGCTCAGCGCTGTATCCGACACTT 89466

QY 263 TGGGAGGCTGAGACGGGTGGATCACCTGAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACA 322
Db 89467 TGGGAGGCCGAGGAGGTGGATCACTTGGAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACA 89526

QY 323 TGGTGAACCGCTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCT 382
Db 89527 TGGTGAACCGCTCTCTCTAAAAATACAAAAATTAGCTGGGTGTGGTGGCACACCT 89586

QY 383 GTAGTCCAGCTACTTGGGAGGCTGAGCGGGAAGATCGCTTGAACCCAGTAGGAGAGG 442
Db 89587 GTATCCAGCTACTCCGAGGCTAAGGAGGAGACTGCTTGAACCTGGGAGGAGAGG 89646

QY 443 TTGAGTGAGCGGAGATAAGAGTCACTGCAGCTCCAGCTGGGTGACAGAGCAAGACTCCC 502
Db 89647 TTGCAGTGAGCGGAGATCTCA-CCACTGCAGCTCCAGCTGGGTGACAGAGCAAGACTCTG 89705

QY 503 TCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 543
Db 89706 TCTCAAAAGAAAAAAGAAAAAAGAAAAAAGAAATGCTGATAT 89746

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Search completed: November 24, 2002, 08:57:14
Job time : 4193 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 10:24:32 ; Search time 2187 Seconds
(without alignments)
7405.344 Million cell updates/sec

Title: US-09-784-423-32

Perfect score: 1000

Sequence: 1 GGTGTGACCTTATCCTCTCT.....CAGAATGATGACGGGGTGC 1000

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_nam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	224	22.4	337	17 AQ356083	AQ356083 CITBI-El-
C 2	66	6.6	490	17 AQ378402	AQ378402 RPC111-16
C 3	62	6.2	703	17 AG089736	AG089736 Pan trogl
C 4	57	5.7	253	12 BF799037	BF799037 CM2-CI003
C 5	57	5.7	327	9 AI216151	AI216151 qm36d06.x
C 6	57	5.7	444	17 AQ284746	AQ284746 RPC111-87

7	57	5.7	455	9	AI886860
8	57	5.7	476	13	BM353489
c 9	57	5.7	558	9	AA402129
c 10	57	5.7	872	14	BQ646204
c 11	57	5.7	928	14	BQ648991
c 12	57	5.7	948	9	AL554221
c 13	57	5.7	1086	14	BM803038
c 14	55	5.5	480	10	AV718952
c 15	55	5.5	501	17	AQ020028
c 16	55	5.5	629	13	BG912932
c 17	54	5.4	479	9	AU158222
c 18	54	5.4	727	17	AG168389
c 19	54	5.4	1103	13	BM477806
c 20	53	5.3	280	17	AZ276522
c 21	53	5.3	320	9	AA552202
c 22	53	5.3	329	12	BF149427
c 23	53	5.3	351	17	AQ125843
c 24	53	5.3	352	9	AA411448
c 25	53	5.3	491	9	AA455483
c 26	53	5.3	577	10	AW973181
c 27	53	5.3	691	17	AG012178
c 28	53	5.3	693	17	AG012177
c 29	53	5.3	702	17	AG012190
c 30	53	5.3	705	17	AG012191
c 31	52	5.2	293	13	BJ396501
c 32	52	5.2	293	13	BJ396501
c 33	52	5.2	303	13	BJ396477
c 34	52	5.2	305	13	BJ394919
c 35	52	5.2	521	17	AQ350115
c 36	52	5.2	596	17	AQ376489
c 37	52	5.2	601	9	AI909139
c 38	52	5.2	617	13	BI861844
c 39	52	5.2	643	17	AZ955691
c 40	52	5.2	865	17	AQ740087
c 41	52	5.2	962	12	BE883679
c 42	51	5.1	306	10	AW795350
c 43	51	5.1	569	17	AZ342219
c 44	51	5.1	588	17	AZ118261
c 45	51	5.1	606	17	AQ932513

ALIGNMENTS

RESULT 1
AQ356083/c
LOCUS
DEFINITION
CITBI-El-2534J20.TF CITBI-El Homo sapiens genomic clone 2534J20,
DNA sequence.
ACCESSION
AQ356083
VERSION
GSS.
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens

AQ356083 337 bp DNA linear GSS 24-JAN-1999
CITBI-El-2534J20.TF CITBI-El Homo sapiens genomic clone 2534J20,
DNA sequence.

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)

Other_GSSs: CITBI-El-2534J20.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeetigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/hungen/bac_end_search.html.

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.

Map Building

Use of BAC End Sequences from CalTech Libraries for Sequence-Ready

Map Building

Unpublished (1997)

Other_GSSs: CITBI-El-2534J20.TF

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200

Fax: 301 838 0208

Email: hbeetigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/hungen/bac_end_search.html.

Seq primer: M13-21
 Class: BAC ends.
 FEATURES
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 Location/Qualifiers
 1. .337
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 /db_xref="taxon:9606"
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 /clone_lib="CITBI-E1"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 78 a 70 c 75 g 114 t
 ORIGIN

Query Match 22.4%; Score 224; DB 17; Length 337;
 Best Local Similarity 99.6%; Pred. No. 2.7e-96;
 Matches 274; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 414 AAGATCGCTGAACCCAGTAGCAGAGGTTGACGTGAGCGGAGATAAGAGTCACTGCAC 473
 DB 276 AAGATCGCTGAACCCAGTAGCAGAGGTTGACGTGAGCGGAGATAAGAGTCACTGCAC 217
 QY 474 TCCAGCTGGGTGACAGAGCAAGACTCCCTCTCAGAGAAATAAAATAAAATAAAAT 533
 DB 216 TCCAGCTGGGTGACAGAGCAAGACTCCCTCTCAGAGAAATAAAATAAAATAAAAT 157
 QY 534 AAATAAAATAAAATAAAATAAAATCTAAAGGGCTGGCATTTGCCGTAGCACTATATG 593
 DB 156 AAATAAAATAAAATAAAATAAAATCTAAAGGGCTGGCATTTGCCGTAGCACTATATG 97
 QY 594 CCATAAGTAATAGCTATCAATATCCGCCCTACCTGCTGTGAAATTTAGTTCT 653
 DB 96 CCCAATAAGTAATAGCTATCAATATCCGCCCTACCTGCTGTGAAATTTAGTTCT 37
 QY 654 TTTTGTACCCGCCATTAGACTTAAGCGAGATTC 688
 DB 36 TTTTGTACCCGCCATTAGACTTAAGCGAGATTC 2

RESULT 2
 LOCUS AQ378402 490 bp DNA linear GSS 20-MAY-1999
 DEFINITION RPI11-164C12-TV RPI-11 Homo sapiens genomic clone RPI-11-164C12,
 DNA sequence.
 ACCESSION AQ378402
 VERSION AQ378402.1 GI:4349425
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 ,J.C.
 TITLE Use of BAC End Sequences from Library RPI-11 for Sequence-Ready
 Map Building
 JOURNAL Map Building
 COMMENT Unpublished (1997)
 Other_GSSs: RPI11-164C12.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are derived from the human BAC library RPI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@jg.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: T7

Class: BAC ends.
 Location/Qualifiers
 1. .490
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 /db_xref="GDB:7562651"
 /db_xref="taxon:9606"
 /clone="RPCI-11-164C12"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACE3 6; Site_1: EcoRI; Site_2: EcoRI;
 RPI11 Human Male BAC Library"
 BASE COUNT 164 a 111 c 112 g 103 t
 ORIGIN

Query Match 6.6%; Score 66; DB 17; Length 490;
 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 346 AAATACAAAATATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGTACTTGGAGGC 405
 DB 325 AAATACAAAATATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGTACTTGGAGGC 384
 QY 406 TGAGGC 411
 DB 385 TGAGGC 390

RESULT 3
 AG089736/c 703 bp DNA linear GSS 03-NOV-2001
 LOCUS Pan troglodytes DNA, clone: PTB-089B08.R, genomic survey sequence.
 DEFINITION AG089736
 ACCESSION AG089736.1 GI:16641538
 VERSION AG089736.1
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 BAC Library clone:PTB-089B08.R.

ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pan.
 REFERENCE
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of Library PTB
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 703)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission

JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS

Sequencing: M13Rev

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1. .703

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="PTB-089B08.R"

/sex="male"

/cell_type="lymphoblast"

/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT

ORIGIN

164 a 164 c 165 g 209 t

1 others

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Query Match          6.2%; Score 62; DB 17; Length 703;
Best Local Similarity 100.0%; Pred. No. 9.7e-19;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGGTGGCACACGCCCTGTAGTCCAGCTA 395
      |||||||
Db 494 TCTCTACTAAATAACAAAAATTAGCCAGGTGGTGGCACACGCCCTGTAGTCCAGCTA 435

QY 396 CT 397
      ||
Db 434 CT 433

RESULT 4
BF799037
LOCUS CM2-CI0031-051000-409-d04 CI0031 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF799037
VERSION BF799037.1 GI:12128026
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-CI0031-
051000-409-d04&t3=2000-10-05&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 253.
FEATURES
source
Location/Qualifiers
1..253
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CI0031"
/dev_stage="Adult"
/note="Organ: colon.ins; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 61 a 69 c 68 g 54 t 1 others
ORIGIN

Query Match          5.7%; Score 57; DB 12; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCGTGGCCACACGGTGAAACCCCATCTCTACTAAATAAAAAATTAGC 225
      |||||||
Db 169 GAGACAGCGTGGCCACACGGTGAAACCCCATCTCTACTAAATAAAAAATTAGC 225

RESULT 6
AQ284746/c
LOCUS AQ284746
DEFINITION RPC111-8705-TV RPC1-11 Homo sapiens genomic clone RPC1-11-8705, DNA
sequence.
ACCESSION AQ284746
VERSION AQ284746.1 GI:3910986
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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```

Db 145 GAGACAGCGTGGCCACACGGTGAAACCCCATCTCTACTAAATAAAAAATTAGC 201

RESULT 5
AI216151/c
LOCUS AI216151
DEFINITION qm36d06.x1 NCI-CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1883915 3'
similar to contains Alu repetitive element;contains element L1
repetitive element ;, mRNA sequence.
ACCESSION AI216151
VERSION AI216151.1 GI:3785192
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 296.
FEATURES
source
Location/Qualifiers
1..327
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1883915"
/clone_lib="NCI-CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: lung; Vector: pVT3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from a
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pVT3 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 62 a 93 c 84 g 88 t
ORIGIN

Query Match          5.7%; Score 57; DB 9; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCGTGGCCACACGGTGAAACCCCATCTCTACTAAATAAAAAATTAGC 225
      |||||||
Db 207 GAGACAGCGTGGCCACACGGTGAAACCCCATCTCTACTAAATAAAAAATTAGC 151

RESULT 6
AQ284746/c
LOCUS AQ284746
DEFINITION RPC111-8705-TV RPC1-11 Homo sapiens genomic clone RPC1-11-8705, DNA
sequence.
ACCESSION AQ284746
VERSION AQ284746.1 GI:3910986
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
ADAMS
1 (bases 1 to 444)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P., and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES

source
1. .444
/organism="Homo sapiens"
/db_xref="GDB:7533364"
/db_xref="taxon:9606"
/clone="RPCI-11-8705"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"

BASE COUNT 93 a 97 c 90 g 164 t
ORIGIN

Query Match 5.7%; Score 57; DB 17; Length 444;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 GAGACCAGCTGGCCACACGGTGAAACCCATCTCTACTATAAAATAAAATTAGC 225
Db 60 GAGACCAGCTGGCCACACGGTGAAACCCATCTCTACTATAAAATAAAATTAGC 4

RESULT 7
AI886860
LOCUS AI886860 465 bp mRNA linear EST 21-DEC-1999
DEFINITION wk29e07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413764 3',
similar to contains Alu repetitive element;; mRNA sequence.
ACCESSION AI886860
VERSION AI886860.1 GI:5592024
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 465)
AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
UNPUBLISHED (1998)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1260 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 449.
FEATURES
source
1. .465
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2413764"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGGACGCCCATGAGTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

BASE COUNT 142 a 112 c 99 g 112 t
ORIGIN

Query Match 5.7%; Score 57; DB 9; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.5e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 GAGACCAGCTGGCCACACGGTGAAACCCATCTCTACTATAAAATAAAATTAGC 225
Db 269 GAGACCAGCTGGCCACACGGTGAAACCCATCTCTACTATAAAATAAAATTAGC 325

RESULT 8
BM353489/c
LOCUS BM353489 476 bp mRNA linear EST 07-JAN-2002
DEFINITION I959g11.x1 HR85 islet Homo sapiens cDNA 3', mRNA sequence.
ACCESSION BM353489
VERSION BM353489.1 GI:18085847
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 476)
AUTHORS Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, J., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y., and Bowers, Y.
UNPUBLISHED (2000)
CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu

LIBRARY was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 451.
FEATURES
source
1. .476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HR85 islet"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:

NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size -1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-747-1916, Fax: 314-747-2692.*

BASE COUNT 110 a 108 c 109 g 150 t

ORIGIN

Query Match 5.7%; Score 57; DB 13; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 225
 |||||
 Db 209 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 153

RESULT 9
 AA402129/c
 LOCUS
 DEFINITION
 2u55a08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
 IMAGE:741878 5' similar to contains Alu repetitive element; contains
 element PRT5 repetitive element ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens

REFERENCE
 AUTHORS
 Hillier, L., Allen, M., Bowles, L., Dubaque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin
 J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
 White, Y., Wylie, T., Waterston, R. and Willson, R.
 WashU-NCI Human EST Project
 Unpublished (1997)
 Contact: Willson RK

TITLE
 JOURNAL
 COMMENT
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 641 Std Error: 0.00
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 483.

FEATURES
 source
 1. 558
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="GDB:5942115"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:741878"
 /sex="Female"
 /tissue_type="ovarian tumor"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: ovary; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCACATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library constructed by Bento Soares and
 M.Fatima Bonaldo."

BASE COUNT 130 a 118 c 122 g 188 t

ORIGIN

Query Match 5.7%; Score 57; DB 9; Length 558;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 225
 |||||
 Db 286 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 230

RESULT 10
 BQ646204/c
 LOCUS
 DEFINITION
 AGENCOURT_8287874 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6297925
 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: Agencourt Bioscience Corporation
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

FEATURES
 source
 1. 872
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="IMAGE:6297925"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 190 a 195 c 222 g 265 t

ORIGIN

Query Match 5.7%; Score 57; DB 14; Length 872;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 225
 |||||
 Db 677 GAGACCGCTGGCCACACACCGGTGAACCCCATCTCTACTATAAAATAAAAAATTAGC 621

RESULT 11
 BQ648991/c
 LOCUS
 DEFINITION
 AGENCOURT_8418892 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6284304
 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 EST.

```

SOURCE
ORGANISM      human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: CGAP (Stanford)
              cDNA Library Preparation: Rubin Laboratory
              DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1CM2481 row: 1 column: 01
              High quality sequence stop: 575.
FEATURES
source
1. .928
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:6284304"
   /clone_lib="NIH_MGC_100"
   /tissue_type="hepatocellular carcinoma, cell line"
   /lab_host="DH10B (phage-resistant)"
   /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
   EcoRI; cDNA made by oligo-dT priming. Directionally cloned
   into EcoRI/XhoI sites using the following 5' adaptor:
   GGCACGAG(G). Size-selected >500bp for average insert size
   1.8kb. Library constructed by Ling Hong in the laboratory
   of Gerald M. Rubin (University of California, Berkeley)
   using ZAP-cDNA synthesis kit (Stratagene) and Superscript
   II RT (Life Technologies). Note: this is a NIH_MGC
   Library."
BASE COUNT    212 a 217 c 230 g 269 t
ORIGIN
Query Match      5.7%; Score 57; DB 14; Length 928;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 GAGACACCTGGCCACACGGTGAAACCCCATCTCTACTTAAATAAAAAATTAGC 225
|||||
Db 678 GAGACACCTGGCCACACGGTGAAACCCCATCTCTACTTAAATAAAAAATTAGC 622
|||||

RESULT 12
AL554221
LOCUS          AL554221 LTI_NFL006_PL2 948 bp mRNA linear EST 16-FEB-2001
DEFINITION    prime, mRNA sequence.
ACCESSION     AL554221
VERSION       AL554221.1 GI:12894792
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT       Contact: Genoscope
              Genoscope - Centre National de Sequencage
              BP 191 91006 Evry cedex - France
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1. .948
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="CSODI082YG14"

us-09-784-423-32.oligo.rst
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT    284 a 231 c 210 g 214 t
ORIGIN
Query Match      5.7%; Score 57; DB 9; Length 948;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 GAGACACCTGGCCACACGGTGAAACCCCATCTCTACTTAAATAAAAAATTAGC 225
|||||
Db 206 GAGACACCTGGCCACACGGTGAAACCCCATCTCTACTTAAATAAAAAATTAGC 262
|||||

RESULT 13
BM803038/c
LOCUS          BM803038 1086 bp mRNA linear EST 05-MAR-2002
DEFINITION    AGENCOURT_6457358 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5560474
              5', mRNA sequence.
ACCESSION     BM803038
VERSION       BM803038.1 GI:19119861
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS      NIH-MGC http://mgs.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: ATCC
              cDNA Library Preparation: Life Technologies, Inc.
              DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: L1AM12286 row: 1 column: 11
              High quality sequence stop: 606.
FEATURES
source
1. .1086
   /organism="Homo sapiens"
   /db_xref="taxon:9606"
   /clone="IMAGE:5560474"
   /clone_lib="NIH_MGC_88"
   /tissue_type="duodenal adenocarcinoma, cell line"
   /lab_host="PH10B (phage-resistant)"
   /note="Organ: small intestine; Vector: pCMV-SPORT6;
   Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
   oligo-dT primed. Average insert size 1.767 kb. Library
   enriched for full-length clones and constructed by Life
   Technologies. Note: this is a NIH_MGC Library."
BASE COUNT    203 a 328 c 234 g 321 t
ORIGIN
Query Match      5.7%; Score 57; DB 14; Length 1086;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 GAGACACCTGGCCACACGGTGAAACCCCATCTCTACTTAAATAAAAAATTAGC 225
|||||

```

Db 627 GAGACCGCTGGCCAAACACGGTGAAACCCCTCTCTACTATAAAATAGG 571

RESULT 14
AV718952/c

LOCUS

AV718952 480 bp mRNA linear EST 16-OCT-2000
DEFINITION AV718952 GLC Homo sapiens cDNA clone GLCPC02 5', mRNA sequence.

ACCESSION

AV718952

VERSION

AV718952.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 480)

Qian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,H.,

Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Zeng,L.,

Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang

,Y., Gu,Y., Chen,Z., and Han,Z.

Homo sapiens cDNA GLC clones

Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

1, 480

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="GLCPC02"

/clone_lib="GLC"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT

107 a 127 c 106 g 140 t

ORIGIN

Query Match

Best Local Similarity 5.5%; Score 55; DB 10; Length 480;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 GCGTGGCTCACACCTGTAATCCAGCACTTGGAGGCTGAGACGGTGGATCA 286

|||||

Db 265 GCGTGGCTCACACCTGTAATCCAGCACTTGGAGGCTGAGACGGTGGATCA 211

|||||

RESULT 15

AQ020028/c

LOCUS

AQ020028 501 bp DNA linear GSS 09-JUN-1998

DEFINITION

CIT-HSP-2312P17.TR CIT-HSP Homo sapiens genomic clone 2312P17, DNA

sequence.

ACCESSION

AQ020028

VERSION

AQ020028.1

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 501)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

Unpublished (1998)

Other GSSs: CIT-HSP-2312P17.TF

CONTACT: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES

source

1, 501

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="2312P17"

/clone_lib="CIT-HSP"

/sex="Male"

/cell_type="Sperm"

/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:

HindIII"

BASE COUNT

117 a 124 c 109 g 151 t

ORIGIN

Query Match

Best Local Similarity 5.5%; Score 55; DB 17; Length 501;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 355 AATTAGCCAGGTGGTGGCACACCGCTGTAGTCCAGCTACTTGGGAGGCTGAG 409

|||||

Db 95 AATTAGCCAGGTGGTGGCACACCGCTGTAGTCCAGCTACTTGGGAGGCTGAG 41

|||||

RESULT 16

BG912932

LOCUS

BG912932 629 bp mRNA linear EST 05-JUN-2001

DEFINITION

602807332F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939639

5', mRNA sequence.

ACCESSION

BG912932

VERSION

BG912932.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 629)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10876 row: p column: 08

High quality sequence stop: 627.

FEATURES

source

1, 629

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4939639"

/clone_lib="NCI_CGAP_Brn67"

/tissue_type="anaplastic oligodendroglioma with lp/19q

loss"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.3 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

```

BASE COUNT      189 a   133 c   150 g   156 t   1 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 55; DB 13; Length 629;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 TACTAAATAACAAAATACCCAGGTGGTGGCAGACGCGCTGTAGTCCAGCT 394
      |||||||
Db 447 TACTAAATAACAAAATACCCAGGTGGTGGCAGACGCGCTGTAGTCCAGCT 501
      |||||||

RESULT 17
AUI58222/c
LOCUS
DEFINITION AUI58222 PLACE1 Homo sapiens cDNA clone PLACE1011576 3', mRNA
sequence.
ACCESSION AUI58222
VERSION AUI58222.1 GI:11019743
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 479)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,
Yamamoto.J., Wakamatsu.A., Ozawa.M., Nakamura.Y., Nagai.T., Sugano
.S. and Isogai.T.Y.
HRI human cDNA project (Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S.,
Saito.K., Kawai.Y., Yamamoto.J., Wakamatsu.A., Ozawa.M., Nakamura
.Y., Nagai.T., Sugano.S., Isogai.T.Y.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="PLACE1"
/tissue_type="placenta"
/note="Vector: PME18SFL3"
BASE COUNT      108 a   120 c   99 g   143 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 54; DB 9; Length 479;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGTGCGGTGCTACACCTGAATCCAGCACTTTGGAGCGCTGAGACGGGTG 281
      |||||||
Db 280 GGTGCGGTGCTACACCTGAATCCAGCACTTTGGAGCGCTGAGACGGGTG 227
      |||||||

RESULT 18
AG168389
LOCUS
DEFINITION AG168389 Pan troglodytes DNA, clone: RP43-036L23.T7, genomic survey
sequence.
ACCESSION AG168389
VERSION AG168389.1 GI:16698067
KEYWORDS GSS.
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-036L23.T7.

ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama.A., Hattori.M., Toyoda.A., Taylor.T.D., Yada.T.,
Totoki.Y., Watanabe.H. and Sakaki.Y.
BAC end sequences of Library RPCI-43
Unpublished
2 (bases 1 to 727)
Fujiyama.A., Hattori.M., Toyoda.A., Taylor.T.D., Yada.T.,
Totoki.Y., Watanabe.H. and Sakaki.Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpsgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the Rad process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..727
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-036L23.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT      258 a   167 c   150 g   150 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 54; DB 17; Length 727;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 AAAAATCAAAAATTAGCCAGGTGGTGGCAGCGCTGTAGTCCAGCTACT 397
      |||||||
Db 241 AAAAATCAAAAATTAGCCAGGTGGTGGCAGCGCTGTAGTCCAGCTACT 294
      |||||||

RESULT 19
BM477806/c
LOCUS
DEFINITION BM477806 1103 bp mRNA linear EST 05-FEB-2002
5', mRNA sequence.
ACCESSION BM477806
VERSION BM477806.1 GI:18526848
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1103)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12274 row: k column: 22
High quality sequence stop: 636.

```


modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT 117 a 76 c 70 g 89 t
ORIGIN

Query Match 5.3%; Score 53; DB 9; Length 352;
Best Local Similarity 100.0%; Pred. No. 2.le-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCCTGGCCACACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 221
|||||
Db 274 GAGACAGCCTGGCCACACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 326
|||||

RESULT 25
AA455483 491 bp mRNA linear EST 06-JUN-1997
LOCUS
DEFINITION
xx76g06.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:809722 3' similar to contains Alu repetitive element; , mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Willson RK

TITLE
JOURNAL
COMMENT
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 417.
Location/Qualifiers
1. .491

/organism="Homo sapiens"
/db_xref="GDB:6039414"
/db_xref="taxon:9606"
/clone="IMAGE:809722"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

BASE COUNT
ORIGIN

Query Match 5.3%; Score 53; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 2.le-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 221
|||||
Db 274 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 326
|||||

BASE COUNT 165 a 111 c 108 g 107 t
ORIGIN

Query Match

5.3%; Score 53; DB 9; Length 491;

Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 221
|||||
Db 267 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAAATAAAAAAT 319
|||||

RESULT 26
AW973181/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

EST385279 WAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.
AW973181
AW973181.1 GI:8163027
human.

REFERENCE
AUTHORS
Hedge,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@tigr.org
Plate: 315
Seq primer: Forward.

TITLE
JOURNAL
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@tigr.org
Plate: 315
Seq primer: Forward.

FEATURES
source
1. .577
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="WAGE resequences, MAGM"
/note="Vector: pBluescriptSkm"

BASE COUNT 146 a 148 c 125 g 158 t
ORIGIN

Query Match 5.3%; Score 53; DB 10; Length 577;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 ATGTGTGAACACGCTCTCTACTATAAAATACAAAATAGCCAGGTGTGTGGC 374
|||||
Db 305 ATGTGTGAACACGCTCTCTACTATAAAATACAAAATAGCCAGGTGTGTGGC 253
|||||

RESULT 27
AG012178/c

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Homo sapiens genomic DNA, 21q region, clone: T1957BG11, genomic survey sequence.
AG012178 AG005159
AG012178.1 GI:3410839
GSS.
Homo sapiens DNA, clone:T1957BG11.
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
Published Only in Database (1998)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
Submitted (09-AUG-1998) Masahira Hattori, Kitasato University,
Department of Science, JST Sequencing Laboratory, Kitasato 1-15-1,

Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp,
Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2865117.
AG005159: Submitted (10-Feb-1998).

FEATURES
source
1. .691
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="T1957BG11"

BASE COUNT 170 a 160 c 150 g 209 t 2 others
ORIGIN

Query Match 5.3%; Score 53; DB 17; Length 691;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 287
|||||
Db 384 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 332
|||||

RESULT 28
AG012177/c

LOCUS AG012177 693 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T1957BG11, genomic survey sequence.
ACCESSION AG012177 AG005158
VERSION AG012177.1 GI:3410838
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone: T1957BG11.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
1 (bases 1 to 693)
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
2 (bases 1 to 693)
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato I-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2865116.
AG005158: Submitted (10-Feb-1998).

FEATURES
source
1. .693
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="T1957BG11"

BASE COUNT 199 a 166 c 144 g 179 t 5 others
ORIGIN

Query Match 5.3%; Score 53; DB 17; Length 693;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 287
|||||
Db 275 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 223
|||||

RESULT 29
AG012190

LOCUS AG012190 702 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T1957BG11, genomic survey sequence.
ACCESSION AG012190 AG005171

AG012190.1 GI:3410851

VERSION GSS.
KEYWORDS Homo sapiens DNA, clone: T1957BG11.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
1 (bases 1 to 702)
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
2 (bases 1 to 702)
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato I-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2865127.
AG005171: Submitted (10-Feb-1998).

FEATURES
source
1. 702
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="T1957BG11"

BASE COUNT 239 a 150 c 163 g 146 t 4 others
ORIGIN

Query Match 5.3%; Score 53; DB 17; Length 702;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 287
|||||
Db 86 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCAC 138
|||||

RESULT 30
AG012191

LOCUS AG012191 705 bp DNA linear GSS 14-APR-1999
DEFINITION Homo sapiens genomic DNA, 21q region, clone: T1957BG11, genomic survey sequence.
ACCESSION AG012191 AG005172
VERSION AG012191.1 GI:3410852
KEYWORDS GSS.
SOURCE Homo sapiens DNA, clone: T1957BG11.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
1 (bases 1 to 705)
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
2 (bases 1 to 705)
TITLE Direct Submission
JOURNAL Submitted (09-AUG-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato I-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2865128.
AG005172: Submitted (10-Feb-1998).

FEATURES
source
1. 705
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="T1957BG11"

BASE COUNT 217 a 143 c 172 g 166 t 7 others
ORIGIN

Query Match 5.3%; Score 53; DB 17; Length 705;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACCTGTATCCAGACATTTGGAGGCTGAGACGGGTGATC 287
|||||
Db 342 GTGGCTCACCTGTATCCAGACATTTGGAGGCTGAGACGGGTGATC 394
|||||

RESULT 31
BJ339324

LOCUS 293 bp mRNA linear EST 07-MAR-2002
DEFINITION BJ339324 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda64n19 5', mRNA sequence.

ACCESSION BJ339324
VERSION BJ339324.1 GI:19247686
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 293)
AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE Full length cDNA of Dictyostelium discoideum at the aggregation
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..293
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
/dev_stage="Aggregation stage"
BASE COUNT 177 a 14 c 18 g 84 t
ORIGIN

Query Match 5.2%; Score 52; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.4e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 66 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 117
|||||

RESULT 32
BJ396501

LOCUS 293 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ396501 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds42102 5', mRNA sequence.

ACCESSION BJ396501
VERSION BJ396501.1 GI:19307587
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 293)
AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856

Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..293
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
/sex="mat A"
/dev_stage="Slug stage"
BASE COUNT 177 a 14 c 18 g 84 t
ORIGIN

Query Match 5.2%; Score 52; DB 13; Length 293;
Best Local Similarity 100.0%; Pred. No. 6.4e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 66 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 117
|||||

RESULT 33
BJ366477

LOCUS 303 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ366477 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc39102 5', mRNA sequence.

ACCESSION BJ366477
VERSION BJ366477.1 GI:19275779
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE 1 (bases 1 to 303)
AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
source
1..303
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone_lib="Dictyostelium discoideum cDNA library, CF"
/sex="mat A"
/dev_stage="Culmination stage"
BASE COUNT 179 a 14 c 19 g 91 t
ORIGIN

Query Match 5.2%; Score 52; DB 13; Length 303;
Best Local Similarity 100.0%; Pred. No. 6.4e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 76 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 127
|||||

RESULT 34
BJ394919

LOCUS 305 bp mRNA linear EST 08-MAR-2002
DEFINITION BJ394919 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds37b01 5', mRNA sequence.

ACCESSION BJ394919

VERSION BJ394919.1 GI:19306005
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum.
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 REFERENCE 1 (bases 1 to 305)
 AUTHORS Urushibara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
 TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source
 1..305
 /organism="Dictyostelium discoideum"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone_lib="Dictyostelium discoideum cDNA library, SF"
 /sex="mat A"
 /dev_stage="Slug stage"
 BASE COUNT 180 a 14 c 19 g 92 t
 ORIGIN

Query Match 5.2%; Score 52; DB 13; Length 305;
 Best Local Similarity 100.0%; Pred. No. 6.4e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 78 AGAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 129

RESULT 35
 AQ350115 521 bp DNA linear GSS 07-MAY-1999
 LOCUS RPC111-110C18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-110C18,
 DEFINITION DNA sequence.
 ACCESSION AQ350115
 VERSION AQ350115.1 GI:4177450
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 JOURNAL Map Building
 COMMENT Unpublished (1997)

Other_GSSs: RPC111-110C18.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208

Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..521

/organism="Homo sapiens"
 /db_xref="GDB:7541921"
 /db_xref="taxon:9606"
 /clone="RPCI-11-110C18"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPC111 Human Male BAC Library"
 BASE COUNT 206 a 103 c 97 g 115 t
 ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 521;
 Best Local Similarity 100.0%; Pred. No. 6.1e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGCTCTACTATAAAATACAAAATAGCCAGGTGTGGTGGCACACGCTGTA 385
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 392 CGCTCTACTATAAAATACAAAATAGCCAGGTGTGGTGGCACACGCTGTA 443

RESULT 36
 AQ376489/c 596 bp DNA linear GSS 20-MAY-1999
 LOCUS RPC111-149C17.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-149C17,
 DEFINITION DNA sequence.
 ACCESSION AQ376489
 VERSION AQ376489.1 GI:4347512
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 596)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
 J.C.
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
 JOURNAL Map Building
 COMMENT Unpublished (1997)

Other_GSSs: RPC111-149C17.TV
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
 Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..596
 /organism="Homo sapiens"
 /db_xref="GDB:7556896"
 /db_xref="taxon:9606"
 /clone="RPCI-11-149C17"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPC111 Human Male BAC Library"
 BASE COUNT 177 a 88 c 71 g 260 t
 ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 596;
 Best Local Similarity 100.0%; Pred. No. 6e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Insert Length: 10000 Std Error: 0.00

Plate: 0221 row: F column: 23

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 643.

Location/Qualifiers

1. .643

source

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0221F23"

/clone_lib="Mouse 10kb plasmid UUGC2M library"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 218 a 101 c 120 g 204 t

ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 643;

Best Local Similarity 100.0%; Pred. No. 6e-14;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTCCT 561

Db 435 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTCCT 384

RESULT 40

AQ740087

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

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401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

cloning, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1079 row: O column: 18

Seq primer: T7

Class: BAC ends

High quality sequence stop: 865.

Location/Qualifiers

1. .865

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-1079 Col-18 Row=O"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="Male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 336 a 178 c 153 g 198 t

ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 865;

Best Local Similarity 100.0%; Pred. No. 5.8e-14;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 385

Db 411 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 462

RESULT 41

BE883679

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

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BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1079 row: O column: 18

Seq primer: T7

Class: BAC ends

High quality sequence stop: 865.

Location/Qualifiers

1. .865

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-1079 Col-18 Row=O"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="Male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 336 a 178 c 153 g 198 t

ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 865;

Best Local Similarity 100.0%; Pred. No. 5.8e-14;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 385

Db 411 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 462

RESULT 41

BE883679

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

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(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1079 row: O column: 18

Seq primer: T7

Class: BAC ends

High quality sequence stop: 865.

Location/Qualifiers

1. .865

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-1079 Col-18 Row=O"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="Male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 336 a 178 c 153 g 198 t

ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 865;

Best Local Similarity 100.0%; Pred. No. 5.8e-14;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 385

Db 411 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 462

RESULT 41

BE883679

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

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Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

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(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)

or from Research Genetics (info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1079 row: O column: 18

Seq primer: T7

Class: BAC ends

High quality sequence stop: 865.

Location/Qualifiers

1. .865

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate-1079 Col-18 Row=O"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="Male"

/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methyase. Size selected DNA was cloned into the pBACE3.6 vector at EcoRI sites"

BASE COUNT 336 a 178 c 153 g 198 t

ORIGIN

Query Match 5.2%; Score 52; DB 17; Length 865;

Best Local Similarity 100.0%; Pred. No. 5.8e-14;

Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 385

Db 411 CGCTCTACTAAAATACAAAATAGCCAGGTGGTGGGCACGCTGTA 462

RESULT 41

BE883679

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA

Query Match 5.2%; Score 52; DB 12; Length 962;
 Best Local Similarity 100.0%; Pred. No. 5.8e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 GCTCTACTTAAATACAAAATTAGCCAGGTGGTGGGACACGCCTGTGA 385
 |||||||
 Db 124 GCTCTACTTAAATACAAAATTAGCCAGGTGGTGGGACACGCCTGTGA 175

RESULT 42
 AW795350/c

LOCUS AW795350 306 bp mRNA linear EST 16-MAY-2000
 DEFINITION PM0-UM0018-130500-003-g05 UM0018 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW795350
 VERSION AW795350.1 GI:7847220

KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 306)

REFERENCE

AUTHORS
 Dias Neto,E., Garcia Correa,R., Verjovsky-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Garvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Bruenstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

COMMENT

Contact: Simpson A.J.G.
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=622=PM0-UM0018-130

500-003-g054t3-2000-05-13&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 306.

FEATURES

source

Location/Qualifiers

1..306

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="UM0018"

/dev_stage="Adult"

/note="Organ: uterus; Vector: puc18; Site:1; SmaI; Site:2;

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 70 a 65 c 74 g 97 t

ORIGIN

Query Match 5.1%; Score 51; DB 10; Length 306;

Best Local Similarity 100.0%; Pred. No. 1.9e-13;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAATAAAAA 219

|||||

Db 89 GAGACAGCCTGGCCACACGGTGAACCCCATCTCTACTATAAATAAAAA 39

RESULT 43

AZ342219

LOCUS AZ342219 569 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0075K08F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
 clone UUGCLM0075K08 F, DNA sequence.

ACCESSION AZ342219

VERSION AZ342219.1 GI:10419239

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 569)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0075 row: K column: 08

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 569.

FEATURES

Location/Qualifiers

1..569

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCLM0075K08"

/clone_lib="Mouse 10kb plasmid UUGCLM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (gll47321141gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT 202 a 120 c 90 g 157 t

ORIGIN

Query Match 5.1%; Score 51; DB 17; Length 569;

Best Local Similarity 100.0%; Pred. No. 1.8e-13;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558

|||||

Db 233 GAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 283

RESULT 44

AZ118261/c

LOCUS
DEFINITION RPCI-23-450D11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-450D11
DNA sequence.
ACCESSION A2118261
VERSION A2118261.1 GI:7782025
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 588)
AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.

TITLE Mouse BAC End Sequences from Library RPCI-23

JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-450D11.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 450 row: D column: 11
Seq primer: SP6
Class: BAC ends

FEATURES
source Location/Qualifiers
1..588
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-450D11"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 158 a 118 c 107 g 205 t
ORIGIN

Query Match 5.1%; Score 51; DB 17; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATT 559
|||||
Db 472 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATT 422

RESULT 45
A0932513/c
LOCUS A0932513
DEFINITION RPCI-23-286D16.TJ RPCI-23 Mus musculus genomic clone RPCI-23-286D16
DNA sequence.
ACCESSION A0932513
VERSION A0932513.1 GI:6621527
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS

1 (bases 1 to 606)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P., and Fraser, C.M.

TITLE
JOURNAL
COMMENT

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 286 row: D column: 16
Seq primer: SP6
Class: BAC ends

FEATURES
source Location/Qualifiers

1..606
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-286D16"
/clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT
ORIGIN

167 a 123 c 116 g 199 t 1 others
Query Match 5.1%; Score 51; DB 17; Length 606;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATT 559
|||||
Db 461 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATT 411

Search completed: November 24, 2002, 12:00:49
Job time : 2204 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 09:16:57 ; Search time 293 Seconds
(without alignments)
7686.001 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGTGACCTTATCCTCTCT.....CAGAATGATGACGGCGTGC 1000

Scoring table: OLIGO_NUC
Gapop 60.0 , capext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
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21: /SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Length	ID	Description
1	1000	100.0	1000	20	AA227732 Human DNA marker c
2	72	7.2	52616	22	AAK70459 Human immune/haema
3	72	7.2	52616	22	AAK78930 Human immune/haema
4	58	5.8	11627	22	AAI07363 Human reproductive
5	58	5.8	11627	23	AB198832 Human testicular a
6	57	5.7	29329	22	ABA18026 Human nervous syst
7	57	5.7	29329	22	ABA20511 Human nervous syst
8	57	5.7	29329	22	AAK70791 Human immune/haema
9	57	5.7	29329	22	AAK78512 Human immune/haema

c	10	56	5.6	122888	24	ABK83569	Human cDNA differe
c	11	55	5.5	476	22	AAF65641	Novel human polynu
c	12	54	5.4	479	22	AAH13151	Human cDNA clone (
c	13	54	5.4	593	24	ABO89372	Human prostate exp
c	14	54	5.4	2298	22	AAH16608	Human cDNA sequenc
c	15	53	5.3	307	22	AA832680	Human genomic DNA
c	16	53	5.3	642	22	AA844882	Human full-length
c	17	52	5.2	700	22	AAH92081	Human inflammatory
c	18	52	5.2	700	22	AAH92081	Human inflammatory
c	19	52	5.2	2701	22	AAI37013	Human musculoskele
c	20	52	5.2	5533	22	AAK74315	Human immune/haema
c	21	52	5.2	5533	22	AAK74317	Human immune/haema
c	22	52	5.2	5536	22	AAK74316	Human immune/haema
c	23	52	5.2	5537	22	AAK74318	Human immune/haema
c	24	52	5.2	12244	22	AAK69991	Human digestive sy
c	25	52	5.2	12392	22	ABA15896	Human nervous syst
c	26	52	5.2	1503900	22	AAK95240	Human neuregulin-1
c	27	52	5.2	1503900	22	AAK95240	Human neuregulin-1
c	28	51	5.1	6523	24	ABN80120	Human chemically m
c	29	51	5.1	43411	24	ABQ88169	Human osteoblast d
c	30	51	5.1	227968	24	ABK83497	Human cDNA differe
c	31	50	5.0	276	22	AA836586	Human cardiovascular
c	32	50	5.0	276	22	AAK75295	Human immune/haema
c	33	50	5.0	276	22	AAK75296	Human immune/haema
c	34	50	5.0	475	23	ABV54360	Human prostate exp
c	35	50	5.0	578	23	ABV55359	Human prostate exp
c	36	50	5.0	737	22	AAI94916	Human neuroblastom
c	37	50	5.0	4243	22	ABA16762	Human nervous syst
c	38	50	5.0	5283	22	AAK74563	Human immune/haema
c	39	50	5.0	5572	22	AAK74320	Human immune/haema
c	40	50	5.0	5573	22	AAK74321	Human immune/haema
c	41	50	5.0	5649	22	AA846383	Tumour suppressor
c	42	50	5.0	5649	22	AA846384	Tumour suppressor
c	43	50	5.0	5649	24	ABK40007	Human chemically p
c	44	50	5.0	5649	24	ABK40008	Human chemically p
c	45	50	5.0	5649	24	ABL32848	Human immune syste

ALIGNMENTS

RESULT 1
AA227732
ID AA227732 standard; DNA; 1000 BP.
XX AC AA227732;
XX DT 23-DEC-1999 (first entry)
XX DE Human DNA marker clone S132.
XX KW Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
KW ITR sequence; pentanucleotide tandem repeat; stutter artifact;
KW DNA typing; DNA profiling; linkage analysis; criminal justice;
KW paternity testing; animal lineage analysis; microsatellite loci;
KW polymorphism detection; ds.
XX OS Homo sapiens.
XX PN W09940194-A1.
XX PD 12-AUG-1999.
XX PF 04-FEB-1999; 99WO-US02345.
XX PR 04-FEB-1998; 98US-0018584.
XX PA (PROM-) PROMEGA CORP.
XX PI Schumm JW, Bacher JW;
XX DR WPI; 1999-590695/50.

PT Isolating DNA containing intermediate tandem repeat sequences, useful
 PS in DNA profiling
 XX Claim 22; Page 78; 111pp; English.

CC This sequence represents a human DNA marker clone used in the method of
 CC the invention. The method is for isolating a fragment of DNA containing
 CC an intermediate tandem repeat (ITR) sequence using hybridization
 CC selection, and comprises: (a) providing several DNA fragments, at least
 CC one of which contains an ITR sequence, a region of the DNA fragment which
 CC contains at least one repeat unit consisting of a sequence of five, six
 CC or seven bases repeated in tandem at least two times; (b) providing a
 CC stationary support having at least one oligonucleotide associated with
 CC it, where the oligonucleotide includes a sequence of nucleotides which is
 CC complementary to a portion of the ITR sequence; and (c) combining the DNA
 CC fragments with the support under conditions where the DNA fragments
 CC including the DNA fragment containing the ITR sequence hybridize to the
 CC support. The method is particularly used to isolate DNA containing
 CC pentanucleotide tandem repeat sequences as well as to detect target ITR
 CC DNA sequences having a low incidence of stutter artifacts (no more than
 CC 2.4%). The method is useful in DNA profiling for linkage analysis,
 CC criminal justice, paternity testing and other forensic and medical
 CC DNA typing is also useful for confirming the lineage of horses, dogs and
 CC other prize animals. The invention overcomes problems related to the use
 CC of microsatellite loci in DNA profiling. The method can detect
 CC polymorphisms with a low incidence of stutter artifacts, which has
 CC previously been a problem in interpreting allelic content of loci. The
 CC development of markers based on larger repeat units, enables easier
 CC separation of the fragments on electrophoretic gels. This allows the
 CC simultaneous analysis of more loci.

XX Sequence 1000 BP; 302 A; 240 C; 231 G; 226 T; 1 other;

Query Match 100.0%; Score 1000; DB 20; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACCTATCTCTGAACTCAGTTTCCTCATCCGTAATGAAAGCTGTAG 60
 DB 1 GGTGTGACCTATCTCTGAACTCAGTTTCCTCATCCGTAATGAAAGCTGTAG 60

QY 61 ATTGTGTAAAAAATAAATGGAATAGGCTAGCGGCTGCTCAGCTGTAATCCA 120
 DB 61 ATTGTGTAAAAAATAAATGGAATAGGCTAGCGGCTGCTCAGCTGTAATCCA 120

QY 121 GCACCTTAGAGGTGCAAGAGGTGGATCAGTTCAGTTCAGGCTTTGAGACCACTG 180
 DB 121 GCACCTTAGAGGTGCAAGAGGTGGATCAGTTCAGGCTTTGAGACCACTG 180

QY 181 GCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTNGGTCGGTGGCT 240
 DB 181 GCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTNGGTCGGTGGCT 240

QY 241 CACACCTGTAAATCCAGCAGCTTTGGGAGGCTGAGACGGTGGATCAGCTGAAGTCAGGAG 300
 DB 241 CACACCTGTAAATCCAGCAGCTTTGGGAGGCTGAGACGGTGGATCAGCTGAAGTCAGGAG 300

QY 301 TTCAGGCCAGCTGGGCAACATGGTGAACACAGCTCTCTACTAAAAATACAAAAATTAG 360
 DB 301 TTCAGGCCAGCTGGGCAACATGGTGAACACAGCTCTCTACTAAAAATACAAAAATTAG 360

QY 361 CCAGGTGTGGTGACACAGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGGGAAGATC 420
 DB 361 CCAGGTGTGGTGACACAGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCGGGAAGATC 420

QY 421 GCTTGAACCCAGTAGGAGAGGTTCAGTTCAGCGGAGATTAAGATCAGCTCCAGGC 480
 DB 421 GCTTGAACCCAGTAGGAGAGGTTCAGTTCAGCGGAGATTAAGATCAGCTCCAGGC 480

QY 481 TGGGTGACAGACAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540
 DB 481 TGGGTGACAGACAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA 540

QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
 DB 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600

QY 601 AGTAATAGCTATCAATATATCCCAACCCCTACCACTGTGTGAAATTTAGTTTCTTTTGTG 660
 DB 601 AGTAATAGCTATCAATATATCCCAACCCCTACCACTGTGTGAAATTTAGTTTCTTTTGTG 660

QY 661 ACCCCCATTTAGACTTAAAGGAGCAATCTCACCCTACTCTCTGTAATTTCTGGTTCCT 720
 DB 661 ACCCCCATTTAGACTTAAAGGAGCAATCTCACCCTACTCTCTGTAATTTCTGGTTCCT 720

QY 721 GGCACATAGTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAAAATGCAAGGAATCTCC 780
 DB 721 GGCACATAGTGGGTCTCAGTGAACATGTTGAGTGAATGAGCAAAATGCAAGGAATCTCC 780

QY 781 AGGCATCTGGGAGCCCTCCAGCGGGTGTGAGTTCGGGAACTCATAGTCTGTCTCAAT 840
 DB 781 AGGCATCTGGGAGCCCTCCAGCGGGTGTGAGTTCGGGAACTCATAGTCTGTCTCAAT 840

QY 841 GGCCCACTGAAAGGTAGAGAGTTCGGTCCCACTCGGCACCCCACTCTCTGACTCAC 900
 DB 841 GGCCCACTGAAAGGTAGAGAGTTCGGTCCCACTCGGCACCCCACTCTCTGACTCAC 900

QY 901 TGTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
 DB 901 TGTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960

QY 961 CAGGACTGCAAGGAGCCGACGAGATGATGACCGGCTGC 1000
 DB 961 CAGGACTGCAAGGAGCCGACGAGATGATGACCGGCTGC 1000

RESULT 2
 AAK70459
 ID AAK70459 standard; DNA; 52616 BP.
 XX
 AC AAK70459;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25271.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ds.
 OS Homo sapiens.
 XX
 PN W0200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-02245119.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0233968.
PR 14-SEP-2000; 2000US-0233997.
PR 14-SEP-2000; 2000US-0233998.
PR 14-SEP-2000; 2000US-0233999.
PR 14-SEP-2000; 2000US-0234000.
PR 14-SEP-2000; 2000US-0234001.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 25271; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAK82169

CC represent sequences used in the exemplification of the present invention.

XX Sequence 52616 BP; 13218 A; 13917 C; 13903 G; 11678 T; 0 other;

SQ Query Match 7.2%; Score 72; DB 22; Length 52616;

Best Local Similarity 100.0%; Pred. No. 3.4e-24;

Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23964 CGTCTCTACTATAAATACAAAAATTAGCCAGGTGGTGCCACAGCCCTGTAGTCCAGC 24023

QY 394 TACTTGGGAGGC 405

Db 24024 TACTTGGGAGGC 24035

RESULT 3

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ID AAK78930 standard; DNA: 52616 BP.

XX

AC AAK78930;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33742.

XX

KW Human; immune; haematopoietic; Immune/haematopoietic antigen; cancer;

XX

KW Cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

PN WO200157182-A2.

XX

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PF 17-JAN-2001; 2001WO-US01354.

XX

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(HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483232/52.

DR Nucleic acids encoding 973 human testicular antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating testicular cancer -
 XX Disclosure; SEQ ID NO 3484; 766pp; English.

XX The present invention provides the protein and coding sequences of 973
 CC human testicular antigens, and fragments of their genomic sequences. The
 CC sequences can be used in the treatment of cardiovascular, urinary system,
 CC reproductive system, immune, respiratory, neurological and
 CC gastrointestinal disorders, infections, and particularly cancer,
 CC especially testicular cancers. The present sequence is a DNA encoding a
 CC protein fragment of the invention.


```

XX SQ Sequence 11627 BP; 3510 A; 2177 C; 2243 G; 3697 T; 0 other;
Query Match 5.8%; Score 58; DB 23; Length 11627;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 340 TACTAATAATACAAAATAGCCAGGTGTGGGACACGCCCTGTAGTCCAGCTACT 397
Db 10819 TACTAATAATACAAAATAGCCAGGTGTGGGACACGCCCTGTAGTCCAGCTACT 10762

RESULT 6
ABAL8026/c
ID ABAL8026 standard; DNA; 29329 BP.
XX AC ABAL8026;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 10357.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antischoling; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX PN W0200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
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PR 08-NOV-2000; 2000US-0246527.
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PR 17-NOV-2000; 2000US-0249210.

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PR 17-NOV-2000; 2000US-0249211.
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PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
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PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases
XX
XX Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABAI1004-ABA21334) and proteins
CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pot_sequences.
XX
SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
Query Match 5.7%; Score 57; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 235 GTGGCTCACCTGATATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCCTGA 291
Db 11642 GTGGCTCACCTGATATCCAGCAGCTTTGGAGGCTGAGACGGGTGATCCTGA 11586
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ID ABA20511 standard; DNA; 29329 BP.
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AC ABA20511;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 12842.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antiskilling; antianemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebrotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 19-MAY-2000; 2000US-0205515.
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PR 30-JUN-2000; 2000US-0215135.
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PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.

PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
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PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-02559678.
PR (HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
PR WPI; 2001-541565/50.
PR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PR useful for preventing, diagnosing and/or treating nervous system
PR cancers and metastases -
PR Disclosure; SEQ ID NO 12842; 1701pp + Sequence Listing; English.
PR The invention relates to novel genes (AB11004-ABA21534) and proteins
PR (AB114678-AB18001) useful for preventing, treating or ameliorating
PR medical conditions e.g. by protein or gene therapy. The genes are
PR isolated from a range of human tissues disclosed in the specification.
PR The nucleic acids, proteins, antibodies and (ant)agonists are useful
PR in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
PR and ovarian cancer and other cancers of the adrenal gland, bone, bone
PR marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
PR (b) immune disorders e.g. Addison's disease, allergies, autoimmune
PR haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
PR disease, multiple sclerosis, rheumatoid arthritis and ulcerative
PR colitis; (c) cardiovascular disorders such as myocardial ischaemia;
PR (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
PR epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
PR and parasitic infections.
PR Note: The sequence data for this patent did not form part of the
PR printed specification, but was obtained in electronic format directly
PR from WIPO at ftp.wipo.int/pub/published_pct_sequences.
PR SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
Query Match 5.7%; Score 57; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 235 GTGGCTCACACCTGTATCCACGACCTTGGAGGCTGAGACGGTGGATCACTGA 291
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XX AAK70791;
AC AAK70791;
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XX 06-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25603.
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
OS
XX
PN WO200157182-A2.

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PD	09-AUG-2001.	
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PR	29-SEP-2000; 2000US-0236327.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
PR	29-SEP-2000; 2000US-0236367.	
PR	29-SEP-2000; 2000US-0236368.	
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PR	17-NOV-2000; 2000US-0249265.	
PR	17-NOV-2000; 2000US-0249297.	
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PR	05-JAN-2001; 2001US-0259678.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		

DR WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 25603; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;

Query Match 5.7%; Score 57; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGACACCGGTGATCACTGA 291
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ID AAK78512 standard; DNA; 29329 BP.
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XX AAK78512;
AC
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XX 07-NOV-2001 (first entry)
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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
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XX Homo sapiens.
XX
XX W0200157182-A2.
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XX 09-AUG-2001.
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XX 17-JAN-2001; 2001W0-US01354.
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XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
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PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.

PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.

PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
XX Disclosure; SEQ ID NO 33324; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,

CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;

Query Match 5.7%; Score 57; DB 22; Length 29329;
Best Local Similarity 100.0%; Pred. No. 4.5e-17;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACACCTGTATCCAGACCTTTGGAGGCTTGAGCGGTGATCACTGA 291
|||||
Db 11642 GTGGCTCACACCTGTATCCAGACCTTTGGAGGCTTGAGCGGTGATCACTGA 11586
|||||

RESULT 10
ABK83569/C
ID ABK83569 standard; cDNA; 122888 BP.
XX
AC ABK83569;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #140.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
XX WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US30821.
XX
PR 03-OCT-2000; 2000US-237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity.
XX
PS Claim 1; SEQ ID No 140; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where

CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from GS in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 SQ Sequence 122888 BP; 28761 A; 33410 C; 31919 G; 28798 T; 0 other;

Query Match 5.6%; Score 56; DB 24; Length 122888;
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 232 GGGTGGCTCACCTGTATCCAGCAGCTTTGGAGGCTGAGCGGTGGATCAC 287
 Db 55450 GGGTGGCTCACCTGTATCCAGCAGCTTTGGAGGCTGAGCGGTGGATCAC 55395

RESULT 11
 AAF65641
 ID AAF65641 standard; cDNA; 476 BP.
 AC AAF65641;
 DT 09-APR-2001 (first entry)
 DE Novel human polynucleotide, SEQ ID NO: 1397.
 KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 OS Homo sapiens.
 PN WC200102568-A2.
 PD 11-JAN-2001.
 PF 30-JUN-2000; 2000WO-US18374.
 PR 02-JUL-1999; 99US-0142310.
 PR 02-JUL-1999; 99US-0142311.
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSE INC.
 PI Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
 PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Krnjajakovic R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 DR WPI; 2001-091805/10.
 XX
 XX Library of polynucleotides for diagnosing a cancerous state of a
 PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX
 XX Claim 9; Page 744; 1046pp; English.

XX The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can
 CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribozymes
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibodies against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.
 SQ Sequence 476 BP; 124 A; 130 C; 120 G; 98 T; 4 other;
 Query Match 5.5%; Score 55; DB 22; Length 476;
 Best Local Similarity 100.0%; Pred. No. 4.4e-16;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 169 GAGACAGCTGGCCACACACGGTGAAACCCCATCTCTACTAAAAATAATTA 223
 Db 305 GAGACAGCTGGCCACACACGGTGAAACCCCATCTCTACTAAAAATAATTA 359
 RESULT 12
 AAH13151/C
 ID AAH13151 standard; cDNA; 479 BP.
 XX AAH13151;
 AC AAH13151;
 DT 26-JUN-2001 (first entry)
 DE Human cDNA clone (3'-primer) SEQ ID NO:9986.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 PN EPI074617-A2.
 PD 07-FEB-2001.
 PF 28-JUL-2000; 2000EP-0116126.
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 PA (HELI-) HELIX RES INST.
 XX
 XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 DR WPI; 2001-318749/34.
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 XX Claim 3; SEQ ID 9986; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH95993 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

SQ Sequence 479 BP; 108 A; 120 C; 99 G; 143 T; 9 other;

Query Match 5.4%; Score 54; DB 22; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGCTGCTACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTG 281
DB 280 GGGTGGGCTGCTACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTG 227
|||||

RESULT 13

ABQ89372
ID ABQ89372 standard; cDNA; 593 BP.

AC ABQ89372;

DT 27-SEP-2002 (first entry)

DE Human prostate expressed polynucleotide SEQ ID NO 628.

KW Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy;
KW gene; ss.

OS Homo sapiens.

PN W0200255700-A2.

XX 18-JUL-2002.

PF 07-DEC-2001; 2001WO-US47349.

PR 07-DEC-2000; 2000US-254648P.

PR 13-MAR-2001; 2001US-275688P.

XX (CHIR) CHIRON CORP.
XX (HYSE-) HYSEQ INC.

PI Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D;
PI Kita D, Garcia V, Jones WL, Stache-Crain B, Scott EM;
XX WPI; 2002-557824/59.

XX New genes and gene products isolated from human prostate, useful for
XX treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
XX cancer), or as vaccines for treating or preventing these diseases -
XX
PS Claim 1; SEQ ID NO 628; 186pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide comprising any of
CC 1477 sequences or its fragment, degenerate variant, antisense or
CC complementary. The polynucleotides and gene products are useful for treating
CC or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer,
CC lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs,

CC cats, rabbits, horse or human). The polynucleotides and polypeptides are
CC also useful as vaccines for treating or preventing these diseases. The
CC polynucleotides are useful for gene therapy. The present sequence is that
CC of one of a group of polynucleotides (ABQ88745-ABQ90015) disclosed
CC electronically as sequences of the invention. However only 1271
CC polynucleotide sequences are given, whereas 1477 polynucleotides and 91
CC proteins are claimed.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence.

SQ Sequence 593 BP; 186 A; 116 C; 141 G; 134 T; 16 other;

Query Match 5.4%; Score 54; DB 24; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGCTGCTACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTG 281
DB 94 GGGTGGGCTGCTACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTG 147
|||||

RESULT 14

AAH16608
ID AAH16608 standard; cDNA; 2298 BP.

XX AAH16608;

XX 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:15707.

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

XX 07-FEB-2001.

PF 28-JUL-2000; 2000EP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Mishikawa T, Hayashi K, Saito K, Yamamoto J;

XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602

XX full-length cDNAs defined in the specification, and for the detection

XX and/or diagnosis of the abnormality of the proteins encoded by the

XX full-length cDNAs -

XX Claim 8; SEQ ID 15707; 2537pp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602

XX full-length cDNAs defined in the specification. Where a primer set

XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary

XX to the complementary strand of a polynucleotide which comprises one of

XX the 5602 nucleotide sequences defined in the specification, where the

XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination

XX of an oligonucleotide comprising a sequence complementary to the

XX complementary strand of a polynucleotide which comprises a 5'-end

XX sequence and an oligonucleotide comprising a sequence complementary to a

XX polynucleotide which comprises a 3'-end sequence, where the

XX oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX
SQ Sequence 2298 BP; 764 A; 473 C; 481 G; 580 T; 0 other;

Query Match 5.4%; Score 54; DB 22; Length 2298;
Best Local Similarity 100.0%; Pred. No. 1.3e-15;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGGTGGCTACACCTGTATCCAGCAGCTTTGGGAGGCTGAGACGGGTG 281
|||||
Db 2019 GGGTGGGGTGGCTACACCTGTATCCAGCAGCTTTGGGAGGCTGAGACGGGTG 2072

RESULT 15

AAS32680

ID AAS32680 standard; DNA; 307 BP.

XX

XX AAS32680;

AC

DT 17-DEC-2001 (first entry)

XX

Human genomic DNA for novel endocrine antigen, SEQ ID No 634.

XX

KW Human; endocrine antigen; ds; cytostatic; antiinfertility; antidiabetic;
KW thyroid-active; adrenal-active; androgenic; gastric; gene therapy;
KW antihensic-therapy; antibody; endocrine disorder; hormone imbalance;
KW reproductive disorder; endocrine cancer; pancreatic disorder;
KW diabetes mellitus; adrenal gland disorder; hirsutism; thyroid disorder;
KW hyperthyroidism; hypothalamic disorder; vanishing testes syndrome.

OS Homo sapiens.
XX

XX WO200155319-A2.
XX

XX 02-AUG-2001.
XX

XX 17-JAN-2001; 2001WO-US01335.
XX

XX 31-JAN-2000; 2000US-0179065.
XX

XX 04-FEB-2000; 2000US-0180628.
XX

XX 24-FEB-2000; 2000US-0184664.
XX

XX 02-MAR-2000; 2000US-0186350.
XX

XX 16-MAR-2000; 2000US-0189874.
XX

XX 17-MAR-2000; 2000US-0190076.
XX

XX 18-APR-2000; 2000US-0198123.
XX

XX 19-MAY-2000; 2000US-0205515.
XX

XX 07-JUN-2000; 2000US-0209467.
XX

XX 28-JUN-2000; 2000US-0214886.
XX

XX 30-JUN-2000; 2000US-0215135.
XX

XX 07-JUL-2000; 2000US-0216647.
XX

XX 07-JUL-2000; 2000US-0216880.
XX

XX 11-JUL-2000; 2000US-0217487.
XX

XX 14-JUL-2000; 2000US-0217496.
XX

XX 26-JUL-2000; 2000US-0218290.
XX

XX 26-JUL-2000; 2000US-0220963.
XX

XX 14-AUG-2000; 2000US-0220364.
XX

XX 14-AUG-2000; 2000US-0224518.
XX

XX 14-AUG-2000; 2000US-0224519.
XX

XX 14-AUG-2000; 2000US-0225213.
XX

XX 14-AUG-2000; 2000US-0225214.
XX

XX 14-AUG-2000; 2000US-0225266.
XX

XX 14-AUG-2000; 2000US-0225267.
XX

XX 14-AUG-2000; 2000US-0225268.
XX

PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234273.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246527.

PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-457726/49.
XX
PT Isolated polypeptide for treating, preventing and prognosing disorders
PT related to the endocrine system including endocrine disorders,
PT reproductive disorders, and gastrointestinal disorders and also for
PT testing and detection e.g. diagnosis -
XX
PS Disclosure; SEQ ID NO 634; 558pp; English.
XX
CC The invention relates to cDNAs encoding novel human endocrine
CC antigens or a fragment having biological activity, a domain, an epitope,
CC full length protein, variant, allelic variant or a species homologue of
CC the cDNA/antigen. The DNAs and polypeptides are useful for preventing,
CC treating or ameliorating a medical condition when administered
CC (e.g. by gene therapy or antisense-therapy). Identifying mutations in
CC the genes coding for the antigens is useful for diagnosing a pathological
CC condition or a susceptibility to a pathological condition. The DNAs,
CC antigens and antibodies raised against the antigens useful for treating,
CC preventing and/or prognosing disorders related to the endocrine system
CC or hormone imbalance or reproductive disorders, cancers of endocrine
CC tissues, disorders of the pancreas (e.g. diabetes mellitus), the adrenal
CC glands (e.g. hirsutism), ovaries, the thyroid (e.g. hyperthyroidism), the
CC hypothalamus and testes (e.g. vanishing testes syndrome), many examples
CC of diseases and disorders are given in the specification. The present
CC sequence is genomic DNA fragment form a gene encoding an endocrine
CC antigen of the invention.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 307 BP; 91 A; 75 C; 93 G; 48 T; 0 other;

Query Match 5.3%; Score 53; DB 22; Length 307;
Best Local Similarity 100.0%; Pred. No. 4e-15;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GGTGGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCA 286
Db 14 GGTGGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCA 66
|||||
RESULT 16
AAS44682/c
ID AAS44682 standard; DNA; 642 BP.
XX
AC AAS44682;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human full-length polynucleotide sequence #107.
XX
KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytostatic; antirheumatic; antiarthritic; vulnary; antinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200164834-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04926.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Drmanac R;
XX
DR WPI; 2001-589862/66.
DR P-PSDB; AAU27782.
XX
PT Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection -
XX
PS Claim 1; SEQ ID No 107; 153pp; English.
XX
CC Sequences AAS44576-AAS44919 represent full-length polynucleotides and
CC contig polynucleotides encoding polypeptides of the invention. The DNA
CC and protein sequences are useful for the treatment, diagnosis and
CC prevention of various types of disorder in a mammalian subject such as a
CC human, dog, monkey, mouse, hamster or rat. The disorders include cancers
CC such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such
CC as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and

CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 642 BP; 145 A; 130 C; 158 G; 209 T; 0 other;

Query Match 5.3%; Score 53; DB 22; Length 642;
Best Local Similarity 100.0%; Pred. No. 3.9e-15;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCTGGCCACACGGTGAAACCCATCTCTACTTAAATAAAAAAT 221
|||||
Db 278 GAGACAGCTGGCCACACGGTGAAACCCATCTCTACTTAAATAAAAAAT 226
|||||

RESULT 17
AAH92080
ID AAH92080 standard; DNA; 700 BP.
XX
AC AAH92080;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease related gene fragment IGR2092a.
XX
KW Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200142511-A2.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US33632.
XX
PR 10-DEC-1999; 99US-0170257.
PR 10-APR-2000; 2000US-0196046.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay -
XX
PS Disclosure; Page 112; 463pp; English.
XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a gene
CC containing a polymorphic site described in the exemplification of the
XX invention.
SQ Sequence 700 BP; 210 A; 141 C; 150 G; 199 T; 0 other;

Query Match 5.2%; Score 52; DB 22; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 379 GCCTGTAGTCCAGCTACTTGGAGCGTGAGCGGAAGAAATCGCTTGAACCC 430
|||||
Db 589 GCCTGTAGTCCAGCTACTTGGAGCGTGAGCGGAAGAAATCGCTTGAACCC 640
|||||

RESULT 18
AAH92081
ID AAH92081 standard; DNA; 700 BP.
XX
AC AAH92081;
XX
DT 09-OCT-2001 (first entry)
XX
DE Human inflammatory bowel disease related gene fragment IGR2093a.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
XX single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
XX chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200142511-A2.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US33632.
XX
PR 10-DEC-1999; 99US-0170257.
PR 10-APR-2000; 2000US-0196046.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;
XX WPI; 2001-367874/38.
XX
PT Testing for the presence of polymorphisms associated with inflammatory
PT bowel disease, using a hybridization assay -
XX
PS Disclosure; Page 112-113; 463pp; English.
XX
CC The present invention describes a method for detecting the presence of
CC polymorphisms associated with inflammatory bowel diseases such as
CC ulcerative colitis and Crohn's disease. The methods can be used to detect
CC the presence of genetic polymorphisms associated with inflammatory bowel
CC disease and correlating their occurrence with disease states. They may be
CC used in this way for phenotypic correlations, forensics, paternity
CC testing, medicine and genetic analysis. The present sequence is a gene
CC containing a polymorphic site described in the exemplification of the
XX invention.

SQ Sequence 700 BP; 178 A; 183 C; 188 G; 151 T; 0 other;

Query Match 5.2%; Score 52; DB 22; Length 700;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GCCTGTAGTCCAGCTACTTGGAGCGTGAGCGGAAGAAATCGCTTGAACCC 430
|||||
Db 90 GCCTGTAGTCCAGCTACTTGGAGCGTGAGCGGAAGAAATCGCTTGAACCC 141
|||||

RESULT 19
AAL37013/c
ID AAL37013 standard; DNA; 2701 BP.
XX
AC AAL37013;
XX

DT 08-JAN-2002 (first entry)
XX Human musculoskeletal system related polynucleotide SEQ ID NO 3378.
DE Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
XX WO200155367-A1.
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01338.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214986.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0245474.
PR 08-NOV-2000; 2000US-0245475.
PR 08-NOV-2000; 2000US-0245476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPT; 2001-451937/48.
 XX
 PT Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 XX
 PS Example 2; SEQ ID NO 3378; 781pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 2701 BP; 774 A; 509 C; 580 G; 838 T; 0 other;
 Query Match 5.2%; Score 52; DB 22; Length 2701;
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 560
 Db 942 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 891
 RESULT 20
 AAK74315
 ID AAK74315 standard; DNA; 5533 BP.
 XX
 AC AAK74315;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29127.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200157182-A2.
 PN
 XX
 PD 09-AUG-2001.
 XX
 XX

PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
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PR 05-JAN-2001; 2001US-0259678.
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PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-483426/52.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT metastasis -
XX
PS Disclosure; SEQ ID NO 29127; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
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SQ Sequence 5533 BP; 1261 A; 1349 C; 1475 G; 1448 T; 0 other;
Query Match 5.2%; Score 52; DB 22; Length 5533;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AAK74317
ID AAK74317 standard; DNA; 5533 BP.
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AC AAK74317;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29129.
XX
KW Human; immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
OS Homo sapiens.
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -
Disclosure; SEQ ID NO 29129; 3071pp + Sequence Listing; English.
AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patient's own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/hematopoietic-related diseases, especially
cancers and cancer metastases of hematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/hematopoietic antigen genomic

CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.

SQ Sequence 5533 BP; 1361 A; 1349 C; 1475 G; 1448 T; 0 other;

Query Match 5.28; Score 52; DB 22; Length 5533;
Best Local Similarity 100.0%; Pred. No. 1.le-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTAAATAACAAAAATTAGCCAGGTGTGGTGGCACGCGCTGTACT 387
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Db 3981 TCTCTAAATAACAAAAATTAGCCAGGTGTGGTGGCACGCGCTGTACT 4032

RESULT 22

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ID AAK74316 standard; DNA; 5536 BP.

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AC AAK74316;

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DT 07-NOV-2001 (first entry)

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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29128.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW

cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

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PN WO200157182-A2.

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PD 09-AUG-2001.

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PF 17-JAN-2001; 2001WO-US01354.

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 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
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 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
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 PS Disclosure; SEQ ID NO 29128; 3071pp + Sequence Listing; English.
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 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 5536 BP; 1263 A; 1348 C; 1474 G; 1451 T; 0 other;
 Query Match 5.2%; Score 52; DB 22; Length 5536;
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 336 TCCTACTAAAAATACAAAATAGCCAGGTGTGGTGGCACACGCCCTGTAGT 387
 DB 3384 TCCTACTAAAAATACAAAATAGCCAGGTGTGGTGGCACACGCCCTGTAGT 4035
 RESULT 23
 AAK74318
 ID AAK74318 standard; DNA; 5537 BP.
 XX
 AC AAK74318;
 XX

DT 07-NOV-2001 (first entry)
 XX Human immune/hematopoietic antigen genomic sequence SEQ ID NO:29130.
 DE Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ds.
 KW Homo sapiens.
 OS
 XX WO200157182-A2.
 PN
 XX 09-AUG-2001.
 PD
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 11-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
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 PR 12-SEP-2000; 2000US-0231968.
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PR 14-SEP-2000; 2000US-0233064.
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PR 01-NOV-2000; 2000US-024617.
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PR 08-NOV-2000; 2000US-0246474.
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PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251866.
PR 08-DEC-2000; 2000US-0251867.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251870.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
XX Disclosure; SEQ ID NO 29130; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/hematopoietic-related diseases, especially
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703
XX to AAK7694 represent human immune/hematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX SQ Sequence 5537 BP; 1271 A; 1331 C; 1454 G; 1481 T; 0 other;
Query Match 5.2%; Score 52; DB 22; Length 5537;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 TCTCTACTAAATAACAAAATTAGCCAGGTGTGGTGACACAGCCTGTAGT 387
Db 3988 TCTCTACTAAATAACAAAATTAGCCAGGTGTGGTGACACAGCCTGTAGT 4039
RESULT 24
AAK89991/c
ID AAK89991 standard; DNA; 12244 BP.
XX AAK89991;
AC AAK89991;
XX 05-NOV-2001 (first entry)
XX Human digestive system antigen genomic sequence SEQ ID NO: 3567.
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
XX ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX digestive system disorder; Meckel's diverticulum; ds.
XX Homo sapiens.
XX OS
XX WO200155314-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01324.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
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PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
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 PR 18-AUG-2000; 2000US-0225759.
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 PR 22-AUG-2000; 2000US-0226681.
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 PR 22-AUG-2000; 2000US-0227182.
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 PR 01-SEP-2000; 2000US-0229344.
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 PR 08-SEP-2000; 2000US-0231242.
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 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
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 PR 21-SEP-2000; 2000US-0234274.
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 PR 25-SEP-2000; 2000US-0234999.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
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 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 23-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
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 PR 02-OCT-2000; 2000US-0237038.
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 PR 20-OCT-2000; 2000US-0241787.
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 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
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 PR 08-NOV-2000; 2000US-0246526.
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 PR 08-NOV-2000; 2000US-0246611.
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 PR 17-NOV-2000; 2000US-0249244.
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 PR 05-DEC-2000; 2000US-0251030.
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 PR 06-DEC-2000; 2000US-0251479.
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 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-502630/55.

Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognosing disorders of the digestive system, particularly cancer and cancer metastases -

Disclosure; SEQ ID NO 3567; 986pp; English.

The present invention provides the protein and coding sequences of a

CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention.
 XX
 SQ Sequence 12244 BP; 3636 A; 2432 C; 2513 G; 3663 T; 0 other;

Query Match 5.2%; Score 52; DB 22; Length 12244;
 Best Local Similarity 100.0%; Pred. No. 1.1e-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 GATCAGCTGAGTCTGAGAGTTTTCAGACAGCCTGGCCACACAGGTGAACG 197
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 Db 10382 GATCAGCTGAGTCTGAGAGTTTTCAGACAGCCTGGCCACACAGGTGAACG 10331

RESULT 25

ABAL5896/G

ID ABAL5896 standard; DNA; 12392 BP.

XX AC ABAL5896;

XX DT 23-JAN-2002 (first entry)

XX DE Human nervous system related polynucleotide SEQ ID NO 8227.

XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
 KW antiparkinsonian; antiskinking; antianemic; antiarthritic; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

XX OS Homo sapiens.

XX PN WO200159063-A2.

XX PD 16-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01334.

XX PR 31-JAN-2000; 2000US-0179065.

XX PR 04-FEB-2000; 2000US-0180628.

XX PR 24-FEB-2000; 2000US-0184664.

XX PR 02-MAR-2000; 2000US-0186350.

XX PR 16-MAR-2000; 2000US-0189874.

XX PR 17-MAR-2000; 2000US-0190076.

XX PR 18-APR-2000; 2000US-0198123.

XX PR 19-MAY-2000; 2000US-0205515.

XX PR 07-JUN-2000; 2000US-0209467.

XX PR 28-JUN-2000; 2000US-0214886.

XX PR 30-JUN-2000; 2000US-0215135.

XX PR 07-JUL-2000; 2000US-0216647.

XX PR 07-JUL-2000; 2000US-0216880.

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XX PR 11-JUL-2000; 2000US-0217496.

XX PR 14-JUL-2000; 2000US-0218290.

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XX PR 14-AUG-2000; 2000US-0225266.

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XX PR 14-AUG-2000; 2000US-0225270.

XX PR 14-AUG-2000; 2000US-0225447.

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XX PR 14-AUG-2000; 2000US-0225758.

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 PR 23-AUG-2000; 2000US-0227182.
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 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
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 PR 14-SEP-2000; 2000US-0232399.
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 PR 14-SEP-2000; 2000US-0233063.
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 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
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 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
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PR 08-NOV-2000; 2000US-0246611.
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 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-541565/60.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX
 PS Disclosure; SEQ ID NO 8227; 1701pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABBI4678-ABBI8001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 12392 BP; 3812 A; 2126 C; 2413 G; 4041 T; 0 other;
 Query Match 5.2%; Score 52; DB 22; Length 12392;
 Best Local Similarity 100.0%; Pred. No. 1.le-14;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 174 CAGCCTGGCCACACGGTGAACCCCATCTCTACTAAAAATAAAATTAGC 225

Db 3234 CAGCCTGGCCACACGGTGAACCCCATCTCTACTAAAAATAAAATTAGC 3183
 RESULT 26
 AAK95240/C
 ID AAK95240 standard; DNA; 1503900 BP.
 XX
 AC AAK95240;
 XX
 DT 17-DEC-2001 (first entry)
 XX
 DE Human neuregulin-1 gene.
 XX
 KW Human; neuregulin-1 associated gene 1; NRGIAG1; Schizophrenia gene;
 KW gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200164876-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US063376.
 XX
 PR 28-FEB-2000; 2000US-0515715.
 XX
 PR (DECO-) DECODE GENETICS EHF.
 PA
 XX Stefansson H, Steinthorsdottir V, Gulcher JR;
 PI WPI; 2001-550179/61.
 DR
 DR P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
 DR AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
 DR AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
 DR AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
 DR AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
 DR AAG67934, AAG67935, AAG67936, AAG67937.
 XX
 PT Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
 PT preventing diagnosing and treating schizophrenia -
 XX
 PS Disclosure; Page 90-501; 750pp; English.
 XX
 CC This sequence represents the human neuregulin-1 associated gene 1
 CC (NRGIAG1) of the invention. The NRGIAG1 gene is also referred to as the
 CC human Schizophrenia gene. The invention also relates to fragments or
 CC variants of the gene and the NRGIAG1 polypeptides they encode. The
 CC NRGIAG1 nucleic acids and polypeptides may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate NRGIAG1
 CC expression. For example, they may be used to treat disorders associated
 CC with decreased expression by rectifying mutations or deletions in a
 CC patient's genome that affect the activity of NRGIAG1 by expressing
 CC inactive proteins or to supplement the patients own production of
 CC NRGIAG1. Additionally, the gene may be used to produce NRGIAG1
 CC polypeptides, by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The gene may also be used as
 CC DNA probes and primers in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acids in samples, and therefore which
 CC patients may be in need of restorative therapy. The NRGIAG1 polypeptides
 CC may also be used as antigens in the production of antibodies against
 CC NRGIAG1 and in assays to identify modulators of NRGIAG1 expression and
 CC activity. Anti-NRGIAG1 antibodies and antagonists may also be used to
 CC down regulate expression and activity. Anti-NRGIAG1 antibodies may
 CC also be used as diagnostic agents for detecting the presence of NRGIAG1
 CC polypeptides in samples. NRGIAG1 is associated with schizophrenia which
 CC may be prevented, diagnosed and/or treated by the above methods.
 XX
 SQ Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;
 Query Match 5.2%; Score 52; DB 22; Length 1503900;
 Best Local Similarity 100.0%; Pred. No. 9.4e-15;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 560
 |||||
 Db 1366726 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 1366675

RESULT 27	
AAK96733/c	
ID	AAK96733 standard; DNA; 1503900 Bp.
AC	
XX	AAK96733;
XX	
DT	17-DEC-2001 (first entry)
XX	
DE	Human neuregulin-1 gene.
XX	
KW	Human; neuregulin 1 gene; schizophrenia; gene therapy; ds. dx.
XX	
OS	Homo sapiens.
PX	
NN	W0200164877-A2.
XX	
PD	07-SEP-2001..
XX	
PF	28-FEB-2001; 2001WO-US063377.
XX	
PR	28-FEB-2000; 2000US-0515716.
XX	
PA	(DECO-) DECODE GENETICS EHF.
PI	Stefansson H, Steinthorsdottir V, Gulcher JR;
XX	
DR	WPI; 2001-514841/56.
DR	P-PSDB; AAG67938, AAG67939, AAG67940, AAG67941, AAG67942, AAG67943,
DR	AAG67944, AAG67945, AAG67946, AAG67947, AAG67948, AAG67949,
DR	AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955,
DR	AAG67956, AAG67957, AAG67958, AAG67959, AAG67960, AAG67961,
DR	AAG67962, AAG67963, AAG67964, AAG67965, AAG67966, AAG67967,
DR	AAG67968, AAG67969, AAG67970, AAG67971, AAG67972, AAG67973,
DR	AAG67974, AAG67975.

Neuregulin 1 nucleic acids and proteins useful for diagnosing preventing and treating schizophrenia -
 Disclosure; Page 345-756; 756pp; English.

This sequence represents the human neuregulin 1 gene of the invention. The invention also relates to fragments or variants of the neuregulin 1 gene. The gene and its proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate neuregulin 1 expression, such as schizophrenia. For example they may be used to treat disorders associated with decreased neuregulin 1 expression by rectifying mutations or deletions in a patient's genome that affect the activity of neuregulin 1 by expressing inactive proteins or to supplement the patients own production of polypeptides. Additionally, the gene may be used to produce the neuregulin 1 protein, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The gene and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. The protein may also be used as antigens in the production of antibodies against neuregulin 1 and in assays to identify modulators of neuregulin 1 expression and activity. The antibodies and antagonists may also be used to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of neuregulin 1 in samples.

Query Match 5.2%; Score 52; DB 22; Length 1503900;
 Best Local Similarity 100.0%; Pred. No. 9.4e-15;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps

QY	509	AAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC	560
Db	1366726	AAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC	1366675
RESULT	28		
	ABN80120		
	ABN80120 standard; DNA; 6523 BP.		
ID	ABN80120	standard; DNA; 6523 BP.	
XX	XX		
AC	AC		
	ABN80120;		
XX	XX		
DT	15-JUL-2002	(first entry)	

RESULT 28

ABN80120
ID ABN80120 standard; DNA; 6523 BP.
XX
ABN80120;
XX
15-JUL-2002 (first entry)
XX
DE Human chemically modified disease associated gene SEQ ID NO 137

Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.

OS	Homo sapiens.
OS	Synthetic.

AA
PN
WO200200927-A2

03-JAN-2002

XX
PF
02-III.-2001.XX
PR 30-JUN-2000: 2000PR-1032520PR 01-SEP-2000; 2000DE-1043826.
YY

PA (EPIG-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

DR WPI; 2002-130908/17.

Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development -

PS Claim 1; SEQ ID NO 137: 27pp: English

The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification with development selected from 87 genes listed in the specification such as ACCPN, ADPN, or AFDL and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is useful for the diagnosis or therapy of diseases associated with development genes, in particular disease related to homeobox containing genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes associated with congenital heart disease, epilepsy, diseases related to histone deacetylation, Curranio syndrome, diseases related to development of the brain and limb girdle muscular dystrophy and dwarfism. Oligomers specific to each of the genes are useful for detecting the methylation state of all CpG dinucleotides within the 350 sequences or (II) and their complementary sequences, as primer oligonucleotides for the amplification of the 350 sequences, (I) and/or their complements as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs).

Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 6523 BP; 1499 A; 356 C; 1860 G; 2808 T; 0 other;

Query Match	5.1%	Score 51;	DB 24;	Length 6523;
Best Local Similarity	100.0%	Pred. No. 3.2e-14;		

QY 509 AAAATAAAATAAAAATAAAAATAAAAATAAAAATAAAAATT 559

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Db 3112 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATT 3162
|||||
RESULT 29
ABQ88169
ID ABQ88169 standard; cDNA; 43411 BP.
XX AC ABQ88169;
XX DT 18-SEP-2002 (first entry)
XX DE Human osteoblast differentiation related cDNA SEQ ID NO 76.
XX KW Human; osteoblast; stem cell differentiation; bone tissue deposition;
XX KW osteoporosis; osteopathic; ss.
XX OS Homo sapiens.
XX PN WO200250301-A2.
XX PD 27-JUN-2002.
XX PF 18-DEC-2001; 2001WO-US48276.
XX PR 18-DEC-2000; 2000US-255882P.
XX PR 24-APR-2001; 2001US-285691P.
XX PA (GENE-) GENE LOGIC INC.
XX PA (PROC ) PROCTER & GAMBLE CO.
XX PI Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
XX PI Mertz L;
XX DR WPI; 2002-557663/59.
XX
XX Use of genes and their expression profiles associated with osteoblast
PT differentiation for screening modulators bone formation, for diagnosing
PT or treating e.g. osteoporosis, or as markers for the differentiation
PT process
XX
PS Claim 1; SEQ ID NO 76; 78pp + Sequence Listing; English.
XX
CC The invention relates to genes and their expression profiles are used
CC for:
CC (a) screening modulators of precursor stem cell differentiation into
CC osteoblasts, or bone tissue deposition;
CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of
CC osteoblast formation or osteoporosis; or
CC (c) treating or monitoring treatment of the conditions cited in (b), or
CC monitoring the progression of bone tissue deposition.
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid
CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,
CC drug-induced abnormalities in bone formation or bone loss, conditions
CC that involve altered bone metabolism (e.g. idiopathic juvenile
CC Fanconi syndrome or fibrous dysplasia. The present sequence is that of an
CC osteoblast differentiation associated cDNA marker of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 43411 BP; 9410 A; 12601 C; 12923 G; 8477 T; 0 other;
Query Match 5.1%; Score 51; DB 24; Length 43411;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 335 GTCTTACTAAATAACAAATAATAGCCAGGTGTGTGGCACAGCGCTGTA 385
|||||
Db 944 GTCTTACTAAATAACAAATAATAGCCAGGTGTGTGGCACAGCGCTGTA 994
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RESULT 30
ABK83497/C
ID ABK83497 standard; cDNA; 227968 BP.
XX AC ABK83497;
XX DT 14-AUG-2002 (first entry)
XX DE Human cDNA differentially expressed in granulocytic cells #68.
XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
XX KW viral infection; parasitic infection; protozoal infection;
XX KW fungal infection; sterile inflammatory disease; psoriasis;
XX KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
XX KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
XX KW adult respiratory distress syndrome; inflammatory bowel disease;
XX KW Crohn's disease; ulcerative colitis; periodontal disease;
XX KW granulocyte activation; chronic inflammation; allergy.
XX OS Homo sapiens.
XX PN WO200228999-A2.
XX PD 11-APR-2002.
XX PF 03-OCT-2001; 2001WO-US30821.
XX PR 03-OCT-2000; 2000US-237189P.
XX PA (GENE-) GENE LOGIC INC.
XX PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX PI WPI; 2002-435328/46.
XX
XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity
XX
PS Claim 1; SEQ ID NO 68; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
```

CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences.

XX Sequence 227968 BP; 53185 A; 60440 C; 61985 G; 52358 T; 0 other;

Query Match 5.1%; Score 51; DB 24; Length 227968;
Best Local Similarity 100.0%; Pred. No. 3e-14;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GTCCTACTAAATACAAAATAGCCAGGTGGTGGCAGCAGCTGTA 385
|||||
Db 47716 GTCCTACTAAATACAAAATAGCCAGGTGGTGGCAGCAGCTGTA 47666

RESULT 31

AAS36586/C

ID AAS36586 standard; DNA; 276 BP.

XX AC AAS36586;

XX XX

DT 17-DEC-2001 (first entry)

XX Human cardiovascular system antigen genomic DNA SEQ ID No 2086.

XX Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
KW chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog;
KW antihemmatic; antiproliferative; cytostatic; cardiant; neuroprotective;
KW cerebroprotective; nontropic; antibacterial; virucide; fungicide; cancer;
KW ophthalmological; vulnary; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; breast; liver; cardiovascular disorder; ds;
KW cerebrovascular disorder; nervous system disorder; bacterial infection;
KW fungal infection; viral infection; ocular disorder; endocrine disorder;
KW gastrointestinal disorder; renal disorder; respiratory disorder;
KW wound healing; skin aging; organ transplantation; tissue regeneration;
KW anti-infertility.

OS Homo sapiens.

XX XX

PN WO200155321-A2.

XX XX

PD 02-AUG-2001.

XX XX

PF 17-JAN-2001; 2001WO-US01340.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184564.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 14-AUG-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 03-SEP-2000; 2000US-0229509.
PR 03-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 01-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.

PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-451930/48.
XX
XX New cardiovascular system related polynucleotides and polypeptides,
PT useful for diagnosing, treating and/or preventing disorders of the
PT cardiovascular system -
XX
XX
XX Claim 1; SEQ ID No 2086; 674pp; English.
XX
XX

Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode the cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition can be determined by detecting the presence or absence of a mutation in a cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cerebral ischaemia, nervous system disorders such as Alzheimer's disease, infections caused by bacteria, viruses and fungi, ocular disorders such as corneal infection, endocrine disorders such as premature labour and infertility, gastrointestinal disorders such as Crohn's disease, renal disorders such as glomerulonephritis and respiratory disorders such as asthma and pleurisy. The polypeptides can also be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Query Match 5.0%; Score 50; DB 22; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 166 TTTGAGACCGCTGGCCACACGGTGAACCCCATCTCTACTAAATA 215
|||||
Db 216 TTTGAGACCGCTGGCCACACGGTGAACCCCATCTCTACTAAATA 167
|||||

RESULT 32
AAK75295/c
ID AAK75295 standard; DNA; 276 BP.
XX
AC AAK75295;
XX
XX 07-NOV-2001 (first entry)
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30107.
XX Human immune/haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216880.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
XX 14-AUG-2000; 2000US-0225213.
XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225266.
XX 14-AUG-2000; 2000US-0225267.
XX 14-AUG-2000; 2000US-0225268.
XX 14-AUG-2000; 2000US-0225270.
XX 14-AUG-2000; 2000US-0225447.
XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
XX 22-AUG-2000; 2000US-0226681.
XX 22-AUG-2000; 2000US-0226868.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 01-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
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 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232091.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
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 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
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 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
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 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
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 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.

PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 03-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 XX
 PS Disclosure; SEQ ID NO 30107; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 276 BP; 50 A; 81 C; 69 G; 76 T; 0 other;

Query Match 5.0%; Score 50; DB 22; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.1e-13;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGTGACACGCTGGCCACACGGTGAACCCCATCTCTACTATAAATA 215
 Db |||||
 Db 216 TTGTGACACGCTGGCCACACGGTGAACCCCATCTCTACTATAAATA 167

RESULT 33

AAK75296/G

ID AAK75296 standard; DNA; 276 BP.

XX

AC AAK75296;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:30108.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX Homo sapiens.
XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US01354.
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.
XX 18-APR-2000; 2000US-0198123.
XX 19-MAY-2000; 2000US-0205515.
XX 07-JUN-2000; 2000US-0209467.
XX 28-JUN-2000; 2000US-0214886.
XX 30-JUN-2000; 2000US-0215135.
XX 07-JUL-2000; 2000US-0216647.
XX 07-JUL-2000; 2000US-0216680.
XX 11-JUL-2000; 2000US-0217487.
XX 11-JUL-2000; 2000US-0217496.
XX 14-JUL-2000; 2000US-0218290.
XX 26-JUL-2000; 2000US-0220963.
XX 26-JUL-2000; 2000US-0220964.
XX 14-AUG-2000; 2000US-0224518.
XX 14-AUG-2000; 2000US-0224519.
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XX 14-AUG-2000; 2000US-0225214.
XX 14-AUG-2000; 2000US-0225366.
XX 14-AUG-2000; 2000US-0225367.
XX 14-AUG-2000; 2000US-0225467.
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XX 14-AUG-2000; 2000US-0225757.
XX 14-AUG-2000; 2000US-0225758.
XX 14-AUG-2000; 2000US-0225759.
XX 18-AUG-2000; 2000US-0226279.
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XX 22-AUG-2000; 2000US-0226686.
XX 22-AUG-2000; 2000US-0227182.
XX 23-AUG-2000; 2000US-0227009.
XX 30-AUG-2000; 2000US-0228924.
XX 01-SEP-2000; 2000US-0229287.
XX 01-SEP-2000; 2000US-0229343.
XX 01-SEP-2000; 2000US-0229344.
XX 05-SEP-2000; 2000US-0229345.
XX 05-SEP-2000; 2000US-0229509.
XX 05-SEP-2000; 2000US-0229513.
XX 06-SEP-2000; 2000US-0230437.
XX 06-SEP-2000; 2000US-0230438.
XX 08-SEP-2000; 2000US-0231242.
XX 08-SEP-2000; 2000US-0231243.
XX 08-SEP-2000; 2000US-0231244.
XX 08-SEP-2000; 2000US-0231413.
XX 08-SEP-2000; 2000US-0231414.
XX 08-SEP-2000; 2000US-0232080.
XX 08-SEP-2000; 2000US-0232081.
XX 12-SEP-2000; 2000US-0231968.
XX 14-SEP-2000; 2000US-0232397.
XX 14-SEP-2000; 2000US-0232398.
XX 14-SEP-2000; 2000US-0232399.
XX 14-SEP-2000; 2000US-0232400.
XX 14-SEP-2000; 2000US-0232401.
XX 14-SEP-2000; 2000US-0233063.
XX 14-SEP-2000; 2000US-0233064.
XX 14-SEP-2000; 2000US-0233065.
XX 21-SEP-2000; 2000US-0234223.
XX 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
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PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
PR 08-NOV-2000; 2000US-0245475.
PR 08-NOV-2000; 2000US-0245476.
PR 08-NOV-2000; 2000US-0245477.
PR 08-NOV-2000; 2000US-0245478.
PR 08-NOV-2000; 2000US-0245523.
PR 08-NOV-2000; 2000US-0245524.
PR 08-NOV-2000; 2000US-0245525.
PR 08-NOV-2000; 2000US-0245526.
PR 08-NOV-2000; 2000US-0245527.
PR 08-NOV-2000; 2000US-0245528.
PR 08-NOV-2000; 2000US-0245532.
PR 08-NOV-2000; 2000US-0245609.
PR 08-NOV-2000; 2000US-0245610.
PR 08-NOV-2000; 2000US-0245611.
PR 08-NOV-2000; 2000US-0245613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.

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PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX Disclosure; SEQ ID NO 30108; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 276 BP; 50 A; 81 C; 69 G; 76 T; 0 other;

Query Match 5.0%; Score 50; DB 22; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 TTGTGAGCAGCGTGGCCACACGCGTGAACCCGATCTCTACTAAATA 215
DB 216 TTGTGAGCAGCGTGGCCACACGCGTGAACCCGATCTCTACTAAATA 167

RESULT 34
ABV54360
ID ABV54360 standard; cDNA; 475 BP.
XX
XX AC ABV54360;
XX
XX 17-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 54351.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
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PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 10509; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 475 BP; 180 A; 62 C; 80 G; 153 T; 0 other;

Query Match 5.0%; Score 50; DB 23; Length 475;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 558
DB 193 AATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT 242

RESULT 35
ABV55359/C
ID ABV55359 standard; cDNA; 578 BP.
XX
XX AC ABV55359;
XX
XX 17-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 55350.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX
XX 16-MAR-2000; 2000US-189862P.
XX
XX 25-MAY-2000; 2000US-207454P.
XX
XX 09-JUN-2000; 2000US-211314P.
XX
XX 18-JUL-2000; 2000US-219007P.
XX
XX 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
```

PT for detecting presence of prostate cancer, stage of prostate cancer -
XX Claim 1; Page 10692-10693; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX
SQ Sequence 578 BP; 160 A; 121 C; 85 G; 211 T; 1 other;

Query Match 5.0%; Score 50; DB 23; Length 578;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
DB 379 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 330

RESULT 36
AAI94916
ID AAI94916 standard; CDNA; 737 BP.
XX
AC AAI94916;
XX
DT 13-NOV-2001 (first entry)
XX
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 991.
XX
KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
XX
KW Homo sapiens.
XX
PN W0200166719-A1.
XX
PD 13-SEP-2001.
XX
PF 02-MAR-2001; 2001WO-JP01629.
XX
PR 07-MAR-2000; 2000JP-0159195.
XX
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM-) HISAMITSU PHARM CO LTD.
XX
PI Nakagawara A;
XX
DR WPI; 2001-565584/63.
XX
PT Nucleic acids originating in gene expressed in human neuroblastoma,
PT useful as probe or primer in diagnosing prognosis of human
PT neuroblastoma, malignancy and susceptibility indicator or tumour marker
PT for anti-cancer agents -
XX
PS Claim 1; Page 763-764; 2979pp; Japanese.
XX
CC The invention relates to novel genes (AAI93926-AAI97963) expressed in
CC human neuroblastoma. The nucleic acids are applicable as a probe or
CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and
CC susceptibility indicators or tumour markers for anti-cancer agents. The
CC gene information for diagnosing prognosis is related to factors similar
CC to that for N-myc and TrkA genes.

XX
SQ Sequence 737 BP; 218 A; 140 C; 140 G; 216 T; 23 other;

Query Match 5.0%; Score 50; DB 22; Length 737;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
DB 361 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 410

RESULT 37
ABA16762/c
ID ABA16762 standard; DNA; 4243 BP.
XX
AC ABA16762;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 9093.
XX
KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN W0200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.

PR	30-AUG-2000;	2000US-0228924.	
PR	01-SEP-2000;	2000US-0229287.	
PR	01-SEP-2000;	2000US-0229343.	
PR	01-SEP-2000;	2000US-0229344.	
PR	01-SEP-2000;	2000US-0229345.	
PR	05-SEP-2000;	2000US-0229509.	
PR	06-SEP-2000;	2000US-0229513.	
PR	06-SEP-2000;	2000US-0230437.	
PR	08-SEP-2000;	2000US-0230438.	
PR	08-SEP-2000;	2000US-0231242.	
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PR	08-SEP-2000;	2000US-0232080.	
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PR	21-SEP-2000;	2000US-0234223.	
PR	21-SEP-2000;	2000US-0234224.	
PR	25-SEP-2000;	2000US-0234997.	
PR	25-SEP-2000;	2000US-0234998.	
PR	26-SEP-2000;	2000US-0235484.	
PR	27-SEP-2000;	2000US-0235834.	
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PR	29-SEP-2000;	2000US-0236327.	
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PR	29-SEP-2000;	2000US-0236370.	
PR	02-OCT-2000;	2000US-0236802.	
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PR	02-OCT-2000;	2000US-0237040.	
PR	13-OCT-2000;	2000US-0239935.	
PR	13-OCT-2000;	2000US-0239937.	
PR	20-OCT-2000;	2000US-0240960.	
PR	20-OCT-2000;	2000US-0241785.	
PR	20-OCT-2000;	2000US-0241786.	
PR	20-OCT-2000;	2000US-0241787.	
PR	20-OCT-2000;	2000US-0241808.	
PR	20-OCT-2000;	2000US-0241809.	
PR	20-OCT-2000;	2000US-0241826.	
PR	01-NOV-2000;	2000US-0242221.	
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PR	08-NOV-2000;	2000US-0246477.	
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PR	08-NOV-2000;	2000US-0246526.	
PR	08-NOV-2000;	2000US-0246527.	
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PR	08-NOV-2000;	2000US-0246532.	
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PR	08-NOV-2000;	2000US-0246610.	
PR	08-NOV-2000;	2000US-0246611.	
PR	08-NOV-2000;	2000US-0246613.	
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PR	17-NOV-2000;	2000US-0249208.	
PR	17-NOV-2000;	2000US-0249209.	
PR	17-NOV-2000;	2000US-0249210.	
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PR	17-NOV-2000;	2000US-0249212.	
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PR	17-NOV-2000;	2000US-0249224.	
PR	17-NOV-2000;	2000US-0249245.	
PR	17-NOV-2000;	2000US-0249264.	
PR	17-NOV-2000;		

ID XX AAK74563 standard; DNA; 5283 BP.
AC XX AAK74563;
XX XX
DT DT 07-NOV-2001 (first entry)
XX XX
DE DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29375.
DE DE
KW KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW KW Cytostatic; gene therapy; vaccine; metastasis; ds.
XX XX
OS OS Homo sapiens.
XX XX
PN PN WO200157182-A2.
XX XX
PD PD 09-AUG-2001.
XX XX
PF PF 17-JAN-2001; 2001WO-US01354.
XX XX
PR PR 31-JAN-2000; 2000US-0179065.
PR PR 04-FEB-2000; 2000US-0180628.
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PR PR 18-APR-2000; 2000US-0198123.
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 PR 17-NOV-2000; 2000US-0249299.
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 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 06-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 PR 05-JAN-2001; 2001US-0254678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and
 metastasis -

XX

PS Disclosure; SEQ ID NO 29132; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 5572 BP; 1315 A; 1312 C; 1444 G; 1501 T; 0 other;
 Query Match 5.0%; Score 50; DB 22; Length 5572;
 Best Local Similarity 100.0%; Pred. No. 9.7e-14;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 338 TCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACACGCTGTAGT 387
 Db 4009 TCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACACGCTGTAGT 4058
 RESULT 40
 AAK74321
 ID AAK74321 standard; DNA; 5573 BP.
 AC AAK74321;
 XX
 DT 07-NOV-2001 (first entry)
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29133.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ds.
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 11-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 14-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-02252114.
PR 14-AUG-2000; 2000US-0225266.
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PR 14-AUG-2000; 2000US-0225368.
PR 14-AUG-2000; 2000US-0225270.
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PR 14-AUG-2000; 2000US-0225757.
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PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.

PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI; 2001-483426/52.

XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis -

XX Disclosure; SEQ ID NO 29133; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK62169
XX represent sequences used in the exemplification of the present invention.

SQ Sequence 5573 BP; 1314 A; 1312 C; 1446 G; 1501 T; 0 other;
Query Match 5.0%; Score 50; DB 22; Length 5573;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 338 TCTACTAAATAACAAATAGCCAGGTGTGGTGCACAGCCTGTAGT 387
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Db 4010 TCTACTAAATAACAAATAGCCAGGTGTGGTGCACAGCCTGTAGT 4059
RESULT 41
AAS46383
ID AAS46383 standard; DNA; 5649 BP.
XX
AC AAS46383;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #105.
XX
DE Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP02955.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer -
XX
PS Claim 1; SEQ ID No 105; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC (SS) and sequences complementary to (SS). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC of diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 5649 BP; 1566 A; 184 C; 1474 G; 2425 T; 0 other;
Query Match 5.0%; Score 50; DB 22; Length 5649;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 4508 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 4557
RESULT 42
AAS46384/C
ID AAS46384 standard; DNA; 5649 BP.
XX
AC AAS46384;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #106.
XX
DE Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP02955.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer -
XX
PS Claim 1; SEQ ID No 106; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes having a sequence taken from 536 (actually 533 since
CC (SS) and sequences complementary to (SS). The nucleic acid may be a
CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC of diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and

CC oncogenes. Sequences with even numbered Seq ID numbers are the
CC complementary sequence of the corresponding odd numbered sequence (e.g.
CC ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence
CC is missing).
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

XX Seq Sequence 5649 BP; 1212 A; 184 C; 1397 G; 2856 T; 0 other;

Query Match 5.0%; Score 50; DB 22; Length 5649;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 1142 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAT 1093
|||||

RESULT 43

ABK40007
ID ABK40007 standard; DNA; 5649 BP.

XX

AC ABK40007;

DT 21-MAY-2002 (first entry)

XX

DE Human chemically pretreated gene sequence #45 strand 1.

XX

KW Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
KW Cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO200202806-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-EP07470.

XX

PR 30-JUN-2000; 2000DE-1032529.

XX

PR 01-SEP-2000; 2000DE-1043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

PI WPI; 2002-154757/20.

XX

DR New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
PT useful for detecting cytosine methylation state of genes associated
PT with pharmacogenomics and for therapy of diseases e.g. cancer

XX

PS Claim 1; SEQ ID No 89; 24pp; English.

XX

CC The invention relates to a nucleic acid comprising a sequence at
CC least 18 bases in length of a segment of the chemically pretreated DNA
CC of genes associated with pharmacogenomics according to one of the
CC sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1
CC (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
CC (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC MRP (NM_004996), NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC from 87 sequences and their complementary sequences, or a sequence (S1) chosen
CC is bisulphite treatment to convert cytosines. The chemical pretreatment
CC into uracils. Also included are an oligomer (II) in particular an
CC oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC each case at least one base sequence having a length of 9 nucleotides
CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in
CC an array for analysing diseases associated with the methylation state

CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC of the 87 sequences. The oligomers may also be used as PCR primers.
CC The set of 87 nucleic acids and their complements is useful for diagnosis
CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

XX Seq Sequence 5649 BP; 1566 A; 184 C; 1474 G; 2425 T; 0 other;

Query Match 5.0%; Score 50; DB 24; Length 5649;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAT 558
|||||

Db 4508 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAT 4557
|||||

RESULT 44

ABK40008/c

XX

ID ABK40008 standard; DNA; 5649 BP.

XX

AC ABK40008;

XX

DT 21-MAY-2002 (first entry)

XX

DE Human chemically pretreated gene sequence #45 strand 2.

XX

KW Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour;
KW Cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1;
KW UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

PN WO200202806-A2.

XX

PD 10-JAN-2002.

XX

PF 29-JUN-2001; 2001WO-EP07470.

XX

PR 30-JUN-2000; 2000DE-1032529.

XX

PR 01-SEP-2000; 2000DE-1043826.

XX

PA (EPIG-) EPIGENOMICS AG.

XX

PI Olek A, Piepenbrock C, Berlin K;

XX

PI WPI; 2002-154757/20.

XX

DR New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers,
PT useful for detecting cytosine methylation state of genes associated
PT with pharmacogenomics and for therapy of diseases e.g. cancer

XX

PS Claim 1; SEQ ID No 90; 24pp; English.

XX

CC The invention relates to a nucleic acid comprising a sequence at
CC least 18 bases in length of a segment of the chemically pretreated DNA
CC of genes associated with pharmacogenomics according to one of the
CC sequences of the genes ALDH6 (NM_000693), CYP11A (NM_000781), CYP11B1
CC (NM_000497), CYP3A3 (NM_000776 and NM_017460), DPYD (NM_000110), EPHX2
CC (NM_001979), OCLN (NM_002538), TXNRD1 (NM_003330), UGT8 (NM_003360),
CC MRP (NM_004996), NM_019900, NM_019901, NM_019902, NM_019862, NM_019898,
CC from 87 sequences and their complementary sequences, or a sequence (S1) chosen
CC is bisulphite treatment to convert cytosines. The chemical pretreatment
CC into uracils. Also included are an oligomer (II) in particular an
CC oligonucleotide or a peptide nucleic acid (PNA)-oligomer, comprising in
CC each case at least one base sequence having a length of 9 nucleotides
CC which hybridises to or is identical to a chemically pretreated DNA of
CC genes associated with pharmacogenomics and their complements, arranged in

CC an array for analysing diseases associated with the methylation state
CC (CpG) and/or detecting SNPs (single nucleotide polymorphisms)
CC of the 87 sequences. The oligomers may also be used as PCR primers.
CC The set of 87 nucleic acids and their complements is useful for diagnosis
CC and therapy of solid tumours and cancer. The present sequence
CC represents one the 87 DNA sequences or its complement.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 5649 BP; 1212 A; 184 C; 1397 G; 2856 T; 0 other;

Query Match 5.0%; Score 50; DB 24; Length 5649;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 1142 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 1093

RESULT 45

ABL32848

ID ABL32848 standard; DNA; 5649 BP.

XX AC ABL32848;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 821.

KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.

XX OS Homo sapiens.

XX PN WO200200928-A2.

XX PD 03-JAN-2002.

XX PF 02-JUL-2001; 2001WO-EP07537.

XX PR 30-JUN-2000; 2000DE-1032529.

XX PR 01-SEP-2000; 2000DE-1043826.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Olek A, Piepenbrock C, Berlin K;

XX DR WPI; 2002-130909/17.

XX PT Nucleic acid comprising fragment of chemically modified gene, useful
XX for diagnosis and treatment of diseases associated with abnormal
XX cytosine methylation

XX PS Claim 1; SEQ ID NO 821; 32pp + Sequence Listing; German.

XX CC The present invention provides a number of human immune system associated
XX genes which are modified by the methylation of cytosines. The sequences
XX can be used in the diagnosis and treatment of immune system disorders,
XX including eye diseases, such as retinopathy, neovascular glaucoma and
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX diseases. The present sequence is a gene of the invention.

XX

SQ Sequence 5649 BP; 1566 A; 184 C; 1474 G; 2425 T; 0 other;
Query Match 5.0%; Score 50; DB 24; Length 5649;
Best Local Similarity 100.0%; Pred. No. 9.7e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 4508 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 4557

Search completed: November 24, 2002, 10:51:00
Job time : 1558 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 09:22:22 ; Search time 3223 Seconds
(without alignments)
9029.726 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GTGTGACCTTACCTCTCT.....CAGATGATGACGGCGTGC 1000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pi.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.cm.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pin.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1000	100.0	1000	6	ARI53982	ARI53982 Sequence
c	879	87.9	69964	9	HS496C20	Z83847 Human DNA s
3	492	49.2	138459	2	AC090795	AC090795 Homo sapi
4	304	30.4	62102	2	AC104363	AC104363 Homo sapi
c	77	7.7	102151	9	HS979N1	AL035659 Human DNA
c	76	7.6	166869	9	AC016395	AC016395 Homo sapi
7	76	7.6	170998	9	AL390071	AL390071 Human DNA
8	76	7.6	290625	2	AL442068	AL442068 Homo sapi
9	75	7.5	59427	9	AC079882	AC079882 Homo sapi
10	75	7.5	124821	9	AC004983	AC004983 Homo sapi
11	74	7.4	167417	9	AC011505	AC011505 Homo sapi
c	72	7.2	96308	9	AF190465	AF190465 Homo sapi
13	72	7.2	173354	9	HS149A16	AL021937 Human DNA
c	72	7.2	273403	9	AC011498	AC011498 Homo sapi
c	71	7.1	162201	2	AC024152	AC024152 Homo sapi
16	71	7.1	186241	9	AC103560	AC103560 Homo sapi
c	70	7.0	163396	9	AL161445	AL161445 Human DNA
c	70	7.0	197143	2	AC069173	AC069173 Homo sapi
c	67	6.7	170513	2	AC023603	AC023603 Homo sapi
c	67	6.7	178361	9	AC006042	AC006042 Homo sapi
c	66	6.6	104656	9	AL731576	AL731576 Human DNA
c	66	6.6	121028	9	AY052369	AY052369 Homo sapi
c	66	6.6	166975	9	AC110023	AC110023 Homo sapi
c	66	6.6	182627	2	AC024262	AC024262 Homo sapi
c	66	6.6	182776	9	AC091078	AC091078 Homo sapi
c	66	6.6	186431	2	AC022281	AC022281 Homo sapi
27	66	6.6	189116	2	CNS01DWM	AL137779 Human chr
28	64	6.4	127140	9	AL136137	AL136137 Human DNA
29	64	6.4	146954	9	AL590640	AL590640 Human DNA
30	64	6.4	173510	9	AL359272	AL359272 Human DNA
31	64	6.4	177422	2	AC021923	AC021923 Homo sapi
c	64	6.4	187349	9	AP003352	AP003352 Homo sapi
33	64	6.4	197870	2	AC091075	AC091075 Homo sapi
34	64	6.4	199208	2	AC019236	AC019236 Homo sapi
c	63	6.3	62443	9	AL136973	AL136973 Human DNA
36	63	6.3	85713	9	HSY237C10_3	Continuation (4 of
37	63	6.3	160010	2	AL844148	AL844148 Homo sapi
c	63	6.3	168071	2	AL391479	AL391479 Homo sapi
c	63	6.3	182789	9	AC021761	AC021761 Homo sapi
c	63	6.3	212730	2	AL354975	AL354975 Homo sapi
41	63	6.3	232162	2	AL591130	AL591130 Homo sapi
c	62	6.2	68122	9	AP000998	AP000998 Homo sapi
43	62	6.2	71530	9	AC025810	AC025810 Homo sapi
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ALIGNMENTS

RESULT 1	ARI53982	1000 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	Sequence 32 from patent US 6238863.				
DEFINITION	ARI53982				
ACCESSION	ARI53982.1	GI:15122035			
VERSION	Unknown.				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1000)				
AUTHORS	Schumm,J.W. and Bachter,J.W.				
TITLE	Materials and methods for indentifying and analyzing intermediate tandem repeat DNA markers				
JOURNAL	Patent: US 6238863-A 32 29-MAY-2001;				

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FEATURES
Source
Location/Qualifiers
1. .1000
BASE COUNT 302 a 240 c 231 g 226 t 1 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 ATTGTTTAAATAATTAATGGATAGGCTAGCGGGTGGCTACGCTGTAATCCCA 120
QY 121 GCACCTTTAGAGGTGGAAGAGGTGGATCAGTGTGAGTCTAGGAGTCTTTGAGACGAGCTG 180
Db 121 GCACCTTTAGAGGTGGAAGAGGTGGATCAGTGTGAGTCTAGGAGTCTTTGAGACGAGCTG 180
QY 181 GCCAACAGGTGAACCCCATCTCTACTTAAATAAATAAATAAATAGCTNGGGTGGCTGGCT 240
Db 181 GCCAACAGGTGAACCCCATCTCTACTTAAATAAATAAATAAATAGCTNGGGTGGCTGGCT 240
QY 241 CACACCTGTAATCCAGCAGCTTTGGAGGCTGAGCGGGTGGATCAGTGAAGTCAAGGAG 300
Db 241 CACACCTGTAATCCAGCAGCTTTGGAGGCTGAGCGGGTGGATCAGTGAAGTCAAGGAG 300
QY 301 TTCAAGCCAGGCTGGGCAACATGGTGAACACCGTCTCTACTTAAATAAATAAATAAATAA 360
Db 301 TTCAAGCCAGGCTGGGCAACATGGTGAACACCGTCTCTACTTAAATAAATAAATAAATAA 360
QY 361 CCAGGTGTGGTGACACAGGCTGTAGTCCAGCTACTTGGAGGCTGAGCGGGAAGAATC 420
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QY 421 GCTTGAACCCAGTAGGAGAGGTTGGAGTGGAGCGAGATGAAGTCACTGCTCCAGCC 480
Db 421 GCTTGAACCCAGTAGGAGAGGTTGGAGTGGAGCGAGATGAAGTCACTGCTCCAGCC 480
QY 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAAATAAATAAATAAATAAATAAATAAATAA 540
Db 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAAATAAATAAATAAATAAATAAATAAATAA 540
QY 541 AATAAATAAATAAATAAATAAAGGCTGGCATTTGGCTAGCAGTATATGCCCAATA 600
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Db 781 AGGCCATCTGGAGCCCTCCAGCGGGTGGTTCGGGAACTCATAGTCTGCTCTCAAT 840
QY 841 GGCACACTGAAGGTAGAGAGTTCGGGTCCCACTCCGACCCCTCTCTCTGACTCAC 900
Db 841 GGCACACTGAAGGTAGAGAGTTCGGGTCCCACTCCGACCCCTCTCTCTGACTCAC 900
QY 901 TGCTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
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Db 961 CAGGACTCCAGGAGCCACGACAGATGATGACCGGCTGC 1000
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RESULT 2

HS496C20/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

HS496C20 69964 bp DNA linear PRI 12-DEC-1999
Human DNA sequence from clone RP3-496C20 on chromosome 22 Contains
STSs, GSSs and two putative CpG islands, complete sequence.

Z83847
Z83847.1 GI:3550060
HTG: CpG island.
Homo sapiens.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Clark G.
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

On Sep 8, 1998 this sequence version replaced gi:3413284.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.

This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C/elegans/wormpep

RP3-496C20 is
from the library RPI-3 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong. For further details see
http://baopac.med.buffalo.edu/

VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-496C20. The true
left end of clone RP3-340K22 is at 21972 in this sequence. The true
right end of clone RPI-140N12 is at 41206 in this sequence. The
start of this sequence overlaps with sequence Z82206. The end of
this sequence overlaps with sequence AL022238.

Location/Qualifiers
1. .69964
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/db_xref="taxon:9606"
/chromosome="22"
/clone="RP3-496C20"
/clone_lib="RPI-3"
/note="match: STS: Em:HS496C20S; match: STS: Em:AL021673"
169. .311
/note="MIR repeat: matches 71. .211 of consensus"
551. .600
/note="10 copies 5 mer tggtt 76 conserved"
2394. .2462
/note="L2 repeat: matches 2626. .2696 of consensus"
3060. .3221
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3226. .3535

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repeat_region
repeat_region
repeat_region
repeat_region

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4446. .4662  
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5924. .5970  
misc_feature /note="L2 repeat: matches 2701. .2748 of consensus"  
6015. .6330  
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6149. .6461  
repeat_region /note="AluSx repeat: matches 1. .312 of consensus"  
6462. .6596  
repeat_region /note="AluSg/x repeat: matches 1. .135 of consensus"  
6632. .6695  
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7817. .8113  
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repeat_region /note="MIR repeat: matches 80. .191 of consensus"  
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9481. .9605  
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10502. .10587  
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10511. .10643  
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11303. .11539  
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13046. .13314  
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13527. .13983  
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13984. .14293  
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14348. .14649  
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14651. .14966  
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14967. .15007  
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repeat_region /note="L1M4 repeat: matches 3784. .5097 of consensus"  
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18511. .18822  
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20302. .20464  
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22217. .22508  
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26997. .27304  
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27326. .27595  
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28098. .28406  
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31120. .31339  
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34776. .34821  
repeat_region /note="L2 repeat: matches 2688. .2733 of consensus"  
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repeat_region /note="AluSx repeat: matches 1. .300 of consensus"  
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repeat_region /note="MER20 repeat: matches 1. .204 of consensus"  
36460. .36544  
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37480. .37620  
repeat_region /note="MIR repeat: matches 4. .150 of consensus"  
37861. .38188  
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 999; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GGTCGACCTATCTCTGACCTCAGTTTCTTCATCCGTAATAATGAAAGCTGCTAG 60
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Db 689 GGTCGACCTATCTCTGACCTCAGTTTCTTCATCCGTAATAATGAAAGCTGCTAG 6624
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Qy 61 ATTGTTGTAATAAATAATGAGTAGGCTAGCGGGTGGCTCACCGCTGATCCCA 120
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Db	6623	ATTGTTGTAATAAATAAATGAATAGGCTAGCGCGTGGCTCAGCGCTGTAATCCCA	6564
QY	121	GCACCTTTAGAGGTGGAAGAGGGTGGATCACTTGGAGTGGAGTTTGGAGACGAGCTG	180
Db	6563	GCACCTTTAGAGGTGGAAGAGGGTGGATCACTTGGAGTGGAGTTTGGAGACGAGCTG	6504
QY	181	GCCAACCGGTGAACCCCACTCTCTAATAAATAAATAATAGCTTGGTGGCGTGGCT	240
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QY	241	CACACCTGTAATCCAGCACTTTGGGAGCGCTGAGACGGGTGGATCACTTGAAGTCAGGAG	300
Db	6444	CACACCTGTAATCCAGCACTTTGGGAGCGCTGAGACGGGTGGATCACTTGAAGTCAGGAG	6385
QY	301	TTCAGGCGAGCGCTGGCAACATGGTGAACACAGCTCTTACTTAAATAAATAAATAATAG	360
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QY	361	CCAGGTGTTGGTGGCACAGCGCTGTAGTCCAGCTACTTGGAGGCTGAGGCGGAAGATC	420
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QY	421	GCTTGAACCCAGTGGCAGAGGTGGCAGTGAGCGGAGATGAAGTCACTGCTCCAGCC	480
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QY	481	TGGGTGACAGCAGCAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAAATAA	540
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QY	541	AATAAATAAATAAATAAATAAAGGCTGGCATTTGGCTAGCATTATATGCCAATA	600
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QY	661	ACCCCCATTAGCTTAAGGCAGATTTCTACCGTACTCTCTGTAATTTCTGTTCT	720
Db	6024	ACCCCCATTAGCTTAAGGCAGATTTCTACCGTACTCTCTGTAATTTCTGTTCT	5965
QY	721	GGCACAATGTTGGTCTCAGTGAACATGTTGAGTGAATGAGCAAAATGCAAGAACTCC	780
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QY	781	AGCCATCTGGAGCCCTCCAGCGGGTGGTGGGAACTCATAGTCTGTCCTCAAT	840
Db	5904	AGCCATCTGGAGCCCTCCAGCGGGTGGTGGGAACTCATAGTCTGTCCTCAAT	5845
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Db	5844	GGCCCACTGAAAGTGAAGTCTTGGGTCCACCTCCGACCCCACTCTCTGCTGACTCAC	5785
QY	901	TGCTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	960
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RESULT	3		
LOCUS	AC090795	138459 bp	DNA linear
DEFINITION	Homo sapiens chromosome 8 clone RP11-254K5 map 8, WORKING DRAFT		
ACCESSION	AC090795		
VERSION	AC090795.2	GI:14336499	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 138459) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-254K5 Unpublished 2 (bases 1 to 138459) Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalil,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galaan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lehotzky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 11, 2001 this sequence version replaced gi:13270664. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html ----- Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www.seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu ----- Project Information Center project name: L12790 Center clone name: 254_K_5 ----- Summary Statistics Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 133567 bases at least Q40 Consensus quality: 135811 bases at least Q30 Consensus quality: 136678 bases at least Q20 Insert size: 139000; agarose-fp Insert size: 137359; sum-of-contigs Quality coverage: 6.5 in Q20 bases; agarose-fp Quality coverage: 6.6 in Q20 bases; sum-of-contigs ----- * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. * 1 1411: contig of 1411 bp in length * 1412 1511: gap of 100 bp * 1512 2165: contig of 654 bp in length * 2166 2265: gap of 100 bp * 2266 3074: contig of 809 bp in length * 3075 3174: gap of 100 bp * 3175 4763: contig of 1589 bp in length * 4764 4863: gap of 100 bp * 4864 6161: contig of 1298 bp in length * 6162 6261: gap of 100 bp

* NOTE: This record contains 81 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 665: contig of 665 bp in length
666 765: gap of 100 bp
766 1454: contig of 689 bp in length
1455 1554: gap of 100 bp
1555 2232: contig of 678 bp in length
2233 2332: gap of 100 bp
3029 3128: gap of 100 bp
3129 3733: contig of 625 bp in length
3754 3853: gap of 100 bp
3854 4459: contig of 606 bp in length
4460 4559: gap of 100 bp
4560 5225: contig of 666 bp in length
5226 5325: gap of 100 bp
5326 5979: contig of 654 bp in length
5980 6079: gap of 100 bp
6080 6752: contig of 673 bp in length
6753 6852: gap of 100 bp
6853 7526: contig of 674 bp in length
7527 7626: gap of 100 bp
7627 8307: contig of 681 bp in length
8308 8407: gap of 100 bp
8408 9090: contig of 683 bp in length
9091 9190: gap of 100 bp
9191 9880: contig of 690 bp in length
9881 9980: gap of 100 bp
10668 10667: contig of 687 bp in length
10668 10767: gap of 100 bp
10768 11436: contig of 669 bp in length
11437 11536: gap of 100 bp
11537 12157: contig of 621 bp in length
12158 12257: gap of 100 bp
12258 12913: contig of 656 bp in length
12914 13013: gap of 100 bp
13014 13667: contig of 654 bp in length
13668 13767: gap of 100 bp
13768 14429: contig of 662 bp in length
14430 14529: gap of 100 bp
14530 15189: contig of 660 bp in length
15190 15289: gap of 100 bp
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15951 16050: gap of 100 bp
16051 16724: contig of 674 bp in length
16725 16824: gap of 100 bp
16825 17505: contig of 681 bp in length
17506 17605: gap of 100 bp
17606 18290: contig of 685 bp in length
18291 18390: gap of 100 bp
18391 19050: contig of 660 bp in length
19051 19150: gap of 100 bp
19151 19807: contig of 657 bp in length
19808 19907: gap of 100 bp
19908 20568: contig of 661 bp in length
20569 20668: gap of 100 bp
20669 21322: contig of 654 bp in length
21323 21422: gap of 100 bp
21423 22079: contig of 657 bp in length
22080 22179: gap of 100 bp
22180 22853: contig of 673 bp in length
22853 22952: gap of 100 bp
22953 23621: contig of 669 bp in length

23622 23721: gap of 100 bp
23722 24386: contig of 665 bp in length
24387 24486: gap of 100 bp
24487 25174: contig of 688 bp in length
25175 25274: gap of 100 bp
25275 25957: contig of 683 bp in length
25958 26057: gap of 100 bp
26058 26729: contig of 672 bp in length
26730 26829: gap of 100 bp
26830 27478: contig of 649 bp in length
27479 27578: gap of 100 bp
27579 28237: contig of 659 bp in length
28238 28337: gap of 100 bp
28338 29002: contig of 665 bp in length
29003 29102: gap of 100 bp
29103 29764: contig of 662 bp in length
29765 29864: gap of 100 bp
29865 30544: contig of 680 bp in length
30545 30644: gap of 100 bp
30645 31330: contig of 686 bp in length
31331 31430: gap of 100 bp
31431 32107: contig of 677 bp in length
32108 32207: gap of 100 bp
32208 32887: contig of 680 bp in length
32888 32987: gap of 100 bp
32988 33679: contig of 692 bp in length
33680 33779: gap of 100 bp
33780 34451: contig of 672 bp in length
34452 34551: gap of 100 bp
34552 35216: contig of 665 bp in length
35217 35316: gap of 100 bp
35317 35978: contig of 662 bp in length
35979 36078: gap of 100 bp
36079 36731: contig of 653 bp in length
36732 36831: gap of 100 bp
36832 37486: contig of 655 bp in length
37487 37586: gap of 100 bp
37587 38249: contig of 663 bp in length
38250 38349: gap of 100 bp
38350 39032: contig of 683 bp in length
39033 39132: gap of 100 bp
39133 39815: contig of 683 bp in length
39816 39915: gap of 100 bp
39916 40576: contig of 661 bp in length
40577 40676: gap of 100 bp
40677 41356: contig of 680 bp in length
41357 41456: gap of 100 bp
41457 42141: contig of 685 bp in length
42142 42241: gap of 100 bp
42242 42899: contig of 658 bp in length
42900 42999: gap of 100 bp
43000 43650: contig of 651 bp in length
43651 43750: gap of 100 bp
43751 44412: contig of 662 bp in length
44413 44512: gap of 100 bp
44513 45169: contig of 657 bp in length
45170 45269: gap of 100 bp
45270 45925: contig of 656 bp in length
45926 46025: gap of 100 bp
46026 46695: contig of 670 bp in length
46696 46795: gap of 100 bp
46796 47481: contig of 686 bp in length
47482 47581: gap of 100 bp
47582 48185: contig of 604 bp in length
48186 48285: gap of 100 bp
48286 48964: contig of 679 bp in length
48965 49064: gap of 100 bp
49065 49751: contig of 687 bp in length
49752 49851: gap of 100 bp
49852 50518: contig of 667 bp in length
50519 50618: gap of 100 bp
50619 51290: contig of 672 bp in length
51291 51390: gap of 100 bp


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/note="FAM_C repeat: matches 130..142 of consensus"
18035..18164
/note="FAM_C repeat: matches 1..130 of consensus"
19499..19566
/note="MUT1A2-internal repeat: matches 1582..1651 of
consensus"
repeat_region 19567..19870
/note="AluSc repeat: matches 1..294 of consensus"
20838..20934
/note="L1M1 repeat: matches -1210..-1134 of consensus"
join(24239..24291,29142..29175,29299..29496,30784..30942,
33601..33681,35749..35805,41891..41981,42579..42769,
43394..43715,44666..44724,46107..46206,46993..47154,
49581..49786,51645..51745,52698..52879,55139..55224,
59047..59180,59335..59440,59532..59640,59921..60054,
60223..60386,60755..61007)
/gene="dj979N1.1"
/codon_start=1
/evidence=not_experimental
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/db_xref="GI:6562060"
/translation="MERKRDADIEKGLQFQSTLPKOEYEAFLKLVNLFASGN
DLFRKDYQALVQIMGLNADYADSDVALPRELLCKLRVNRACVFTGLYERAL
EDEKALGDSEIRALFRKARALNELGRHKEAVEYSSRCSALPHDESVTJUGLEA
OKGLRVKRVKRPQELTFSLNSGTAGVAGDQSGSLSDIDTGNVPDTRQV
EGAPRCYVDPGSPALLPSTPTPLPPLPHVLDLAPLDSSTLSDLSDFSDGV
FGELDTLLDSLSVQLGSGSGVSELPQIPVFRGTPPLPVPVGGSPVSPSP
ASGLVMDPSKLAASYDALDPGPTLDPLDLPKSETRDALDSGTRGSLKPD
SFEETNSQDHRPPSGAQPAPSPPCMTALLKNPLAATHEKQACQICPKTGP
RAGDITYREGLEHKRDILLGLRSEDQWRRIRPRTKNSFVGSYILCKDMINKQ
DCKYDNCTEAYHOEIDVWTERKGTNLDLPLGKVRGSLTAKLLKHOGIF
TFELCEIDSPRIISGNDSPSVCSNLAHKSFYNNKLVHIVRSTLSKSIKQF
QEFQFDVREHYRGCLRDESHFAHSFELKVLWLLQYQSWTHDIVQESKYYWQ
MEAHGAKSSMGAPRTGPFSTFDLQMKFVCGWNGOVVPDKOLKYSARHWO
TERRVLLVSKARKWVRPLRNFPOQYDLCIHAQGRKCOYVGNCSFAISPE
ERDMTFMKNKILDMQVDMWLAKHNPCKPGEGTPISSREGEKQIOMPTDYADIM
GYHWCCKNSKKQOQHQHSEKHEKFTSDSDASGAFRPFMGFEFLCDLQMG
KACPGDKRCAGHGBELNEDLRVLKQKAKRKMLLCPDRDDDFGRYNFLLED
GLAGATPEAPAAAGAAATTGT"
23406..23716
/note="AluYa5 repeat: matches 1..311 of consensus"
26153..26298
/note="MER69A repeat: matches 1..133 of consensus"
28743..29117
/note="L1M3e repeat: matches -429..737 of consensus"
complement(30252..30637)
/note="match: STS: Em:G14621"
join(33626..33681,35749..35805,41891..41933,42579..42630)
/gene="dj979N1.2"
join(<33626..33681,35749..35805,41891..41933,
42579..42630)
/gene="dj979N1.2"
/note="supported by GENSCAN
GENSCAN, CpG island and polyA features suggest this gene
fragment and fragments dj979N1.1..-3 and -4 are part of
one gene
match: ESTs: Em:AI122015 Em:AA306154"
/codon_start=3
/evidence=not_experimental
/product="dj979N1.2 (novel protein)"
/protein_id="CAB62494.1"
/db_xref="GI:6562061"
/translation="ELAQKGLRVKAYKRPQELTFSLNSGTAGVADQTSNGLG
SIDDIETDCYDVPGRSPALLPSTPT"
34507..35006
/gene="dj979N1.2"
/note="CpG island"
/evidence=not_experimental
34636..34823
/gene="dj979N1.2"
/note="Single clone region. region contains only reads

repeat_region 166869 bp DNA linear PRI 14-MAY-2002
AC016395 Homo sapiens chromosome 10 clone RF11-153K11, complete sequence.
LOCUS AC016395
DEFINITION AC016395
ACCESSION AC016395
VERSION AC016395.5 GI:20564406
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Smith,D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
Unpublished
2 (bases 1 to 166869)
Smith,D.R.
Direct Submission
3 (bases 1 to 166869)
Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
Smith,D.R.
Direct Submission
4 (bases 1 to 166869)
Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
Smith,D.R.
Direct Submission
4 (bases 1 to 166869)
Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On May 14, 2002 this sequence version replaced gi:9929646.
Location/Qualifiers
1..166869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-153K11"
/clone_lib="RPI-11"
BASE COUNT 47408 a 35216 c 35336 g 48909 t
ORIGIN

Query Match 7.6%; Score 77; DB 9; Length 166869;
Best Local Similarity 100.0%; Pred. No. 1.le-33;
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GTCCTACTATAAAATACAAAATATAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGACT 394
|||||
Db 19376 GTCCTACTATAAAATACAAAATATAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGACT 394
|||||
QY 395 ACTTGGGAGCGTGAGGC 411
|||||
Db 18316 ACTTGGGAGCGTGAGGC 18300
|||||

RESULT 6
AC016395/c
LOCUS AC016395 166869 bp DNA linear PRI 14-MAY-2002
DEFINITION Homo sapiens chromosome 10 clone RF11-153K11, complete sequence.
ACCESSION AC016395
VERSION AC016395.5 GI:20564406
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Smith,D.R.
Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
Unpublished
2 (bases 1 to 166869)
Smith,D.R.
Direct Submission
3 (bases 1 to 166869)
Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
Smith,D.R.
Direct Submission
4 (bases 1 to 166869)
Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On May 14, 2002 this sequence version replaced gi:9929646.
Location/Qualifiers
1..166869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-153K11"
/clone_lib="RPI-11"
BASE COUNT 47408 a 35216 c 35336 g 48909 t
ORIGIN

Query Match 7.6%; Score 76; DB 9; Length 166869;
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Best Local Similarity 100.0%; Pred. No. 4.5e-33;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATATACAAATAATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTA 395
|||||
Db 73964 TCTCTACTAAATATACAAATAATAGCCAGGTGTGGTGGCACACGCTGTAGTCCAGCTA 73905
|||||
QY 396 CTTGGAGGCTGAGGC 411
|||||
Db 73904 CTTGGAGGCTGAGGC 73889

RESULT 7
AL3900071
LOCUS Human DNA sequence from clone RP11-98D3 on chromosome 13, complete
DEFINITION AL3900071 170998 bp DNA linear PRI 25-MAR-2001
ACCESSION AL3900071
VERSION AL3900071.9 GI:13373975
KEYWORDS HPG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Phillimore, B.
Direct Submission
Submitted (23-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Mar 16, 2001 this sequence version replaced gi:12743811.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-98D3 is from the library RP11-11.1 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
This sequence is the entire insert of clone RP11-98D3 The true left
end of clone RP11-88019 is at 112608 in this sequence. The true
right end of clone RP11-29G24 is at 33813 in this sequence.
FEATURES
source
1..170998
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-98D3"
/clone_lib="RP11-11"
1..132
/note="match: STS: Em:HSPH27EB"
1332..1494
repeat_region /note="MER20 repeat: matches 73..217 of consensus"
1495..1736
repeat_region /note="CpG island"
/note="L2 repeat: matches 2339..2594 of consensus"

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repeat_region 1848..1965
/note="L1P5 repeat: matches 6026..6143 of consensus"
2110..2412
/note="AluSq repeat: matches 1..303 of consensus"
4254..4301
/note="L2 copies 4 mer ttcc 75% conserved"
7203..7239
/note="L2 repeat: matches 2620..2656 of consensus"
7563..7708
/note="MIR repeat: matches 110..257 of consensus"
7989..8060
/note="3 copies 24 mer 80% conserved"
8003..8060
/note="29 copies 2 mer at 91% conserved"
8005..8060
/note="14 copies 4 mer atat 92% conserved"
8062..8718
/note="L1P5 repeat: matches 5486..6142 of consensus"
9019..9070
/note="13 copies 4 mer tata 80% conserved"
10761..10991
/note="L2 repeat: matches 2482..2710 of consensus"
11163..11609
/note="L2 repeat: matches 2010..2492 of consensus"
12426..12736
/note="AluJb repeat: matches 1..299 of consensus"
13347..13654
/note="AluY repeat: matches 1..309 of consensus"
14005..14129
/note="MIR repeat: matches 19..148 of consensus"
16812..17120
/note="AluY repeat: matches 1..309 of consensus"
17927..18055
/note="MIR repeat: matches 86..218 of consensus"
19169..19260
/note="46 copies 2 mer at 69% conserved"
19195..19254
/note="15 copies 4 mer atat 76% conserved"
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/note="L1MB8 repeat: matches 5830..6173 of consensus"
19846..20139
/note="AluY repeat: matches 1..295 of consensus"
20140..20489
/note="L1MB8 repeat: matches 5462..5830 of consensus"
23000..23410
/note="MSTRC repeat: matches 15..405 of consensus"
24771..25102
/note="L2 repeat: matches 1900..2247 of consensus"
25229..25415
/note="L2 repeat: matches 1485..1683 of consensus"
25574..25874
/note="AluJb repeat: matches 1..304 of consensus"
26566..26693
/note="L2 repeat: matches 2352..2476 of consensus"
26816..26994
/note="MIR repeat: matches 29..226 of consensus"
27529..27694
/note="L2 repeat: matches 2495..2644 of consensus"
28745..29001
/note="AluJo repeat: matches 1..256 of consensus"
29425..29716
/note="AluSq repeat: matches 1..292 of consensus"
30387..30983
/note="MER90 repeat: matches 1..615 of consensus"
31050..31356
/note="AluX repeat: matches 1..306 of consensus"
32941..33577
/note="CpG island"
/evidence=not_experimental
37667..38255
/note="CpG island"
/evidence=not_experimental
38473..38928

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misc_feature /note="20 copies 3 mer ctg 98% conserved"
40650. .41215
/note="CpG island"
repeat_region /evidence=not_experimental
44973. .45123
repeat_region /note="L1ME1 repeat: matches 6016. .6159 of consensus"
46468. .46527
repeat_region /note="30 copies 2 mer tg 85% conserved"
48732. .48843
repeat_region /note="MIR repeat: matches 60. .196 of consensus"
52923. .53162
repeat_region /note="MIR repeat: matches 11. .245 of consensus"
53167. .53264
repeat_region /note="MIR repeat: matches 106. .213 of consensus"
53297. .53386
repeat_region /note="MIR repeat: matches 8. .98 of consensus"
53543. .53889
repeat_region /note="L2 repeat: matches 1651. .2047 of consensus"
54290. .54575
repeat_region /note="L1PB1 repeat: matches 5852. .6155 of consensus"
56551. .56667
repeat_region /note="L1M4 repeat: matches 2267. .2282 of consensus"
56668. .56746
repeat_region /note="MAD1 repeat: matches 1. .80 of consensus"
56747. .56968
repeat_region /note="L1M4 repeat: matches 2282. .2155 of consensus"
56969. .57270
repeat_region /note="AluDb repeat: matches 4. .311 of consensus"
57271. .57702
repeat_region /note="L1M4 repeat: matches 2154. .2583 of consensus"
57788. .57860
repeat_region /note="MER47 repeat: matches 1. .73 of consensus"
57862. .58057
repeat_region /note="L1M4 repeat: matches 2600. .2811 of consensus"
58394. .58520
repeat_region /note="FLAM_A repeat: matches 1. .121 of consensus"
58586. .58893
repeat_region /note="AluTo repeat: matches 1. .311 of consensus"
64210. .64446
repeat_region /note="L2 repeat: matches 2453. .2706 of consensus"
64871. .64953
repeat_region /note="MER63 repeat: matches 685. .766 of consensus"
66867. .67144
repeat_region /note="AluTb repeat: matches 1. .299 of consensus"
68291. .68591
repeat_region /note="AluDo repeat: matches 11. .305 of consensus"
69232. .69973
repeat_region /note="L2 repeat: matches 1244. .2019 of consensus"
70272. .70418
repeat_region /note="MIR repeat: matches 23. .172 of consensus"
70713. .71105
repeat_region /note="L2 repeat: matches 1629. .2037 of consensus"
71119. .71618
repeat_region /note="MER54B repeat: matches 1. .498 of consensus"
71602. .71825
repeat_region /note="MER54B repeat: matches 459. .674 of consensus"
71894. .72125
repeat_region /note="L2 repeat: matches 1300. .1544 of consensus"
72923. .73109
repeat_region /note="MIR repeat: matches 58. .249 of consensus"
75367. .75683
repeat_region /note="AluXx repeat: matches 1. .303 of consensus"
78989. .79225
repeat_region /note="MIR repeat: matches 12. .256 of consensus"
80308. .80410
repeat_region /note="L2 repeat: matches 2577. .2692 of consensus"

Query Match 7.6%; Score 76; DB 9; Length 170998;
Best Local Similarity 100.0%; Pred. No. 4.5e-33;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAATACAAAATAGCCAGGTGTGGTGACACACCGCTGTAGTCCAGCTA 395
|||||
Db 163825 TCTCTACTAAATAATACAAAATAGCCAGGTGTGGTGACACACCGCTGTAGTCCAGCTA 163884
|||||
QY 396 CTTGGAGGCTGAGGC 411
|||||
Db 163885 CTTGGAGGCTGAGGC 163900
|||||
RESULT 8
AL442068
LOCUS Homo sapiens chromosome 10 clone RP11-331G8, *** SEQUENCING IN
DEFINITION
ACCESSION AL442068
VERSION AL442068.16 GI:17043795
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sims.S.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (19-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
JOURNAL Cambridgehire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT On Nov 21, 2001 this sequence version replaced gi:14575284.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA331G8
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 277809 bases at least Q40
Consensus quality: 281712 bases at least Q30
Consensus quality: 284299 bases at least Q20
Insert size: 286425; sum-of-contigs
Insert size: 156064; 7.4% error; agarose-fp
Quality coverage: 5.79x in Q20 bases; sum-of-contigs Quality
coverage: 15.47x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 43 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 103320: contig of 103320 bp in length
* 103321 103420: gap of 100 bp
* 103421 140724: contig of 37304 bp in length
* 140725 140824: gap of 100 bp
* 140825 162687: contig of 21863 bp in length
* 162688 162787: gap of 100 bp
* 162788 165269: contig of 2482 bp in length
* 165270 165369: gap of 100 bp
* 165370 167787: contig of 2418 bp in length
* 167788 167887: gap of 100 bp
* 167888 170672: contig of 2785 bp in length
* 170673 170772: gap of 100 bp
* 170773 173340: contig of 2568 bp in length
* 173341 173440: gap of 100 bp
* 173441 176369: contig of 2929 bp in length
* 176370 176469: gap of 100 bp
* 176470 179660: contig of 3191 bp in length
* 179661 179760: gap of 100 bp

179761 181788: contig of 2028 bp in length
181789 181888: gap of 100 bp
181889 185591: contig of 3703 bp in length
185592 185691: gap of 100 bp
185692 187897: contig of 2206 bp in length
187898 187997: gap of 100 bp
187998 190151: contig of 2154 bp in length
190152 190251: gap of 100 bp
190252 192977: contig of 2726 bp in length
192978 193077: gap of 100 bp
193078 195504: contig of 2427 bp in length
195505 195605: gap of 100 bp
195606 198738: contig of 3134 bp in length
198739 198838: gap of 100 bp
198839 202505: contig of 3667 bp in length
202506 202605: gap of 100 bp
202606 206757: contig of 4152 bp in length
206758 206857: gap of 100 bp
206858 211910: contig of 5053 bp in length
211911 212010: gap of 100 bp
212011 218152: contig of 6142 bp in length
218153 218252: gap of 100 bp
218253 221882: contig of 3630 bp in length
221883 221982: gap of 100 bp
221983 225735: contig of 3753 bp in length
225736 225835: gap of 100 bp
225836 229907: contig of 4072 bp in length
229908 230007: gap of 100 bp
230009 233016: contig of 3009 bp in length
233017 233116: gap of 100 bp
233117 236145: contig of 3029 bp in length
236146 236245: gap of 100 bp
236246 239609: contig of 3364 bp in length
239610 239709: gap of 100 bp
239710 241796: contig of 2087 bp in length
241797 241896: gap of 100 bp
241897 243915: contig of 2019 bp in length
243916 244015: gap of 100 bp
244016 246442: contig of 2427 bp in length
246443 246542: gap of 100 bp
246543 249599: contig of 3057 bp in length
249600 249699: gap of 100 bp
249700 252680: contig of 2981 bp in length
252681 252780: gap of 100 bp
252781 256312: contig of 3532 bp in length
256313 256412: gap of 100 bp
256413 259563: contig of 3151 bp in length
259564 259663: gap of 100 bp
259664 262204: contig of 2541 bp in length
262205 262304: gap of 100 bp
262305 264799: contig of 2495 bp in length
264800 264899: gap of 100 bp
264900 267645: contig of 2746 bp in length
267646 267745: gap of 100 bp
267746 271525: contig of 3780 bp in length
271526 271625: gap of 100 bp
271626 275798: contig of 4173 bp in length
275799 275898: gap of 100 bp
275899 278025: contig of 2127 bp in length
278026 278125: gap of 100 bp
278126 281433: contig of 3308 bp in length
281434 281533: gap of 100 bp
281534 284437: contig of 2904 bp in length
284438 284537: gap of 100 bp
284538 286727: contig of 2190 bp in length
286728 286827: gap of 100 bp
286828 290625: contig of 3798 bp in length.
Location/Qualifiers
1. .290625
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-331G8"

FEATURES
source

misc_feature
1. .103320
/note="assembly_fragment:07950
fragment_chain:1
vector_side:left"
103421..140724
/note="assembly_fragment:01658
fragment_chain:1"
140825..162687
/note="assembly_fragment:01866
fragment_chain:1"
162788..165269
/note="assembly_fragment:01933
fragment_chain:2"
165370..167787
/note="assembly_fragment:02386
fragment_chain:2"
167888..170672
/note="assembly_fragment:02267
fragment_chain:3"
170773..173340
/note="assembly_fragment:02094
fragment_chain:3"
173441..176369
/note="assembly_fragment:00062"
176470..179660
/note="assembly_fragment:00157"
179761..181788
/note="assembly_fragment:00471"
181889..185591
/note="assembly_fragment:00485"
185692..187897
/note="assembly_fragment:00607"
187998..190151
/note="assembly_fragment:01019"
190252..192977
/note="assembly_fragment:01432"
193078..195504
/note="assembly_fragment:01879"
195605..198738
/note="assembly_fragment:01944"
198839..202505
/note="assembly_fragment:02174"
202606..206757
/note="assembly_fragment:02200"
206858..211910
/note="assembly_fragment:02684"
212011..218152
/note="assembly_fragment:03379"
218253..221882
/note="assembly_fragment:03527"
221983..225735
/note="assembly_fragment:03880"
225836..229907
/note="assembly_fragment:04098"
230008..233016
/note="assembly_fragment:04166"
233117..236145
/note="assembly_fragment:04570"
236246..239609
/note="assembly_fragment:04709"
239710..241796
/note="assembly_fragment:04939"
241897..243915

Query Match 7.6%; Score 76; DB 2: Length 290625;
Best Local Similarity 100.0%; Pred. No. 4.6e-33;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGCAGCCTGTAGTCCACGCTA 395
|||||
Db 254811 TCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCAGCAGCCTGTAGTCCACGCTA 254870
|||||

QY 396 CTTGGGAGGCTGAGC 411
 |||||
 Db 254871 CTTGGGAGGCTGAGC 254886

RESULT 9
 AC079882 59427 bp DNA linear PRI 09-JAN-2002
 LOCUS Homo sapiens BAC clone RP11-577018 from 7, complete sequence.
 DEFINITION AC079882
 ACCESSION AC079882
 VERSION AC079882.6 GI:16950366
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 59427)
 Sulston, J.E. and Waterston, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 99063792
 PUBMED 9847074

2 (bases 1 to 59427)
 Shah, N., Abbott, A. and Creason, K.
 The sequence of Homo sapiens BAC clone RP11-577018
 Unpublished (2001)
 3 (bases 1 to 59427)
 Waterston, R.H.
 Direct Submission
 Submitted (15-SEP-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 59427)
 Waterston, R.H.
 Direct Submission
 Submitted (16-NOV-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 59427)
 Waterston, R.H.
 Direct Submission
 Submitted (03-JAN-2002) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 6 (bases 1 to 59427)
 Waterston, R.
 Direct Submission
 Submitted (09-JAN-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Nov 16, 2001 this sequence version replaced gi:15624994.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: http://genome.wustl.edu/gsc
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0577018

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by
 restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and
 sequencing collaboration between the NHGRI Chromosome 7 Mapping
 Project (Eric D. Green, Director), John D. McPherson in the
 Department of Genetics (Washington University), and the Washington
 University Genome Sequencing Center. For additional information
 about the map position of this sequence, see
 http://www.nhgri.nih.gov/DIR/OTB/CHR7, send
 mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
 donor, as described by Osogawa, K., Woon, P.Y., Zhao, B., Frengen, E.,
 Tatenio, M., Catanese, J.J. and de Jong, P.J. (1998) An improved
 approach for construction of bacterial artificial chromosome
 libraries. Genomics 51:1-8. The clone may be obtained either from
 Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
 and coworkers at the Roswell Park Cancer Institute
 (http://bacpac.med.buffalo.edu)
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-611L7, 2000 bp overlap; the
 clone sequenced to the right is RP11-740N7, 2000 bp overlap.
 Actual start of this clone is at base position 99588 of RP11-611L7;
 Actual end is at base position 85919 of RP11-740N7.

FEATURES

Source	Location/Qualifiers
repeat_region	1..59427 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="7" /map="7"
repeat_region	/clone="RP11-577018" /clone_lib="RP11-11" 347..657 /rpt_family="Alu"
misc_feature	763..943 /rpt_family="Alu"
repeat_region	921..939 /note="match to EST BF038607 (NID: g10744968)"
misc_feature	944..1243 /rpt_family="Alu"
misc_feature	946..959 /note="match to EST AA503424 (NID: g2236391) ng77g09.s1"
misc_feature	947..959 /note="similar to Homo sapiens EST BGL93651 (NID: g13715338)"
repeat_region	1244..1377 /rpt_family="Alu"
repeat_region	1704..1833 /rpt_family="Alu"
misc_feature	1717..1739 /note="similar to Homo sapiens EST T84464 (NID: g712752) y047c10.r1"
repeat_region	2002..2249 /rpt_family="L1"
repeat_region	2273..2559 /rpt_family="Alu"
misc_feature	2538..2571 /note="similar to Homo sapiens EST T84464 (NID: g712752) y047c10.r1"
repeat_region	2575..2703 /rpt_family="Alu"
repeat_region	2718..2817 /rpt_family="L1"
misc_feature	3024..3032 /note="match to EST AA382672 (NID: g2034990)"
repeat_region	3069..3174 /rpt_family="L2"
repeat_region	3248..3415 /rpt_family="MIR"
repeat_region	3557..3926 /rpt_family="L2"
repeat_region	3929..4224

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repeat_region /rpt_family="Alu"
4273..4573
misc_feature /rpt_family="Alu"
4273..4285
repeat_region /note="match to EST AW014562 (NID:g5863319)"
4692..4714
repeat_region /rpt_family="AT-rich"
4735..5036
misc_feature /rpt_family="Alu"
5017..5036
repeat_region /note="match to EST AL550875 (NID:g12888273)"
5017..5036
repeat_region /rpt_family="(A)n"
5076..5110
misc_feature /rpt_family="AT-rich"
5177..5270
repeat_region /note="match to EST AA382672 (NID:g2034990)"
5355..5491
misc_feature /rpt_family="Alu"
5433..5454
misc_feature /note="match to EST BF898161 (NID:g12289620)"
5555..5859
misc_feature /note="match to EST BG941778 (NID:g14341150) axl7b11.x1"
5699..6115
repeat_region /note="match to EST BI021363 (NID:g14427993)"
6035..6063
repeat_region /rpt_family="(TTTC)n"
6036..6329
misc_feature /rpt_family="Alu"
6333..6348
repeat_region /note="match to EST BG184060 (NID:g13705747)"
6337..6360
misc_feature /rpt_family="(T)n"
6337..6355
repeat_region /note="match to EST AL550875 (NID:g12888273)"
6341..6624
repeat_region /rpt_family="Alu"
6642..6836
repeat_region /rpt_family="L2"
6837..7141
repeat_region /rpt_family="Alu"
7142..7192
misc_feature /rpt_family="L2"
7402..7405
misc_feature /note="match to EST AL570071 (NID:g12926034)"
7407..7808
repeat_region /note="match to EST BE062598 (NID:g8407248)"
8127..8421
repeat_region /rpt_family="Alu"
8764..9034
repeat_region /rpt_family="Alu"
9045..9233
repeat_region /rpt_family="Alu"
9311..9614
repeat_region /rpt_family="Alu"
9588..9614
misc_feature /rpt_family="(A)n"
9742..10149
misc_feature /note="match to EST BF898161 (NID:g12289620)"
9841..9989
misc_feature /note="match to EST AA382672 (NID:g2034990)"
9870..10039
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Query Match 7.5%; Score 75; DB 9; Length 59427;
Best Local Similarity 100.0%; Pred.No. 1.6e-32;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAAAATACAAAATTAGCCAGGTGTGGTGGCACAGCCCTGTAGTCCAGCTA 395
|||||
Db 6947 TCCTCTACTAAAAATACAAAATTAGCCAGGTGTGGTGGCACAGCCCTGTAGTCCAGCTA 7006
|||||

QY 396 CTTGGGAGCTGAGG 410
|||||
```

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Db 7007 CTTGGGAGCTGAGG 7021

RESULT 10
AC004983
LOCUS
DEFINITION Homo sapiens PAC clone RP5-1163J12 from 7q21.2-q31.1, complete
sequence.
AC004983
VERSION AC004983.3 GI:21321875
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 124821)
AUTHORS Kozlowicz,A. and Ozersky,P.
TITLE The sequence of Homo sapiens PAC clone RP5-1163J12
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 124821)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 124821)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 5 (bases 1 to 124821)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 6 (bases 1 to 124821)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 4, 2002 this sequence version replaced gi:4309885.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
-----
Center project name: H_DJ1163J12
```

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the

Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GB/CHR7>, send mailto:egreen@nhgri.nih.gov, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at <http://www.chori.org> using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong. VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

Actual start of this clone is at base position 1 of D1163J12; actual end is at 124821 of D1163J12.

The region from base 102149 to 102310 of D1163J12 is covered only by PCR product of D1163J12 clone DNA. The data was generated using two different chemistries, sequenced in the same direction.

FEATURES

```

source
location/Qualifiers
1..124821
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7q21.2-q31.1"
/clone="RP5-1163J12"
518..818
/rpt_family="Alu"
1248..1551
/rpt_family="Alu"
1616..1773
/rpt_family="Alu"
1774..2080
/rpt_family="Alu"
2081..2093
/rpt_family="Alu"
2094..2411
/rpt_family="Alu"
2412..2532
/rpt_family="Alu"
3308..3613
/rpt_family="Alu"
4131..4429
/rpt_family="Alu"
4881..4994
/rpt_family="Alu"
4995..5050
/rpt_family="Alu"
5204..5392
/rpt_family="Alu"
5433..5569
/rpt_family="Alu"
5917..6238
/rpt_family="Alu"
6242..6547
/rpt_family="Alu"
6555..6850
/rpt_family="Alu"
6882..7183
/rpt_family="Alu"
7254..7303
/rpt_family="Alu"
7305..7458
/rpt_family="Alu"
7807..7973
/rpt_family="MIR"
7974..8275
/rpt_family="L1"
/rpt_family="Alu"

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repeat_region
8344..8473
/rpt_family="L1"
repeat_region
8561..8854
/rpt_family="Alu"
repeat_region
9013..9281
/rpt_family="MIR"
repeat_region
9305..9599
/rpt_family="Alu"
repeat_region
9605..9890
/rpt_family="Alu"
10159..10463
/rpt_family="Alu"
repeat_region
10704..11017
/rpt_family="Alu"
repeat_region
11120..11268
/rpt_family="Alu"
repeat_region
11269..11563
/rpt_family="Alu"
repeat_region
11564..11708
/rpt_family="Alu"
repeat_region
11730..11865
/rpt_family="Alu"
repeat_region
11978..12276
/rpt_family="Alu"
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12404..12448
/Note="similar to EST AW437628 (NID:g6972934)"
repeat_region
12524..12823
/rpt_family="Alu"
repeat_region
13160..13453
/rpt_family="Alu"
repeat_region
13466..13722
/rpt_family="L1"
repeat_region
13723..13906
/rpt_family="Alu"
repeat_region
13907..14193
/rpt_family="Alu"
repeat_region
14194..14341
/rpt_family="Alu"
repeat_region
14342..14425
/rpt_family="L1"
repeat_region
14588..14886
/rpt_family="Alu"
repeat_region
15000..15292
/rpt_family="Alu"
misc_feature
15117..15573
/Note="similar to EST AW872691 (NID:g8006744) hm26g04.xl"
misc_feature
15334..15523
/Note="similar to EST AW437628 (NID:g6972934)"
repeat_region
15572..15854
/rpt_family="Alu"
repeat_region
15888..15997
/rpt_family="MIR_type"
repeat_region
15998..16310
/rpt_family="Alu"
misc_feature
16024..16203
/Note="similar to EST AI351591 (NID:g4088797) qr-07a04.xl"
repeat_region
16311..16749

Query Match
Best Local Similarity 100.0%; DB 9; Length 124821;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAAAATACAAAATTAGCCAGGTGTGGTCACACGCTGTAGTCCAGCTA 395
|||||
Db 32622 TCTTACTTAAAAATACAAAATTAGCCAGGTGTGGTCACACGCTGTAGTCCAGCTA 32681
|||||

QY 396 CTTGGGAGGCTGAGG 410
|||||
Db 32682 CTTGGGAGGCTGAGG 32696
```

RESULT 11

AC011505
 LOCUS Homo sapiens chromosome 19 clone CTD-2081K17, complete sequence.
 DEFINITION AC011505
 AC011505
 VERSION AC011505.6 GI:21747445
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 167417)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished
 AUTHORS 2 (bases 1 to 167417)
 DIRECT SUBMISSION
 TITLE DOE Joint Genome Institute.
 JOURNAL Direct Submission
 SUBMITTED (07-OCT-1999) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 167417)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Direct Submission
 SUBMITTED (01-JUN-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 REFERENCE 4 (bases 1 to 167417)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Direct Submission
 SUBMITTED (14-JUL-2002) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jul 14, 2002 this sequence version replaced gi:21306640.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 Finishing Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.9% of Sequence;
 Estimated Total Number of Errors is 0.1.
 NOTE: Shatter libraries failed to resolve the dinucleotide repeat
 region. Unsure number of repeat copies 49544-50135. False join
 49658.

FEATURES

source
 1. .167417
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /clone="CTD-2081K17"
 49544..50135
 misc_feature
 /note="NOTE: Shatter libraries failed to resolve the
 dinucleotide repeat region. Unsure number of repeat
 copies 49544-50135. False join 49658."
 BASE COUNT 44976 a 40334 c 40235 g 41872 t
 ORIGIN
 Query Match 7.4%; Score 74; DB 9; Length 167417;
 Best Local Similarity 100.0%; Pred. No. 6.9e-32;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 335 GTCTCTACTAAATAACAAATATGACAGGTGTGGTGGACACAGCGCTGTAGTCCAGCT 394
 Db 36358 GTCTCTACTAAATAACAAATATGACAGGTGTGGTGGACACAGCGCTGTAGTCCAGCT 36417
 QY 395 ACTTGGGAGCTGA 408
 Db 36418 ACTTGGGAGCTGA 36431
 RESULT 12
 AF190465/c
 LOCUS Homo sapiens SH3-containing protein EEN (EEN) and chromatin
 assembly factor-I p150 subunit (CAF) genes, complete cds, complete
 sequence.
 ACCESSION AF190465
 AF190465.1 GI:6120105
 HTG.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 96308)
 AUTHORS Chen, S., Xiong, H., Dong, H., Lin, W., Zhang, C., Fu, G., Qi, Z. and
 Huang, G.M.
 TITLE Homo sapiens SH3-containing protein EEN gene
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 96308)
 AUTHORS Chen, S., Xiong, H., Dong, H., Lin, W., Zhang, C., Fu, G., Qi, Z. and
 Huang, G.M.
 TITLE Direct Submission
 JOURNAL Direct Submission
 SUBMITTED (28-SEP-1999) Chinese Human Genome Center at Shanghai,
 351 Guoshoujing Road, Zhangjiang Hi-Tech Park, Shanghai 201203,
 People's Republic of China
 FEATURES
 Location/Qualifiers
 1. .96308
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /map="19p13"
 /clone="BAC 335C9"
 complement[<2348. .>41096]
 /gene="EEN"
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 complement[<2348. .2544,3075. .3131,3358. .3482,
 4116. .4219,4464. .4622,4832. .4965,6230. .6373,7250. .7322,
 7675. .7743,41052. .>41096])
 /gene="EEN"
 /product="SH3-containing protein EEN"
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 4116. .4219,4464. .4622,4832. .4965,6230. .6373,7250. .7322,
 7675. .7743,41052. .41096])
 /gene="EEN"
 /codon_start=1
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 /protein_id="AAF04290.1"
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 /translation="MSVAGLKQFYKASQLYSEKVGAGETKLDLDDFKEMKKVDVTS
 KAVTEVLARTIEYLOPNPASRAKLWLNVTSKIQGVKNPGYQSGELGECMRHGK
 ELGGSNFGDALLDAGSMKELAEVYDSDIEVKQNFIDPLNCEKDKLQIHLKK
 LEGRRLDFDYKKKGKQIPDELRQALEKFEESKEVYAEVSMNLLETIEQVLSQAL
 VDAQLDYHRQAVQQLDELAELKLRMRREASSRKREYKPKPREFDLGEPSQNGGFP
 CTAPKIAASSFRSSDKPIRTPSRMPPLDQPSCKALYDFEPENDGELGFHGEDVIT
 LTNQIDENYEGMLDGGSGFFPLSYVEVLVLPQ."
 complement[<2348. .2544)
 /gene="EEN"
 /number=10
 complement(3075. .3131)
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 /number=9
 complement(3358. .3482)
 /gene="EEN"
 /number=8
 complement(4116. .4219)
 /gene="EEN"
 /number=7
 complement(4464. .4622)
 /gene="EEN"
 /number=6
 complement(4832. .4965)
 /gene="EEN"
 /number=5
 complement(5036. .5177)
 /rpt_family="FRAM"
 repeat_region
 complement(5190. .5471)
 /rpt_family="Alusg"
 repeat_region
 5473. .5501
 /rpt_family="(TTTGTG)n"
 repeat_region
 complement(5509. .5611)
 /rpt_family="Alusp"

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repeat_region 5612...5654
repeat_region /rpt_family="TG)n"
exon complement(5655...5803)
exon /rpt_family="AluSp"
exon /gene="EEN"
exon /number=4
exon complement(7250...7322)
exon /gene="EEN"
exon /number=3
exon complement(7675...7743)
exon /gene="EEN"
exon /number=2
exon /rpt_family="MER5B"
exon /number=9847
exon /rpt_family="AluY"
exon complement(12727...12855)
exon /rpt_family="FLAM_C"
exon /number=13882
exon /rpt_family="AGGGGG)n"
exon /number=18905
exon /rpt_family="L2"
exon /number=19141
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exon /number=19487
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exon /number=20192
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exon complement(22420...22646)
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exon complement(23286...23475)
exon /rpt_family="MLTID"
exon /number=23488
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exon complement(23640...23944)
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exon /rpt_family="AluJb"
exon /number=24263
exon /rpt_family="MER82"
exon /number=24616
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exon complement(25217...25305)
exon /rpt_family="FAM"
exon /number=25398
exon /rpt_family="LIME"
exon /number=25555
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exon complement(27234...27366)
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exon complement(27665...27965)
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exon complement(28030...28320)
exon /rpt_family="AluJb"
exon complement(28328...28417)
exon /rpt_family="MER113"
exon complement(28458...28580)
exon /rpt_family="AluSg/x"
exon complement(28581...28886)
exon /rpt_family="AluSg"
exon complement(30425...30568)
exon /rpt_family="L2"
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exon /rpt_family="CAGA)n"
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repeat_region 33398...33680
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repeat_region 33710...34020
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repeat_region 34027...34240
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repeat_region 34243...34535
repeat_region /rpt_family="AluSg"
repeat_region 34536...34573
repeat_region /rpt_family="AT-rich"
repeat_region complement(35523...35699)
repeat_region /rpt_family="MER20"
repeat_region complement(35895...35992)
repeat_region /rpt_family="AluJb"
repeat_region 36356...36644
repeat_region /rpt_family="AluSg"
repeat_region 36845...37156
repeat_region /rpt_family="AluSg"
repeat_region complement(37214...37315)
repeat_region /rpt_family="Alu"
repeat_region complement(37408...37610)
repeat_region /rpt_family="MER20"
repeat_region 37625...37760
repeat_region /rpt_family="MIR"
repeat_region complement(38577...38873)
repeat_region /rpt_family="AluJb"
repeat_region complement(39109...39402)
repeat_region /rpt_family="AluSx"
repeat_region 39565...39768
repeat_region /rpt_family="LMB6"
repeat_region 39769...40073
repeat_region /rpt_family="AluSx"
repeat_region 40123...40228
repeat_region /rpt_family="GA-rich"
repeat_region 40238...40416
repeat_region /rpt_family="MER20"
exon complement(41052...41096)
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Best Local Similarity 100.0%; Pred. No. 1e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATACAAAATAGCCAGGTGGTGCCACACGCGCTGTAGTCCAGC 393
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Db 72056 CGTCTCTACTAAATACAAAATAGCCAGGTGGTGCCACACGCGCTGTAGTCCAGC 393
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QY 394 TACTTGGGAGGC 405
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Db 71996 TACTTGGGAGGC 71985

RESULT 13

HS149A16

LOCUS

DEFINITION

Human DNA sequence from clone RPI-149A16 on chromosome 22 Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RPL3 gene for Ret finger protein-like 3, the RPL3S gene for Ret finger protein-like 3 antisense, the gene for a novel Immunoglobulin Lambda Chain V family protein, the gene for a novel protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, the gene for a novel protein

(ortholog of worm F16A11.2 and bacterial and archaea-bacterial predicted proteins), the gene for a novel protein similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein) and the 5' part of a novel gene. Contains ESTs, STSs, GSSs and three putative CpG islands, complete sequence.

ACCESSION

AL021937

VERSION

AL021937.1

KEYWORDS

BPI; CpG island; IGLC; Immunoglobulin; LBP; RALGDS; RALGER; Ret Finger; RFLP3; RFLP3S; RGDS; RSC.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

Smith, M.

AUTHORS

Direct Submission

TITLE

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

JOURNAL

On Jan 21, 1999 this sequence version replaced gi:4164331.

COMMENT

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpepfrom the library RPI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pCYPAC2

This sequence is the entire insert of clone RPI-149A16. The true right end of clone RPI-90G24 is at 14164 in this sequence. The start of this sequence overlaps with sequence AL008723.

FEATURES

Location/Qualifiers

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/db_xref="taxon:9606"

/chromosome="22"

/clone="RPI-149A16"

/clone_lib="RPI-1"

188..318

/note="L2 repeat: matches 2574..2706 of consensus"

857..932

/note="38 copies 2 mer ac 67 conserved"

1512..1686

/note="L1M4 repeat: matches 4064..4254 of consensus"

1795..1924

/note="MER94 repeat: matches 2..134 of consensus"

2270..2338

/note="MLTJ1 repeat: matches 112..181 of consensus"

2767..2977

/note="L2 repeat: matches 2546..2750 of consensus"

3195..3560

/note="THE1B repeat: matches 1..364 of consensus"

3561..3661

/note="L1M3 repeat: matches 6080..6184 of consensus"

4429..4642

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

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repeat_region

/note="AluSg repeat: matches 1..212 of consensus"
4668..4813
/note="L1M3 repeat: matches 6041..6183 of consensus"
4814..5025
/note="L1P repeat: matches 2279..2491 of consensus"
5071..5379
/note="AluSx repeat: matches 1..301 of consensus"
5477..5504
/note="L14 copies 2 mer tg 100 conserved"
5523..5944
/note="L1M4 repeat: matches 2684..3149 of consensus"
5990..6307
/note="AluJo repeat: matches 1..310 of consensus"
6398..6773
/note="L2 repeat: matches 1217..1566 of consensus"
6774..6856
/note="Alu repeat: matches 247..293 of consensus"
6857..7348
/note="L2 repeat: matches 1566..2231 of consensus"
7410..7811
/note="MLT2CB repeat: matches 2..377 of consensus"
7800..7908
/note="MLT2CB repeat: matches 272..377 of consensus"
7889..8186
/note="MLT2CB repeat: matches 267..504 of consensus"
8374..8480
/note="L2 repeat: matches 2640..2745 of consensus"
9222..9288
/note="L1M1 repeat: matches 6258..6327 of consensus"
9548..9843
/note="AluSp repeat: matches 1..298 of consensus"
9845..9998
/note="AluSg/x repeat: matches 134..287 of consensus"
10011..10380
/note="L1P13 repeat: matches 5785..6144 of consensus"
10850..11152
/note="AluSg repeat: matches 1..308 of consensus"
11489..11990
/note="LTR36 repeat: matches 53..611 of consensus"
12755..12842
/note="L2 repeat: matches 2381..2502 of consensus"
13036..13154
/note="L2 repeat: matches 25..123 of consensus"
14217..14389
/note="L1P13 repeat: matches 50..233 of consensus"
14813..15096
/note="AluSx repeat: matches 1..298 of consensus"
15236..15658
/note="L1M1 repeat: matches 64..499 of consensus"
15666..15818
/note="L1M1 repeat: matches 5647..5800 of consensus"
16125..16188
/note="L2 repeat: matches 2643..2708 of consensus"
16632..16832
/note="match: STS: Em:251415
match: STS: Em:HS331WC9"
16705..16747
/note="L1M4 repeat: matches 102..145 of consensus"
16786..17335
/note="MLT1F repeat: matches 1..541 of consensus"
17821..17925
/note="L1M1 repeat: matches 117..259 of consensus"
18006..19786
/note="forced join in tandem repeat; single clone region;
assembly confirmed by restriction digest"
18099..18383
/note="95 copies 3 mer tgg 55 conserved"
18448..18663
/note="72 copies 3 mer tgg 56 conserved"
19169..19250
/note="41 copies 2 mer gt 63 conserved"

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repeat_region 20817..20983
/note="L2 repeat: matches 2276..2440 of consensus"
repeat_region 21858..21938
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repeat_region 21962..22065
/note="L2 repeat: matches 2595..2707 of consensus"
repeat_region 22311..22446
/note="68 copies 2 mer ac 61 conserved"
repeat_region 24135..24225
/note="MIR repeat: matches 26..118 of consensus"
misc_feature 24808..25247
/note="match: GSS: Em:AQ881697"
repeat_region 25356..25474
/note="L2 repeat: matches 2586..2710 of consensus"
repeat_region 25815..26103
/note="AluX repeat: matches 23..312 of consensus"
repeat_region 26197..26384
/note="MERG3B repeat: matches 1..436 of consensus"
repeat_region 26909..27216
/note="AluSg repeat: matches 1..286 of consensus"
repeat_region 28889..29892
/note="L2 repeat: matches 1496..2750 of consensus"
repeat_region 30213..30484
/note="L2 repeat: matches 2214..2502 of consensus"
repeat_region 30569..30651
/note="L2 repeat: matches 2665..2747 of consensus"
repeat_region 32066..32175
/note="MLR1J repeat: matches 401..514 of consensus"
misc_feature complement(32187..32629)
/note="match: GSS: Em:AQ825726"
misc_feature complement(32796..33149)
/note="match: GSS: Em:AQ571968"
misc_feature 33171..33361
/note="match: STS: Em:F08813"
misc_feature 33242..33663
/note="match: GSS: Em:AQ153435"
repeat_region 34859..36399
/note="L1P2 repeat: matches 4602..6144 of consensus"
repeat_region 36506..36623
/note="MIR repeat: matches 59..187 of consensus"
repeat_region 37039..37108
/note="MER41D repeat: matches 485..557 of consensus"
repeat_region 37114..37291
/note="Harlequin repeat: matches 2301..2476 of consensus"

Query Match 7.2% Score 72; DB 9; Length 173354;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGAGGCTGATCAGCTGA 291
Db 110975 CGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGAGGCTGATCAGCTGA 111034

QY 292 AGTCAGGAGTTC 303
Db 111035 AGTCAGGAGTTC 111046

RESULT 14
AC011498/c
LOCUS AC011498
DEFINITION Homo sapiens chromosome 19 clone CTB-50L17, complete sequence.
ACCESSION AC011498
VERSION AC011498.7 GI:16258980
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.

repeat_region 19818..19877
/note="MIR repeat: matches 69..128 of consensus"
repeat_region 20817..20983
/note="L2 repeat: matches 2276..2440 of consensus"
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/note="L2 repeat: matches 2407..2488 of consensus"
repeat_region 21962..22065
/note="L2 repeat: matches 2595..2707 of consensus"
repeat_region 22311..22446
/note="68 copies 2 mer ac 61 conserved"
repeat_region 24135..24225
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misc_feature 24808..25247
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repeat_region 25815..26103
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repeat_region 26197..26384
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repeat_region 26909..27216
/note="AluSg repeat: matches 1..286 of consensus"
repeat_region 28889..29892
/note="L2 repeat: matches 1496..2750 of consensus"
repeat_region 30213..30484
/note="L2 repeat: matches 2214..2502 of consensus"
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repeat_region 32066..32175
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misc_feature complement(32187..32629)
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misc_feature 33242..33663
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repeat_region 36506..36623
/note="MIR repeat: matches 59..187 of consensus"
repeat_region 37039..37108
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repeat_region 37114..37291
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Query Match 7.2% Score 72; DB 9; Length 173354;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGAGGCTGATCAGCTGA 291
Db 110975 CGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGAGGCTGATCAGCTGA 111034

QY 292 AGTCAGGAGTTC 303
Db 111035 AGTCAGGAGTTC 111046

RESULT 14
AC011498/c
LOCUS AC011498
DEFINITION Homo sapiens chromosome 19 clone CTB-50L17, complete sequence.
ACCESSION AC011498
VERSION AC011498.7 GI:16258980
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.

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TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 273403)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
3 (bases 1 to 273403)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Oct 18, 2001 this sequence version replaced gi:15022009.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 1.3.
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BASE COUNT 59422 a 76105 c 73388 g 54488 t
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Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAATAGCCAGGTGTGGTGGCAGCGCTGTATGCCAGC 393
Db 62956 CGTCTCTACTAAAAATACAAATAGCCAGGTGTGGTGGCAGCGCTGTATGCCAGC 62957

QY 394 TACTTGGGAGGC 405
Db 62896 TACTTGGGAGGC 62895

RESULT 15
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LOCUS AC024152
DEFINITION 162201 bp DNA linear HTG 04-NOV-2000
ACCESSION AC024152
VERSION AC024152.11 GI:11079270
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 162201)
AUTHORS Muzny,D.M., Adams,C., Ali-Osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbara,J.,
Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Bivaga,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burke,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escott,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T.,
Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A.,
Hernandez,J., Hernandez,O., Hodgson,A., Hoques,M., Holloway,C.,
Hollins,B., Homsif., Howard,S., Huber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,

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Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, B., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newton, E., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenwo, S., Oguh, M., Okwodu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoostari, N., Sisson, I., Sodergren, E., Sonaite, P., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, K., Woodden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., and Gibbs, R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 162201)
Worley, K.C.

Submitted (25-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 3, 2000 this sequence version replaced gi:9430318.

COMMENT

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: RPI1-24E1
Center clone name: RPI1-24E1
----- Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 5% of reads
Chemistry: Dye-terminator Big Dye: 95% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 137709 bases at least Q40
Consensus quality: 149473 bases at least Q30
Consensus quality: 154220 bases at least Q20
Estimated insert size: 155558; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; agarose-fp estimation
Quality coverage: 3.7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 39130: contig of 39130 bp in length
39131 39230: gap of unknown length
39231 56697: contig of 17467 bp in length
56698 56797: gap of unknown length
56798 74326: contig of 17529 bp in length
74327 74426: gap of unknown length
74427 90214: contig of 15788 bp in length
90215 90314: gap of unknown length
90315 106525: contig of 16211 bp in length
106526 106625: gap of unknown length
106626 119989: contig of 13364 bp in length
119990 120089: gap of unknown length
120090 130101: contig of 10012 bp in length
130102 130201: gap of unknown length

* 130202 138941: contig of 8740 bp in length
* 138942 139041: gap of unknown length
* 139042 145294: contig of 6253 bp in length
* 145295 150375: gap of unknown length
* 150376 150375: contig of 4881 bp in length
* 150376 150375: gap of unknown length
* 150376 155117: contig of 4642 bp in length
* 155118 157939: contig of 2822 bp in length
* 157940 158009: gap of unknown length
* 158010 160008: gap of unknown length
* 160009 161069: contig of 1064 bp in length
* 161070 161169: gap of unknown length
* 161170 162201: contig of 1032 bp in length.
FEATURES
Location/Qualifiers
1..162201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RPI1-24E1"
BASE COUNT 44663 a 34049 c 34232 g 47778 t 1479 others
ORIGIN
Query Match 7.1%; Score 71; DB 2; Length 162201;
Best Local Similarity 100.0%; Pred. No. 4.1e-30;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 GGATCACTTGAGGTCAGAGTGGTGGACCGCTGGCCACACGGTGAACCCCAATCTC 204
|||||
Db 23363 GGATCACTTGAGGTCAGAGTGGTGGACCGCTGGCCACACGGTGAACCCCAATCTC 204
|||||
QY 205 TACTAAAATA 215
|||||
Db 23303 TACTAAAATA 23293

RESULT 16

AC103560

LOCUS

DEFINITION

AC103560 AC022908

VERSION

AC103560.2 GI:21553246

KEYWORDS

HTG

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Unpublished

REFERENCE

AUTHORS

Kaul, R.K., Olson, M.V.,

Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (28-NOV-2001) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

REFERENCE

AUTHORS

Kaul, R.K., Olson, M.V.,

Zhou, Y., James, R.A., Rouse, G., Wu, Z.,

Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.

and Haugen, E.D.

Direct Submission

Submitted (25-JUN-2002) Genome Center, University of Washington,

Box 352145, Seattle, WA 98195, USA

On Jun 25, 2002 this sequence version replaced gi:17136120.

COMMENT

----- Genome Center

Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: wgchgtg@u.washington.edu

Drafting Center: BCM

----- Project Information

Center project name: chr-3
Center clone name: RP11-673E20 (bc0526)

----- Summary Statistics

Sequencing vector: unknown; 53% of reads
Sequencing vector: plasmid; 47% of reads
Chemistry: Dye-terminator ET; 80% of reads
Chemistry: Dye-terminator Big Dye; 20% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 18599 bases at least Q40
Consensus quality: 186199 bases at least Q30
Consensus quality: 186239 bases at least Q20
Insert size: 186241; sum-of-contigs
Quality coverage: 9.7x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': Mapping in progress
3': RP11-252010 (UMGC:bc0324) AC024102

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI				HindIII				BglII			
SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt	SeqDerMap	FgPrnt
8696	8757	2175	2179	3135	3386						
6	<800	6382	6493	2067	1978						
1052	1002	512	<800	5815	5770						
17118	16865	449	<800	6118	6083						
9222	8960	2668	2671	1999	1978						
45	<800	1406	1394	5551	5770						
862	886	1120	1137	3666	3646						
982	1002	166	<800	221	<800						
2317	2306	6933	6956	2789	2866						
7842	7838	4355	4624	1175	1171						

1417	1383	4893	4874	2090	1978
3428	3541	8783	8743	4135	4303
9648	9521	3313	3337	2904	2866
1701	1691	657	<800	1627	1594
157	<800	1892	1892	751	758
2197	2306	4295	4303	8173	8038
3444	3362	1900	1892	948	958
2946	3189	3426	3647	3399	3646
1267	1255	3682	3925	1976	1978
999	1002	10582	10486	7002	6945
558	<800	3894	4184	10589	10321
3330	3189	649	<800	1130	1139
2257	2306	565	<800	1638	1594
1095	1067	298	<800	750	758
887	886	3312	3337	7554	7330
2276	2306	566	<800	382	<800
2533	2665	544	<800	45	<800
2593	2665	8816	8743	2967	3097
993	1002	1717	1711	5871	5770
1403	1383	1620	1547	3777	4021
1912	1876	343	<800	868	958
9030	8960	1144	1137	2198	2178
339	<800	457	<800	6062	5770
6659	6780	9478	9430	937	958
6650	6780	9092	9157	1764	1749
7426	7503	2445	2462	950	958
1570	1514	148	<800	984	958
1506	1514	4668	4874	520	<800
2275	2306	10544	10486	1650	1594
10930	10522	6248	6209	1338	1341
995	1002	7286	7252	1957	1978
737	<800	4827	4874	3561	3646
6846	6939	961	957	3658	3646
4499	4491	12517	12544	2545	2581
268	<800	6185	6209	4378	4611
3112	3189	572	<800	5041	5391

Query Match 7.1%; Score 71; DB 9; Length 186241;
 Best Local Similarity 100.0%; Pred. No. 4.2e-30;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 145 GGATCATTGAGTCAGGAGTTTGTAGACCGAGCTGGCCACACGCTGAAACCCCATCTC 204
 |||||
 DB 28955 GGATCATTGAGTCAGGAGTTTGTAGACCGAGCTGGCCACACGCTGAAACCCCATCTC 29014
 |||||

QY 205 TACTAAATA 215
 |||||

DB 29015 TACTAAATA 29025
 |||||

RESULT 17
 AL161445/c
 LOCUS
 DEFINITION Human DNA sequence from clone Rp11-326F20 on chromosome 9 Contains
 the GGTAL gene for glycoprotein alpha-galactosyl transferase 1, the
 SPINK4 gene for Kazal type 4 serine protease inhibitor, the 3' end
 of the BAG1 gene for BCL2-associated athanogene and a CpG island,
 complete sequence.

ACCESSION AL161445
 VERSION AL161445.10 GI:11137678
 KEYWORDS HTG; athanogene; BAG1; BCL2; CpG island; galactosyltransferase;
 GGTAL; glycoprotein; Kazal; serine protease inhibitor; SPINK4.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 163396)
 Ramsay, H.
 Direct Submission
 Submitted (04-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humbri@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Nov 10, 2000 this sequence version replaced gi:11071610.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr9
 This sequence is the entire insert of clone Rp11-326F20 The true

left end of clone Rp11-344B24 is at 100362 in this sequence. The
 true right end of clone Rp11-54K16 is at 54767 in this sequence.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. Rp11-326F20 is from
 the library RPI-11.2 constructed by the group of Pieter de Jong.
 For further details see
 http://www.chori.org/dacpac/home.htm
 VECTOR: pBAC3.6.

FEATURES

Source	Location/Qualifiers
repeat_region	1..163396
repeat_region	/organism="Homo sapiens"
repeat_region	/db_xref="taxon:9606"
repeat_region	/chromosome="9"
repeat_region	/clone="Rp11-326F20"
repeat_region	/clone_lib="RPI-11.2"
repeat_region	5..237
repeat_region	/note="AluY repeat: matches 77..309 of consensus"
repeat_region	239..314
repeat_region	/note="L1M4 repeat: matches 2591..2666 of consensus"
repeat_region	331..438
repeat_region	/note="MER44A repeat: matches 225..331 of consensus"
repeat_region	440..555
repeat_region	/note="AluSq/x repeat: matches 11..126 of consensus"
repeat_region	566..708
repeat_region	/note="AluJo/FRAM repeat: matches 158..298 of consensus"
repeat_region	795..1193
repeat_region	/note="L1M4 repeat: matches 3657..4070 of consensus"
repeat_region	1194..1491
repeat_region	/note="AluSp repeat: matches 1..296 of consensus"
repeat_region	1492..1680
repeat_region	/note="L1M4 repeat: matches 4070..4265 of consensus"
repeat_region	1681..1981
repeat_region	/note="AluSx repeat: matches 1..301 of consensus"
repeat_region	1982..2181
repeat_region	/note="L1M4 repeat: matches 4265..4471 of consensus"
repeat_region	2182..2486
repeat_region	/note="Aluub repeat: matches 1..304 of consensus"
repeat_region	2487..2783
repeat_region	/note="L1M4 repeat: matches 4471..4701 of consensus"
repeat_region	3046..3192
repeat_region	/note="AluSq/x repeat: matches 1..147 of consensus"
repeat_region	3196..3247
repeat_region	/note="MIR repeat: matches 17..66 of consensus"
repeat_region	4038..4566
repeat_region	/note="MER41B repeat: matches 150..635 of consensus"
repeat_region	4567..4862
repeat_region	/note="AluSq repeat: matches 1..300 of consensus"
repeat_region	4863..5008
repeat_region	/note="MER41B repeat: matches 1..150 of consensus"
repeat_region	6433..6490
repeat_region	/note="MIR repeat: matches 81..138 of consensus"
repeat_region	7523..7596
repeat_region	/note="L1P1 repeat: matches 5753..5825 of consensus"
repeat_region	8418..8461
repeat_region	/note="L1MB4 repeat: matches 6132..6184 of consensus"
repeat_region	8482..8769
repeat_region	/note="AluSx repeat: matches 1..304 of consensus"
repeat_region	8770..8783
repeat_region	/note="L1MB4 repeat: matches 6145..6132 of consensus"
repeat_region	8784..9085
repeat_region	/note="AluSp repeat: matches 1..302 of consensus"
repeat_region	9086..9106
repeat_region	/note="L1MB4 repeat: matches 6122..6146 of consensus"
repeat_region	9152..9751
repeat_region	/note="L1MB3 repeat: matches 5512..6125 of consensus"
repeat_region	10464..10534
repeat_region	/note="MIR repeat: matches 61..130 of consensus"
repeat_region	11734..11790

```
/note="L2 repeat: matches 2688. .2742 of consensus"
11747. .11869
repeat_region
/note="MIR repeat: matches 132. .252 of consensus"
11874. .12110
repeat_region
/note="FAM_C repeat: matches 1. .134 of consensus"
12121. .12219
repeat_region
/note="MIR repeat: matches 35. .142 of consensus"
12243. .12346
repeat_region
/note="52 copies 2 mer tg 71% conserved"
12254. .12343
repeat_region
/note="9 copies 10 mer gtgtgtgtgt 72% conserved"
complement(12461. .12790)
/note="match: GSS: Em:AQ210501"
misc_feature
complement(12571. .12678)
/note="match: GSS: Em:AQ177335"
repeat_region
12602. .13170
/note="MER21B repeat: matches 232. .794 of consensus"
13171. .13289
repeat_region
/note="FAM_A repeat: matches 1. .122 of consensus"
13290. .13517
repeat_region
/note="MER21B repeat: matches 4. .232 of consensus"
14033. .14159
repeat_region
/note="MIR repeat: matches 112. .257 of consensus"
complement(14283. .70891)
/gene="GGTA1"
mRNA
complement(join(14283. .17232,17420. .17524,19637. .19759,
24065. .24252,38835. .39070,70404. .70891))
/gene="GGTA1"
/product="ba326F20.1 (glycoprotein, alpha-galactosyl
transferase 1)"
/note="glycoprotein, alpha-galactosyl transferase 1
match: cDNAs: Em:J03980 Em:D00314 Em:E02227 Em:M13569
Em:X14085 Em:A23697 Em:X14558 Em:M22921 Em:U10473
Em:E02228 Em:X13223 Em:D29805 Em:M13214 Em:X55415
Em:U19890 Em:Y12510 Em:M13701 Em:U19889 Em:AF038660
Em:U10474 Em:AB024434 Em:AB019541 Em:U10472 Em:AF142670
match: ESTs: Em:BF124086 Em:AW467118 Em:AA769459
Em:AA476930 Em:AI192425 Em:AI572046 Em:AI149377
Em:AA830559 Em:AA889902 Em:AI028425 Em:AW362033
Em:AI149203 Em:AI565973"
/evidence=not_experimental
complement(14283)
/gene="GGTA1"
polyA_site
complement(14305. .14310)
polyA_signal
/gene="GGTA1"
repeat_region
14897. .14934
/note="19 copies 2 mer aa 92% conserved"
misc_feature
complement(15755. .17099)
/gene="GGTA1"
/note="match: STS: Em:G05861"
misc_feature
complement(16658. .16912)
/gene="GGTA1"
/note="match: STS: Em:G59840"
CDS
complement(join(17100. .17232,17420. .17524,19637. .19759,
24065. .24252,38835. .39070,70404. .70815))
/gene="GGTA1"
/note="match: proteins: Tr:O60512"
/codon_start=1
/evidence=not_experimental
/product="ba326F20.1 (glycoprotein, alpha-galactosyl
transferase 1)"
/protein_id="CAD13306.1"
/db_xref="GI:17384434"
/translation="MRLREPLLSGAAMPASIQRACLRLLVAVCALHLGVILVYLAG
RLSLRLPOLGVSTPLQGSNSAAIGQSGELRTGGARPPPLGASPPRGDSSP
VDSGPGASNLTVVPVHTTALSIPACPEESPLLGVPMLEFNMVDLELVAKQNP
VMGRTAPRDCVSPKVALIIPERNQERHLKLYLYLHPVQLQVDCIGIYVINOAG
DTIFNRKLLNVGFQALKDQYTCFVFSVDVLIIPMDHNAYRCFSQPRHSVAMDKF
GESLPYQYFGVSALSQQQLTINGFPNNYWGSGEDDDIFNKLFRGMSISRNAY
VGRCMIRHSRDKKNEPNPQRFDRIAHTKETMLSDGLNSLYQLVDQRYPLTYITV
DIGTFS"
repeat_region
17945. .18109
/note="L2 repeat: matches 2241. .2411 of consensus"
```

```
19126. .19243
/note="L1MC5 repeat: matches 7805. .7927 of consensus"
19877. .20157
repeat_region
/note="AluSc repeat: matches 11. .299 of consensus"
20168. .20468
repeat_region
/note="AluSx repeat: matches 1. .301 of consensus"
22027. .22341
repeat_region
/note="AluJo repeat: matches 4. .309 of consensus"
22507. .22807
repeat_region
/note="AluSx repeat: matches 1. .301 of consensus"
23081. .23376
repeat_region
/note="AluJo repeat: matches 1. .297 of consensus"
23549. .23852
repeat_region
/note="AluJb repeat: matches 1. .305 of consensus"
24409. .24625
repeat_region
/note="L1ME repeat: matches 5615. .5826 of consensus"
25003. .25292
repeat_region

Query Match 7.0%; Score 70; DB 9; Length 163396;
Best Local Similarity 100.0%; Pred. No. 1.6e-29;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 TACTAAATAACAAAATTAGCCAGGTGTGGTCACACGCTGTAGTCCAGCTACTTG 399
|||||
Db 20352 TACTAAATAACAAAATTAGCCAGGTGTGGTCACACGCTGTAGTCCAGCTACTTG 20293
|||||

QY 400 GGAGGCTGAG 409
|||||
Db 20292 GGAGGCTGAG 20283

RESULT 18
AC069173/c
LOCUS
DEFINITION Homo sapiens chromosome 3 clone RP11-594G13 map 3, WORKING DRAFT
SEQUENCE, 29 unordered pieces.
ACCESSION AC069173
VERSION AC069173.2 GI:10567947
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 197143)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castelle,A., Choquel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galligan,J., Gardyna,S., Glinde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lechoczy,J.,
Levine,R., Liu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,A., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
TITLE
JOURNAL
Submitted (21-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 4, 2000 this sequence version replaced gi:7960339.
```



```

misc_feature 121415..134427
              /note="assembly_fragment"
misc_feature 134528..147968
              /note="assembly_fragment"
misc_feature 148069..161342
              /note="assembly_fragment"
misc_feature 161443..177031
              /note="assembly_fragment"
misc_feature 177132..197143
              /note="assembly_fragment"
BASE COUNT 49796 a 47285 c 47847 g 49412 t 2803 others
ORIGIN
Query Match      7.0%; Score 70; DB 2; Length 197143;
Best Local Similarity 100.0%; Pred. No. 1.6e-29;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGAGC 393
      |||
Db 155629 CGTCTCTACTAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGAGC 155570

QY 394 TACTTGGGAG 403
      |||
Db 155569 TACTTGGGAG 155560

RESULT 19
AC023603/c
LOCUS      170513 bp      DNA      linear      HTG 17-MAR-2000
DEFINITION Homo sapiens chromosome 3p clone RP11-330614, WORKING DRAFT
ACCESSION  AC023603
VERSION     AC023603.1 GI:6980169
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 170513)
AUTHORS     Zhao,Y., Zhang,C., Lin,W., Dong,H., Wan,M., Xu,S., Gu,W., Tu,Y.,
            Jia,J., Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. and
            Huang,M.
            Direct Submission
            Submitted (16-FEB-2000) Genomic Dept., Chinese National Human
            Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai,
            Shanghai 201203, P. R. China
            -----Genome Center Information-----
            Center: Chinese National Human Genome Center at Shanghai
            Center Code: CHGC
            Web site: http://www.chgc.sh.cn
            Email: mhuang@chgc.sh.cn or fugang@chgc.sh.cn
            -----End Genome Center Information-----
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 14 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *
            * 1 2230: contig of 2230 bp in length
            * gap of unknown length
            * 2231 4248: contig of 2018 bp in length
            * gap of unknown length
            * 4249 9512: contig of 5264 bp in length
            * gap of unknown length
            * 9513 14048: contig of 4536 bp in length
            * gap of unknown length
            * 14049 18094: contig of 4045 bp in length
            * gap of unknown length
            * 18095 23536: contig of 5442 bp in length
            * gap of unknown length
            * 23537 29239: contig of 5703 bp in length

```

```

* 29240 39461: gap of unknown length
* contig of 10222 bp in length
* 39462 49383: contig of 9922 bp in length
* gap of unknown length
* 49384 62126: contig of 12743 bp in length
* gap of unknown length
* 62127 84920: contig of 22794 bp in length
* gap of unknown length
* 84921 108776: contig of 23836 bp in length
* gap of unknown length
* 108777 135846: contig of 27070 bp in length
* gap of unknown length
* 135847 170513: contig of 34667 bp in length.
FEATURES             Location/Qualifiers
     source           1..170513
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3p"
                     /clone="RP11-330614"
BASE COUNT  53252 a 32291 c 31832 g 53096 t 42 others
ORIGIN

Query Match      6.7%; Score 67; DB 2; Length 170513;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 340 TACTAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGACTACTTG 399
      |||
Db 119984 TACTAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCTGTAGTCCCGACTACTTG 119925

QY 400 GGAGGCT 406
      |||
Db 119924 GGAGGCT 119918

RESULT 20
AC006042/c
LOCUS      178361 bp      DNA      linear      PRI 21-DEC-1999
DEFINITION Homo sapiens BAC clone RP11-505D17 from 7p22-p21, complete
            sequence.
ACCESSION  AC006042
VERSION     AC006042.2 GI:4508120
KEYWORDS    HTG.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 178361)
AUTHORS     Sulston,J.E. and Waterston,R.
            Title
            Toward a complete human genome sequence
            JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
            MEDLINE   99063792
            PUBMED     9847074
            REFERENCE 2 (bases 1 to 178361)
            AUTHORS    Hou,S., Wohlman,P. and Le,T.
            Title
            The sequence of Homo sapiens BAC clone RP11-505D17
            JOURNAL   Unpublished
            REFERENCE 3 (bases 1 to 178361)
            AUTHORS    Waterston,R.H.
            Title
            Direct Submission
            JOURNAL   Submitted (22-NOV-1998) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            REFERENCE 4 (bases 1 to 178361)
            AUTHORS    Waterston,R.H.
            Title
            Direct Submission
            JOURNAL   Submitted (24-MAR-1999) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            REFERENCE 5 (bases 1 to 178361)
            AUTHORS    Waterston,R.
            Title
            Direct Submission

```

JOURNAL

Submitted (19-AUG-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 178361)
Waterston,R.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:3980487.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@watson.wustl.edu

----- Summary Statistics

----- Center project name: H_NH0505D17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgrl.nih.gov/DIR/GB/CHR7/>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frenken, E., Tatenio, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-438H20; the clone sequenced to the right is RP11-560C1. The actual start of this clone is at base position 1 of RP11-505D17; actual end is at base position 178361 of RP11-505D17.

FEATURES

Source

Location/Qualifiers

1..178361
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7p22-p21"
/clone="RP11-505D17"
/clone_lib="RPCI-11"
18..267

repeat_region

/rpt_family="L2"

repeat_region

334..762

repeat_region

775..802

repeat_region

817..1043

misc_feature

838..1267

/note="match to EST AI025912 (NID:g3241525) ov95e10.sl"

repeat_region

1301..1515

/rpt_family="Alu"

misc_feature

2041..2511

/note="match to EST AA759276 (NID:g2807139) ah90e10.sl"

repeat_region

5336..5468

/rpt_family="MIR"

repeat_region

6287..6449

/rpt_family="L1"

repeat_region

7747..8030

/rpt_family="Alu"

repeat_region

8032..8058

/rpt_family="(TAAAA)n"

misc_feature

8237..8585

/note="match to EST AI223166 (NID:g3805369) qg53d05.sl"

misc_feature

8241..8581

/note="match to EST AA770501 (NID:g2821739) ah74b12.sl"

misc_feature

8248..8649

/note="match to EST AA926996 (NID:g3075893) om26d02.sl"

repeat_region

9367..9603

/rpt_family="MaLR"

repeat_region

9604..9896

/rpt_family="Alu"

repeat_region

9897..10077

/rpt_family="MaLR"

repeat_region

10680..10981

/rpt_family="Alu"

repeat_region

10998..11037

/rpt_family="(CA)n"

repeat_region

11186..11220

/rpt_family="AT-rich"

repeat_region

11587..11713

/rpt_family="MIR"

repeat_region

11834..12132

/rpt_family="Alu"

repeat_region

13508..13607

/rpt_family="(GAAA)n"

repeat_region

13611..13902

/rpt_family="Alu"

repeat_region

14757..14932

/rpt_family="MIR"

repeat_region

16538..16686

/rpt_family="MERL_type"

repeat_region

16819..17280

/rpt_family="MaLR"

repeat_region

17727..18009

/rpt_family="Alu"

repeat_region

18104..18313

/rpt_family="L2"

repeat_region

18487..18974

/rpt_family="L2"

repeat_region

18975..19361

/rpt_family="Alu"

repeat_region

19262..20642

/rpt_family="L2"

repeat_region

21084..21133

/rpt_family="A-rich"

repeat_region

21186..21766

/rpt_family="L2"

repeat_region

23013..23147

/rpt_family="Alu"

repeat_region

23416..23768

/rpt_family="L2"

repeat_region

25129..25424

/rpt_family="Alu"

repeat_region

25553..25603

/rpt_family="AT-rich"

repeat_region

25755..25989

/rpt_family="MIR"

misc_feature

26095..26418

/note="match to EST AI302527 (NID:g3961873) qn47g06.sl"

misc_feature

26132..26418

/note="match to EST AI271704 (NID:g3890871) qj87f01.sl"

misc_feature

26865..28262

/note="CpG_island (%GC=73.1, o/e=0.80, #CpGs=164)"

repeat_region 27225..27245
/rpt_family="CGG)n"
repeat_region 27658..27758
/rpt_family="L1"
repeat_region 27759..27778
/rpt_family="(GGA)n"
repeat_region 27779..28238
/rpt_family="L1"
misc_feature 28108..28205
/note="match to EST N32168 (NID:g1152567) YY23f11.s1"
gene <28109..144935
/gene="WUGSC:H.NH0505D17.1"
CDS join(<28109..28205,62305..62456,80880..80966,
113833..113946,118493..118645,129318..129528,
143294..143414,144590..144935)
/gene="WUGSC:H.NH0505D17.1"
/note="supported by human ESTs
AI681256.1(NID:g4891438),N32168.1(NID:g1152567), and

Query Match 6.7%; Score 67; DB 9; Length 178361;
Best Local Similarity 100.0%; Pred. No. 9.8e-28;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 340 TACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCAGCTACTTG 399
|||||
Db 39904 TACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCAGCTACTTG 39845
QY 400 GGAGGCT 406
|||||
Db 39844 GGAGGCT 39838

RESULT 21
AL731576/c
LOCUS AL731576 104656 bp DNA linear PRI 26-JUL-2002
DEFINITION Human DNA sequence from clone RP11-178C16 on chromosome 10,
complete sequence.

ACCESSION AL731576 AC025425
VERSION AL731576.9 GI:22002710
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104656)
AUTHORS Lawlor,S.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 29, 2002 this sequence version replaced gi:21322404.
COMMENT Draft Sequence Produced by Genome Therapeutics Corp, 100 Beaver
Street, Waltham, MA 02453, USA
http://www.genomecorp.com

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Emi, EMBL; Swi,
SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence

was generated from part of bacterial clone contigs of human
chromosome 10, constructed by the Sanger Centre Chromosome 10
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/AGP/Chr10
RP11-178G16 is from the library RPCR-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk

FEATURES

source 1..104656
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-178G16"
/clone_lib="RPCI-11.1"
BASE COUNT 29430 a 21161 c 22634 g 31431 t
ORIGIN
Query Match 6.6%; Score 66; DB 9; Length 104656;
Best Local Similarity 100.0%; Pred. No. 3.7e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GTCCTACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCAGCT 394
|||||
Db 72280 GTCCTACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCAGCT 72221

QY 395 ACTTGG 400
|||||

Db 72220 ACTTGG 72215

RESULT 22
AY052369/c

LOCUS AY052369 121028 bp DNA linear PRI 16-APR-2002
DEFINITION Homo sapiens PP2A B56 gamma gene, complete cds, alternative splice
products.
ACCESSION AY052369
VERSION AY052369.1 GI:16303629
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 121028)
AUTHORS Muneer,S., Ramalingam,V., Wyatt,R., Schultz,R.A., Minna,J.D. and
Kamibayashi,C.
TITLE Genomic organization and mapping of the gene encoding the PP2A
B56gamma regulatory subunit
JOURNAL Genomics 79 (3), 344-348 (2002)
MEDLINE 21853305
PUBMED 11863364

REFERENCE 2 (bases 1 to 121028)
AUTHORS Muneer,S., Kamibayashi,C. and Minna,J.D.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-2001) Hamon Center for Therapeutic Oncology,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd, Dallas, TX 75390, USA

FEATURES

source 1..121028
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14q32.2"
join(2507..2643,49292..49491,74767..74877,75863..75955,
76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105076,
110434..110550,117745..120289)

mRNA

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mRNA
/product="PP2A B56 gamma 3"
join(2507..2643,49292..49491,74767..74877,75863..75955,
76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105076,
117745..120289)
/product="PP2A B56 gamma 2"
join(2507..2643,49292..49491,74767..74877,75863..75955,
76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105226)
/product="PP2A B56 gamma 1"
2507..2643
/number=1
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76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105076,
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/note="protein phosphatase; splice variant 3"
/codon_start=1
/product="PP2A B56 gamma 3"
/protein_id="AAL14779.1"
/db_xref="GI:16303632"
/translation="MVVDAANSNGFPQPVLLHIRDVPPADQEKLFIOKLROCCVLFD
FVSDPLDLKWEKRAALSEMVEYITHNRNVTETIYPEVHMFVAVNFRILPSSN
PTGAEDPEDEPTLEAAWPHLOLVYEFRLFESDPQPNIAKKYIDQKVLQLEL
FQSDPRERDLKTLHRIYCKFLGLRAYIRKQINNIYFIYETEHNGIAELLEIL
GSILINGFALPLKEEHKIFLLKVLPLHVKLSVYHPQLAYCVVQFLEKDSITPEVY
MALKYWPKTHSPKEVFMLELEILDVIEPSEFVKIMEPLFROLAKCVSPHFQVAE
RALIYWNNEYIMSLISDNAKILPIMFPSLYRNSTHWNKTIHGLIYNALKLFEMNQ
KLFDCTQOQFAEKLEKLEKMEREAWVKIENLAKANPQVTVYSOASPMSTIPVAMET
DQPLFEDVLRKTVKDEAHQAQDKPKKRLALRKSLELPDPHTKKALEACHRADEL
ASQDGR"
join(2580..2643,49292..49491,74767..74877,75863..75955,
76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105076,
117745..117876)
/note="protein phosphatase; splice variant 2"
/codon_start=1
/product="PP2A B56 gamma 2"
/protein_id="AAL14778.1"
/db_xref="GI:16303631"
/translation="MVVDAANSNGFPQPVLLHIRDVPPADQEKLFIOKLROCCVLFD
FVSDPLDLKWEKRAALSEMVEYITHNRNVTETIYPEVHMFVAVNFRILPSSN
PTGAEDPEDEPTLEAAWPHLOLVYEFRLFESDPQPNIAKKYIDQKVLQLEL
FQSDPRERDLKTLHRIYCKFLGLRAYIRKQINNIYFIYETEHNGIAELLEIL
GSILINGFALPLKEEHKIFLLKVLPLHVKLSVYHPQLAYCVVQFLEKDSITPEVY
MALKYWPKTHSPKEVFMLELEILDVIEPSEFVKIMEPLFROLAKCVSPHFQVAE
RALIYWNNEYIMSLISDNAKILPIMFPSLYRNSTHWNKTIHGLIYNALKLFEMNQ
KLFDCTQOQFAEKLEKLEKMEREAWVKIENLAKANPQADPKDPLALRKSLE
PDPHTKKALEACHRADELASQDGR"
join(2580..2643,49292..49491,74767..74877,75863..75955,
76038..76168,82840..82899,85603..85711,87110..87163,
94322..94492,99005..99132,102192..102293,105004..105100)
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/codon_start=1
/product="PP2A B56 gamma 1"
/protein_id="AAL14777.1"
/db_xref="GI:16303630"
/translation="MVVDAANSNGFPQPVLLHIRDVPPADQEKLFIOKLROCCVLFD
FVSDPLDLKWEKRAALSEMVEYITHNRNVTETIYPEVHMFVAVNFRILPSSN
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FQSDPRERDLKTLHRIYCKFLGLRAYIRKQINNIYFIYETEHNGIAELLEIL
GSILINGFALPLKEEHKIFLLKVLPLHVKLSVYHPQLAYCVVQFLEKDSITPEVY
MALKYWPKTHSPKEVFMLELEILDVIEPSEFVKIMEPLFROLAKCVSPHFQVAE
RALIYWNNEYIMSLISDNAKILPIMFPSLYRNSTHWNKTIHGLIYNALKLFEMNQ
KLFDCTQOQFAEKLEKLEKMEREAWVKIENLAKANPQVLKKRIT"
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/number=2
74767..74877
/number=3
75863..75955
/number=4
76038..76168
/number=5

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exon      82840..82899
/number=6
exon      85603..85711
/number=7
exon      87110..87163
/number=8
exon      94322..94492
/number=9
exon      99005..99132
/number=10
exon      102192..102293
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exon      105004..105076
/number=12
exon      105077..105226
/number=12A
exon      110434..110550
/number=13
exon      117745..120289
/number=14

BASE COUNT 31520 a 26430 c 27189 g 35887 t 2 others
ORIGIN

Query Match      6.6%  Score 66;  DB 9;  Length 121028;
Best Local Similarity 100.0%;  Pred. No. 3.8e-27;
Matches 66;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY 142 GGTGGATCACTTGAGTGTAGAGTGTGAGACCAAGCTGCGCAACACGGTGAACCCCAT 201
|||||
Db 26660 GGTGGATCACTTGAGTGTAGAGTGTGAGACCAAGCTGCGCAACACGGTGAACCCCAT 26601

QY 202 CTCATC 207
|||||
Db 26600 CTCATC 26595

RESULT 23
AC110023/c
LOCUS      AC110023      166975 bp      DNA      linear      PRI 11-APR-2002
DEFINITION Homo sapiens chromosome 15, clone RP11-739G5, complete sequence.
ACCESSION  AC110023
VERSION     AC110023.3  GI:20043183
KEYWORDS    HTG.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166975)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-739G5
Unpublished
2 (bases 1 to 166975)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,I., Boukhgalter,B.,
Brown,A., Camarata,J., Campoliano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyua,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McKwan,P., McKernan,K., Meidrim,J., Meneus,L., Mithova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuppback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

```



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repeat_region      /rpt_family="MERS8A"
16310..16553
repeat_region      /rpt_family="MIR"
17063..17083
repeat_region      /rpt_family="AT_Rich"
complement(17197..17482)
repeat_region      /rpt_family="AluSc"
complement(17483..17626)
repeat_region      /rpt_family="MIR"
complement(18296..18429)
repeat_region      /rpt_family="MIR"
complement(20132..20502)
repeat_region      /rpt_family="MIRII"
21039..21062
repeat_region      /rpt_family="AT_Rich"
21276..21302
repeat_region      /rpt_family="AT_Rich"
21896..22065
repeat_region      /rpt_family="L1PB3"

Query Match          6.6%; Score 66; DB 9; Length 166975;
Best Local Similarity 100.0%; Pred. No. 3.8e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 AAATACAAAATTAGCCAGGTGTGTGGCACAGCGCTGACTGCCAGCTACTTGGGAGGC 405
|||||
Db 23765 AAATACAAAATTAGCCAGGTGTGTGGCACAGCGCTGACTGCCAGCTACTTGGGAGGC 405

QY 406 TGAGGC 411
Db 23705 TGAGGC 23700

RESULT 24
AC024262          182627 bp      DNA      linear      HTG 28-MAR-2001
LOCUS             Homo sapiens chromosome 15 clone RP11-164C12, WORKING DRAFT
SEQUENCE          4 unordered pieces.
AC024262
AC024262.17 GI:13470160
HTG; HTGS-PHASE1; HTGS-DRAFT; HTGS-FULLTOP.
Homo sapiens.
ORGANISM           Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182627)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Mao,J., Komp,C., Kottler,S., Lam,B., Marathe,R., Miranda,M.,
Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D.,
Southwick,A.M., Webb,C., Wilhelmy,J., Yu,S. and Davis,R.W.
Unpublished
2 (bases 1 to 182627)
Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D., Federspiel,N.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
Yu,S. and Davis,R.W.
Direct Submission
Submitted (28-FEB-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT
----- Genome Center
Center: Stanford DNA Sequencing and Technology Development
Center code: SOSTDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
----- Project Information
Center project name: 854
Center clone name: RP11-164C12
----- Summary Statistics
Sequencing Vector: M13mp18; X02513

```

Chemistry: Dye-primer; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 181410 bases at least Q40
 Consensus quality: 181662 bases at least Q30
 Consensus quality: 181772 bases at least Q20
 Insert size: 182311; agarose-fp
 Insert size: 182327; sum-of-contigs
 Quality coverage: 10.2x in Q20 bases; agarose-fp
 Quality coverage: 10.2x in Q20 bases; sum-of-contigs.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

* 1 17671: contig of 17671 bp in length
* 17672 17771: gap of unknown length
* 17772 55704: contig of 37933 bp in length
* 55705 55804: gap of unknown length
* 55805 114621: contig of 58817 bp in length
* 114622 114721: gap of unknown length
* 114722 182627: contig of 67906 bp in length.

```

FEATURES source

```

1..182627
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/clone_lib="RP11-164C12"
/clone_lib="RP11-164C12"
/misc_feature 1..17671
/notes="assembly_name:Contig10"
17772..55704
/misc_feature /notes="assembly_name:Contig11"
55805..114621
/misc_feature /notes="assembly_name:Contig12"
clone_end:17*
/misc_feature 114722..182627
/notes="assembly_name:Contig13"

```

```

BASE COUNT 53714 a 38503 c 38339 g 51766 t 305 others
ORIGIN
Query Match          6.6%; Score 66; DB 2; Length 182627;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 346 AAATACAAAATTAGCCAGGTGTGTGGCACAGCGCTGACTGCCAGCTACTTGGGAGGC 405
|||||
Db 56133 AAATACAAAATTAGCCAGGTGTGTGGCACAGCGCTGACTGCCAGCTACTTGGGAGGC 56192

QY 406 TGAGGC 411
|||||
Db 56193 TGAGGC 56198

```

```

RESULT 25
AC091078/c
LOCUS             AC091078 182776 bp      DNA      linear      PRI 25-JUL-2002
DEFINITION        Homo sapiens, clone RP11-164C12, complete sequence.
ACCESSION          AC091078
VERSION            AC091078.7 GI:21700642
KEYWORDS           HTG.
SOURCE             Homo sapiens.
ORGANISM           Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182776)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-164C12
Unpublished
REFERENCE          2 (bases 1 to 182776)

```

AUTHORS

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
 Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
 Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
 Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
 Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K.,
 Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
 MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
 McWan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
 Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
 Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

Direct Submission
 Submitted (28-MAR-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 182776)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

TITLE

Direct Submission
 Submitted (06-JUL-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 182776)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
 Liu,G., Maclean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mienga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.

TITLE

Direct Submission
 Submitted (25-JUL-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 6, 2002 this sequence version replaced gi:21392507.

COMMENT

All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RW/RepeatMasker.html
 ----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WtBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: I12380
 Center clone name: 164_C_12

FEATURES

source	Location/Qualifiers
repeat_region	1..154 /rpt_family="Charliel"
repeat_region	155..456 /rpt_family="AluY"
repeat_region	457..551 /rpt_family="Charliel"
repeat_region	590..929 /rpt_family="LIM4"
repeat_region	complement(930..1228) /rpt_family="AluSp"
repeat_region	1229..1284 /rpt_family="LIM4"
repeat_region	complement(1572..2004) /rpt_family="MLTIC"
repeat_region	2262..2287 /rpt_family="(T)n"
repeat_region	2288..2458 /rpt_family="AluSg/x"
repeat_region	2460..2685 /rpt_family="LIMed"
repeat_region	2845..3116 /rpt_family="LIMed"
repeat_region	3139..3295 /rpt_family="LIMed"
repeat_region	complement(3296..3601) /rpt_family="AluSx"
repeat_region	3602..3662 /rpt_family="LIMed"
repeat_region	4030..4186 /rpt_family="LIMed"
repeat_region	4940..5021 /rpt_family="MIR"
repeat_region	5956..5965 /rpt_family="AT-rich"
repeat_region	complement(5966..6290) /rpt_family="LIPB1"
repeat_region	complement(6578..6693) /rpt_family="AluJb"
repeat_region	6816..6838 /rpt_family="(TTCA)n"
repeat_region	complement(7035..7086) /rpt_family="L2"
repeat_region	8170..8622 /rpt_family="MLTIC"
repeat_region	8715..8785 /rpt_family="MIR3"
repeat_region	9382..9588 /rpt_family="L3"
repeat_region	9940..9973 /rpt_family="(CA)n"
repeat_region	9974..10017 /rpt_family="(GA)n"
repeat_region	complement(10608..10909) /rpt_family="AluY"
repeat_region	complement(11914..11975) /rpt_family="MER5B"
repeat_region	11976..12279 /rpt_family="AluSp"
repeat_region	12288..12583

```

repeat_region      /rpt_family="AluJb"
complement(12584..12703)
repeat_region      /rpt_family="MERSB"
12714..12793
repeat_region      /rpt_family="MIR"
complement(13588..13770)
repeat_region      /rpt_family="LIMA5A"
13765..13838
repeat_region      /rpt_family="LIMA5A"
16006..16312
repeat_region      /rpt_family="AluY"
17503..17620
repeat_region      /rpt_family="MER46C"
18030..18330
repeat_region      /rpt_family="AluY"
complement(18370..18544)
repeat_region      /rpt_family="AluX"
complement(18545..18848)
repeat_region      /rpt_family="AluSg"
complement(18849..18981)
repeat_region      /rpt_family="AluX"
19509..19566
repeat_region      /rpt_family="MER46C"
complement(20146..20513)
repeat_region      /rpt_family="MIR1A1"
complement(20681..20719)
repeat_region      /rpt_family="AluSg"
complement(20720..20796)
repeat_region      /rpt_family="Alu"
21232..21316
repeat_region      /rpt_family="ORSL"
21325..21622
repeat_region      /rpt_family="AluJb"
21651..21757
repeat_region      /rpt_family="ORSL"
21994..22045
repeat_region      /rpt_family="AT_rich"
22163..22214
repeat_region      /rpt_family="r-rich"
complement(22321..28436)

Query Match      6.6%; Score 66; DB 9; Length 182776;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 AAATACAAATATAGCAGGTGTGGCACACGCTGTAGTCCACGCTACTTGGGAGGC 405
|||||
Db 182452 AAATACAAATATAGCAGGTGTGGCACACGCTGTAGTCCACGCTACTTGGGAGGC 182393
|||||

QY 406 TGAGGC 411
|||||
Db 182392 TGAGGC 182387

RESULT 26
AC022281/c
LOCUS      186431 bp DNA linear HTG 24-JAN-2002
DEFINITION Homo sapiens chromosome 10 clone RP11-10E13, WORKING DRAFT
SEQUENCE, 9 unordered pieces.
ACCESSION AC022281
VERSION AC022281.3 GI:13399348
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN;
HTGS_CANCELLED.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 186431)
AUTHORS Smith,D.R.
TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome
Sequence Data
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186431)

```

AUTHORS
TITLE
JOURNAL
COMMENT

Smith,D.R.
Direct Submission
Submitted (28-JAN-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Mar 21, 2001 this sequence version replaced gi:9929643.

Genome Center
Center: Genome Therapeutics Corporation
Center code: GTC
Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com

Project Information
Center project name: hg143

Summary Statistics
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 395389 bases at least Q40
Consensus quality: 405067 bases at least Q30
Consensus quality: 410525 bases at least Q20
Insert size: 185631; sum-of-contigs
Quality coverage: 6.4x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 124725: contig of 124725 bp in length
* 124726 124825: gap of unknown length
* 124826 125924: contig of 1099 bp in length
* 125925 126024: gap of unknown length
* 126025 128493: contig of 2469 bp in length
* 128494 128593: gap of unknown length
* 128594 156515: contig of 27922 bp in length
* 156516 156615: gap of unknown length
* 156616 170011: contig of 13396 bp in length
* 170012 170111: gap of unknown length
* 170112 176430: contig of 6319 bp in length
* 176431 176530: gap of unknown length
* 176531 179019: contig of 2489 bp in length
* 179020 179120: gap of unknown length
* 179120 181965: contig of 2846 bp in length
* 181966 182065: gap of unknown length
* 182066 186431: contig of 4366 bp in length.

FEATURES

source

1..186431
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone_lib="RP11-10E13"
/clone_lib="RPC1-11"
1..124725
/note="assembly_name:Contig243"

misc_feature

clone_end:SP6"
124826..125924
/note="assembly_name:Contig204"
126025..128493
/note="assembly_name:Contig233"
128594..156515
/note="assembly_name:Contig240"
156616..170011
/note="assembly_name:Contig239"
170112..176430
/note="assembly_name:Contig235"
176531..179019
/note="assembly_name:Contig231"
179120..181965
/note="assembly_name:Contig232"
182066..186431
/note="assembly_name:Contig236"

```

BASE COUNT 48827 a 41798 c 41896 g 53062 t 848 others
ORIGIN
Query Match 6.6%; Score 66; DB 2; Length 186431;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GTGGATCACTTGGTTCAGGAGTTTTCAGACACGCTGGCCACACGGTGAACCCCAT 201
|||||
Db 41809 GTGGATCACTTGGTTCAGGAGTTTTCAGACACGCTGGCCACACGGTGAACCCCAT 41750
|||||

QY 202 CTCCTAC 207
|||||
Db 41749 CTCCTAC 41744

RESULT 27
CNSOLDWM 189116 bp DNA linear PRI 08-JAN-2002
LOCUS Human chromosome 14 DNA sequence BAC C-2017C7 of library CalTech-D
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL137779
VERSION AL137779.6 GI:18103850
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 189116)
AUTHORS Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., DeBerardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissbach, J.
TITLE Sequencing of the human chromosome 14
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 189116)
GENOSCOPE.
Direct Submission
Submitted (08-JAN-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
On Jan 9, 2002 this sequence version replaced gi:15718346.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Gen code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-1017G21 (AC-ALL18558)
Downstream BAC (overlapping the SP6 end) : R-79666 -----
Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 7.29x in Q20 bases; sum-of-contigs
-----
Overall quality chart :
Range : bases
0 : 2
1 - 9 : 47
10 - 19 : 204
20 - 29 : 463
30 - 39 : 1585
40 - 49 : 5020
50 - 59 : 8017
60 - 69 : 8705
70 - 79 : 19573
80 - 89 : 53510
90 - 99 : 91990
-----
Percentage of bases with a quality value >= 40 : 98 %.
Location/Qualifiers

```

```

1. 189116
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone="C-2017C7"
/clone_lib="CalTech-D"
33932..34056
/note="matching EMBL:T96367
RHdb:RH53659
dbSTS:STS4719
Identified using the e-PCR software (G. Schuler)"
42542..42731
/note="matching EMBL:AA236880
RHdb:RH91926
dbSTS:STS64930
Identified using the e-PCR software (G. Schuler)"
80798..80947
/note="matching EMBL:T88698
RHdb:RH53754
dbSTS:STS31753
Identified using the e-PCR software (G. Schuler)"
89772..89898
/note="matching EMBL:H64944
RHdb:RH53858
dbSTS:STS24743
Identified using the e-PCR software (G. Schuler)"
101676..101841
/note="matching EMBL:T52954
RHdb:RH44791
dbSTS:STS37859
Identified using the e-PCR software (G. Schuler)"
114961..115136
/note="matching EMBL:Z51483
RHdb:RH31332
dbSTS:STS25252
Identified using the e-PCR software (G. Schuler)"

BASE COUNT 53622 a 42176 c 42426 g 50890 t 2 others
ORIGIN
Query Match 6.6%; Score 66; DB 9; Length 189116;
Best Local Similarity 100.0%; Pred. No. 3.9e-27;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 GTGGATCACTTGGTTCAGGAGTTTTCAGACACGCTGGCCACACGGTGAACCCCAT 201
|||||
Db 45000 GTGGATCACTTGGTTCAGGAGTTTTCAGACACGCTGGCCACACGGTGAACCCCAT 45059
|||||

QY 202 CTCCTAC 207
|||||
Db 45060 CTCCTAC 45065

RESULT 28
AL136137 127140 bp DNA linear PRI 06-DEC-2001
LOCUS Human DNA sequence from clone RP11-377B2 on chromosome Xp11.23-11.4
DEFINITION Contains a novel pseudogene, a pseudogene similar to RPL19
(ribosomal protein L19), complete sequence.
ACCESSION AL136137
VERSION AL136137.15 GI:10119664
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 127140)
AUTHORS Whitehead, S.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 12, 2000 this sequence version replaced gi:10086012.
During sequence assembly data is compared from overlapping clones.
COMMENT

```

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/C-elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-377B2 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-377B2. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP6-105D16 is at 127041 in this sequence. The true right end of clone RP4-551E13 is at 100 in this sequence.

FEATURES

Source	Location/Qualifiers
misc_feature	1..127140
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="X"
	/map="p11.23-11.4"
	/clone_lib="RPC1-377B2"
	/complement(1..428)
	/note="match: GSS: Em:AQ027029"
	972..1271
	/note="AluY repeat: matches 2..302 of consensus"
repeat_region	complement(1321..1598)
	/note="match: STS: Em:L47514"
	2140..2253
	/note="FLAM_C repeat: matches 1..117 of consensus"
	2602..2887
	/note="AluSx repeat: matches 1..286 of consensus"
	2912..3224
	/note="AluSx repeat: matches 1..303 of consensus"
	3238..3526
	/note="AluJo repeat: matches 1..290 of consensus"
repeat_region	3527..3648
	/note="61 copies 2 mer ca 77% conserved"
	3830..3982
	/note="HAL1 repeat: matches 24..164 of consensus"
	4044..4081
	/note="19 copies 2 mer ac 100% conserved"
	4130..4390
	/note="L1MC3 repeat: matches 6875..7167 of consensus"
	4391..4691
	/note="AluSx repeat: matches 1..302 of consensus"
misc_feature	4796..5146
	/note="match: GSS: Em:AQ633427"
	complement(4822..4963)
	/note="match: STS: Em:HSA058XH1"
	4836..5129
	/note="AluSg repeat: matches 1..292 of consensus"
	5626..5935
	/note="AluY repeat: matches 1..311 of consensus"
	6060..6377
	/note="AluJb repeat: matches 1..312 of consensus"
repeat_region	6384..6444
	/note="HAL1 repeat: matches 289..354 of consensus"
	6492..6502
	/note="BC200 repeat: matches 1..10 of consensus"
	6503..6621
	/note="AluJo repeat: matches 10..139 of consensus"
	6622..6641
	/note="BC200 repeat: matches 10..161 of consensus"
	6642..7142
	/note="HAL1 repeat: matches 357..947 of consensus"
repeat_region	7143..7443
	/note="AluSx repeat: matches 1..305 of consensus"
	7444..7555
	/note="HAL1 repeat: matches 947..1044 of consensus"
	7664..7977
	/note="AluY repeat: matches 1..311 of consensus"
	7982..8294
	/note="AluSg repeat: matches 1..309 of consensus"
	8302..8615
	/note="AluSg repeat: matches 1..299 of consensus"
repeat_region	8632..8733
	/note="L1MAC repeat: matches 1564..1666 of consensus"
	8861..9122
	/note="HAL1 repeat: matches 1427..1704 of consensus"
	10252..10559
	/note="AluSg repeat: matches 3..308 of consensus"
	11009..11135
	/note="L1MC5 repeat: matches 7754..7900 of consensus"
	11573..11941
	/note="MUTIC repeat: matches 6..416 of consensus"
repeat_region	11955..12244
	/note="AluSx repeat: matches 1..291 of consensus"
	12693..12724
	/note="16 copies 2 mer tg 96% conserved"
	15518..15901
	/note="MER31A repeat: matches 1..375 of consensus"
	MER31A repeat: matches 1..375 of consensus"
	15902..16194
	/note="AluJo repeat: matches 1..292 of consensus"
	16195..16277
repeat_region	/note="MER31A repeat: matches 375..458 of consensus"
	MER31A repeat: matches 375..458 of consensus"
	16586..16893
	/note="AluSx repeat: matches 1..301 of consensus"
	17240..17283
	/note="MADEL repeat: matches 35..80 of consensus"
	17638..18226
	/note="LTR10C repeat: matches 1..586 of consensus"
	LTR10C repeat: matches 1..586 of consensus"
	18309..18597
repeat_region	/note="AluSp repeat: matches 1..288 of consensus"
	18621..18909
	/note="AluSx repeat: matches 1..284 of consensus"
	19245..19569
	/note="match: GSS: Em:AQ663911 Em:B94529"
	19245..19512
	/note="match: GSS: Em:AQ128461"
	complement(19373..19569)
	/note="match: GSS: Em:AQ240745"
	19381..19521
misc_feature	/note="match: GSS: Em:AQ037473"
	19405..19614
	/note="MER4D repeat: matches 764..981 of consensus"
	19615..19829
	/note="AluSg/X repeat: matches 92..306 of consensus"
	19830..20397
	/note="MER4D repeat: matches 233..764 of consensus"
	20430..20567
	/note="AluJo repeat: matches 1..119 of consensus"
	20568..20869
repeat_region	/note="AluSx repeat: matches 1..301 of consensus"
	20870..20999
	/note="AluJo repeat: matches 119..306 of consensus"

```

repeat_region 21447..21599
/Note="LTR repeat: matches 1..156 of consensus
LTR8 repeat: matches 1..156 of consensus"
21600..21919
/Note="AluX repeat: matches 1..310 of consensus"
21920..22306
/Note="LTR repeat: matches 156..524 of consensus
LTR8 repeat: matches 156..524 of consensus"
22307..22614
/Note="AluSg repeat: matches 1..310 of consensus"
22615..22779
/Note="LTR repeat: matches 524..691 of consensus
LTR8 repeat: matches 524..691 of consensus"
22930..23226
/Note="Alu repeat: matches 6..302 of consensus"
23239..23324
/Note="MER57-internal repeat: matches 7149..7239 of
consensus"
23445
/Note="match: GSS: Em:AQ826300"
23449..23755
/Note="AluX repeat: matches 3..311 of consensus"
23464..23755
/Note="match: STS: Em:HS138B7S"
24354..24509
/Note="AluY repeat: matches 137..292 of consensus"
24510..24806
/Note="AluY repeat: matches 1..297 of consensus"
24807..24943
/Note="AluY repeat: matches 1..137 of consensus"
25494..25683
/Note="MER58C repeat: matches 1..81 of consensus
MER58C repeat: matches 1..81 of consensus"
complement(25685..25976)
/Note="match: GSS: Em:AQ590309"

Query Match 6.4%; Score 64; DB 9; Length 127140;
Best Local Similarity 100.0%; Pred. No. 5.8e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATAACAAAATTAGCCAGGTGGTGGGCACACGCCCTGTAGTCCGAGC 393
Db 51506 CGTCTCTACTAAATAACAAAATTAGCCAGGTGGTGGGCACACGCCCTGTAGTCCGAGC 51565

QY 394 TACT 397
|||||
Db 51566 TACT 51569

RESULT 29
AL590640
LOCUS
DEFINITION Human DNA sequence from clone RP11-40H20 on chromosome 1, complete
sequence.
ACCESSION AL590640
VERSION AL590640.18 GI:18476678
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146954)
Harrison,E.
Direct Submission
Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:18181688.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with

```

```

only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sg:
SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
RP11-40H20 is from the library RPI1-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-40H20 it may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RP11-40H20 is at 1 in this sequence. The
true left end of clone RP4-633N17 is at 144955 in this sequence.
The true right end of clone RP11-4K3 is at 7274 in this sequence.
LOCATION/Qualifiers
Source
1..146954
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-40H20"
/clone_lib="RPI1-11.1"
5405..5468
/Note="Sequence from overlapping clone RP11-4K3
(AL591050). Assembly confirmed by restriction digest."
26429..26442
/Note="Single clone region. Reads generated from a
transposon library derived from a single pUC clone.
Restriction digest data confirm the assembly."
108250..108261
/Note="Sequence from uni-directional dGTP big dye
terminator reads only."
Single clone region. Reads generated from a transposon
library derived from a single pUC clone. Restriction
digest data confirm the assembly."
139312..139369
/Note="Sequence from uni-directional dGTP big dye
terminator reads only."
BASE COUNT 41970 a 33288 c 33765 g 37930 t
ORIGIN

Query Match 6.4%; Score 64; DB 9; Length 146954;
Best Local Similarity 100.0%; Pred. No. 5.9e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAATAACAAAATTAGCCAGGTGGTGGGCACACGCCCTGTAGTCCGAGC 393
Db 40427 CGTCTCTACTAAATAACAAAATTAGCCAGGTGGTGGGCACACGCCCTGTAGTCCGAGC 40486

QY 394 TACT 397
|||||
Db 40487 TACT 40490

RESULT 30
AL359272
LOCUS
DEFINITION Human DNA sequence from clone RP11-554P16 on chromosome X. Contains
the first coding exon of the gene KIAA1202, STSS, GSSs and a CpG
island, complete sequence.
ACCESSION AL359272

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VERSION	AL359272.9	GI:9650579
KEYWORDS	HTG; CpG Island; KIAA1202.	
SOURCE	human.	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Bird,C.	
AUTHORS	Direct Submission	
JOURNAL	Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk	
COMMENT	requests: clonerequests@sanger.ac.uk On Aug 1, 2000 this sequence version replaced gi:9588592. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX RP11-554P16 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pBACe3.6 This sequence is the entire insert of clone RP11-554P16. FEATURES source 1..173510 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="X" /clone="RP11-554P16" /clone_lib="RPCI-11.2" repeat_region 2..192 /note="L1MEC repeat: matches 1913..2098 of consensus" misc_feature 7..674 /note="match: GSS: Em:AQ373815" repeat_region 195..511 /note="AluSp repeat: matches 1..312 of consensus" repeat_region 543..845 /note="AluX repeat: matches 1..304 of consensus" repeat_region 950..1127 /note="L1MEC repeat: matches 1968..2136 of consensus" repeat_region 1190..2306 /note="L1M4b repeat: matches -180..888 of consensus" repeat_region 2425..3343 /note="L1M4 repeat: matches 3078..4092 of consensus" repeat_region 3344..3717 /note="MSTD repeat: matches 1..394 of consensus" repeat_region 3718..4412 /note="L1M4 repeat: matches 4092..4274 of consensus" repeat_region 4413..4452 /note="THE1B repeat: matches 1..42 of consensus" repeat_region 4453..4763 /note="AluX repeat: matches 1..310 of consensus" repeat_region 4764..5111 /note="THE1B repeat: matches 42..364 of consensus" repeat_region 5112..5774 /note="L1M4 repeat: matches 4274..5344 of consensus" repeat_region 5775..6080	

repeat_region 29523..30381
/note="L1MB8 repeat: matches 2496. .3231 of consensus"
repeat_region 30382..30685
/note="AluJo repeat: matches 2. .299 of consensus"
repeat_region 30686..31069
/note="L1MB8 repeat: matches 2110. .2496 of consensus"
repeat_region 31088..31421
/note="L1P4 repeat: matches 5820. .6156 of consensus"
repeat_region 31422..31617
/note="L1P4 repeat: matches 5374. .5552 of consensus"
repeat_region 31618..31909
/note="AluX repeat: matches 1. .294 of consensus"
repeat_region 31910..31976
/note="L1P4 repeat: matches 5304. .5374 of consensus"
repeat_region 31978..32359
/note="L1MB repeat: matches 1951. .2330 of consensus"
repeat_region 32354..33592
/note="L1M4C repeat: matches 969. .2197 of consensus"
repeat_region 33935..34790
/note="L1M4B repeat: matches -266. .602 of consensus"
repeat_region 34856..35219
/note="L1MB repeat: matches 1. .364 of consensus"
repeat_region 36043..36159
/note="L2 repeat: matches 2576. .2710 of consensus"
misc_feature 38455..39057
/note="match: GSS: Em:AQ008362"
misc_feature 41978..42373
/note="match: STS: Em:L18363"
repeat_region 42056..42087
/note="16 copies 2 mer tg 96% conserved"
repeat_region 42311..42540
/note="MIR repeat: matches 19. .262 of consensus"
repeat_region 42824..42914
/note="L2 repeat: matches 2606. .2709 of consensus"
repeat_region 43119..43173
/note="L2 repeat: matches 2687. .2742 of consensus"
repeat_region 43122..43185
/note="MIR repeat: matches 194. .257 of consensus"
repeat_region 44700..44743
/note="22 copies 2 mer aa 75% conserved"
repeat_region 45956..46137
/note="MIR repeat: matches 20. .199 of consensus"
repeat_region 46401..46617
/note="MIR repeat: matches 23. .262 of consensus"
repeat_region 46729..47035
/note="AluJb repeat: matches 1. .309 of consensus"
repeat_region 47439..47682
/note="L1MB repeat: matches 5666. .5914 of consensus"
repeat_region 48430..48527

Query Match 6.4%; Score 64; DB 9; Length 173510;
Best Local Similarity 100.0%; Pred. No. 5.9e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 334 CGTCTCTACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCGACG 393
Db 169132 CCGTCTCTACTAAATAACAAAATAGCCAGGTGGTGGCACACGCTGTAGTCCGACG 169191
QY 394 TACT 397
|||||
Db 169192 TACT 169195

RESULT 31
AC021923
LOCUS AC021923 177242 bp DNA linear HTG 09-MAY-2001
DEFINITION Homo sapiens clone RP11-2707, WORKING DRAFT SEQUENCE, 7 unordered
pieces.
ACCESSION AC021923
VERSION AC021923.4 GI:12656831
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177242)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-2707
Unpublished
2 (bases 1 to 177242)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArelano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,B., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lechoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
MacDonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheders,R., Meldrum,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 2, 2001 this sequence version replaced gi:7249099.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4730
Center clone name: 27_0_7
----- Summary Statistics
Sequencing vector: M13; M7815; 49% of reads
Sequencing vector: Plasmid; n/a; 51% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 175551 bases at least Q40
Consensus quality: 176231 bases at least Q30
Consensus quality: 176426 bases at least Q20
Insert size: 180000; agarose-fp
Insert size: 176642; sum-of-contigs
Quality coverage: 9.8 in Q20 bases; agarose-fp
Quality coverage: 10.0 in Q20 ba.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 3850: contig of 3850 bp in length
* 3851 3950: gap of 100 bp
* 3951 9386: contig of 5436 bp in length
* 9387 9486: gap of 100 bp
* 9487 17804: contig of 8318 bp in length
* 17805 17904: gap of 100 bp
* 17905 71191: contig of 53287 bp in length
* 71192 71291: gap of 100 bp
* 71292 112250: contig of 40959 bp in length
* 112251 112350: gap of 100 bp
* 112351 154709: contig of 42359 bp in length
* 154710 154809: gap of 100 bp
* 154810 177242: contig of 22433 bp in length.
Location/Qualifiers

FEATURES

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source
1. .177242
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-2707"
/clone_lib="RPC1-11 Human Male BAC"
1. .3850
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
misc_feature
3951. .9386
/note="assembly_fragment"
9487. .17804
/note="assembly_fragment"
17905. .71191
/note="assembly_fragment"
71292. .112250
/note="assembly_fragment"
112351. .154709
/note="assembly_fragment"
154810. .177242
/note="assembly_fragment"
clone_end:T7
vector_side:right"
BASE COUNT 49940 a 37600 c 38021 g 51078 t 603 others
ORIGIN

Query Match 6.4%; Score 64; DB 2; Length 177242;
Best Local Similarity 100.0%; Pred. No. 5.9e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGCGGTACACCTGTAATCCAGCACCTTGGAGGCTGAGACGGTGGATCAC 287
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Db 85852 GGGTGGGCGGTACACCTGTAATCCAGCACCTTGGAGGCTGAGACGGTGGATCAC 85911

QY 288 CTGA 291
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Db 85912 CTGA 85915

RESULT 32
AP003352/c
LOCUS 187349 bp DNA linear PRI 03-APR-2001
DEFINITION Homo sapiens genomic DNA, chromosome 8q23, clone: KB1208A12.
ACCESSION AP003352
VERSION AP003352.2 GI:13516385
KEYWORDS
SOURCE Homo sapiens cell_line:FLEB 14 - 14 DNA, clone_lib:Keio BAC library
clone:KB1208A12.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. (sites)
Shimizu,N. and Asakawa,S.
TITLE Homo sapiens DNA chromosome 8 SEQUENCE
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 187349)
Shimizu,N. and Asakawa,S.
TITLE Direct Submission
JOURNAL Submitted (28-FEB-2001) Nobuyoshi Shimizu, Keio University, School
of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo
160-8582, Japan (E-mail:ashimizu@cmb.med.keio.ac.jp,
Tel:81-3-3351-2370, Fax:81-3-3351-2370)
COMMENT On Apr 2, 2001 this sequence version replaced gi:13359068.
FEATURES
Location/Qualifiers
1. .187349
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8q23"
/clone="KB1208A12"
/cell_line="FLEB 14 - 14"
/clone_lib="Keio BAC library"
307. .407
repeat_region
/evidence=not_experimental
/rpt_family="L2"
complement(752. .1291)
/evidence=not_experimental
/rpt_family="LIM4"
1735. .2095
/evidence=not_experimental
/rpt_family="Charlie4a"
complement(2109. .2538)
/evidence=not_experimental
/rpt_family="LIMB5"
complement(2539. .2849)
/evidence=not_experimental
/rpt_family="AluSg"
complement(2850. .3129)
/evidence=not_experimental
/rpt_family="LIMB5"
3130. .3228
/evidence=not_experimental
/rpt_family="Charlie4a"
complement(3887. .4189)
/evidence=not_experimental
/rpt_family="AluSx"
complement(4202. .4509)
/evidence=not_experimental
/rpt_family="AluY"
4526. .4729
/evidence=not_experimental
/rpt_family="MIR"
4731. .4752
/evidence=not_experimental
/rpt_family="AT_Rich"
4762. .4925
/evidence=not_experimental
/rpt_family="AluSg"
5042. .5157
/evidence=not_experimental
/rpt_family="AluSg"
5217. .5339
/evidence=not_experimental
/rpt_family="FLAM_C"
complement(5513. .5813)
/evidence=not_experimental
/rpt_family="AluSx"
complement(5835. .6120)
/evidence=not_experimental
/rpt_family="AluJb"
complement(6185. .6288)
/evidence=not_experimental
/rpt_family="LIM4"
6308. .6337
/evidence=not_experimental
/rpt_family="(TTTTC)n"
complement(6374. .6674)
/evidence=not_experimental
/rpt_family="L2"
complement(6675. .6951)
/evidence=not_experimental
/rpt_family="AluY"
complement(6954. .7245)
/evidence=not_experimental
/rpt_family="AluSx"
complement(7246. .7360)
/evidence=not_experimental
/rpt_family="L2"
7570. .7814
/evidence=not_experimental
/rpt_family="MIR"
complement(7870. .8167)
/evidence=not_experimental
/rpt_family="AluSx"
8317. .8619
/evidence=not_experimental

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repeat_region /rpt_family="AluSc"
complement(8629..8716)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(8754..8929)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(10203..10502)
/evidence-not_experimental
repeat_region /rpt_family="AluSx"
complement(10504..10802)
/evidence-not_experimental
repeat_region /rpt_family="AluSg"
complement(11247..11541)
/evidence-not_experimental
repeat_region /rpt_family="AluJb"
complement(11862)
/evidence-not_experimental
repeat_region /rpt_family="L2"
complement(11863..12179)
/evidence-not_experimental
repeat_region /rpt_family="AluJo"
complement(12180..12285)
/evidence-not_experimental
repeat_region /rpt_family="L2"
complement(12747..12781)
/evidence-not_experimental
repeat_region /rpt_family="(TG)n"
complement(12930..12973)
/evidence-not_experimental
repeat_region /rpt_family="(TTTTA)n"
complement(12974..13257)
/evidence-not_experimental
repeat_region /rpt_family="AluSx"
complement(13274..13504)
/evidence-not_experimental
repeat_region /rpt_family="LIPAL3"
complement(13820..13844)
/evidence-not_experimental
repeat_region /rpt_family="(TTTCC)n"
complement(14691..14990)
/evidence-not_experimental
repeat_region /rpt_family="AluSx"
complement(15114..15249)
/evidence-not_experimental
repeat_region /rpt_family="L2"
complement(15666..15819)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(16065..16162)
/evidence-not_experimental
repeat_region /rpt_family="MERSA"
complement(16166..16419)
/evidence-not_experimental
repeat_region /rpt_family="AluSg"
complement(17087..17114)
/evidence-not_experimental
repeat_region /rpt_family="(TARG)n"
complement(17115..17395)
/evidence-not_experimental
repeat_region /rpt_family="AluSx"
complement(17570..17647)
/evidence-not_experimental
repeat_region /rpt_family="AluSc"
complement(18742..19066)
/evidence-not_experimental
repeat_region /rpt_family="MER1B"
complement(20245..20422)
/evidence-not_experimental
repeat_region /rpt_family="L2"
complement(20424..20452)
/evidence-not_experimental
repeat_region /rpt_family="(TC)n"

```

```

repeat_region complement(20453..20743)
/evidence-not_experimental
repeat_region /rpt_family="AluSg"
complement(20744..21255)
/evidence-not_experimental
repeat_region /rpt_family="L2"
complement(21787..21863)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(21864..22286)
/evidence-not_experimental
repeat_region /rpt_family="MER57A"
complement(22287..22492)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(22461..22637)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(23449..23484)
/evidence-not_experimental
repeat_region /rpt_family="MIR"
complement(23897..24018)

```

Query Match 6.4% Score 64; DB 9; Length 187349;
Best Local Similarity 100.0%; Pred. No. 6e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCAC 287
|||||
Db 181566 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCAC 181507

QY 288 CTGA 291
|||||
Db 181506 CTGA 181503

RESULT 33

AC091075 197870 bp DNA linear HTG 11-JUN-2001
LOCUS Homo sapiens chromosome 8 clone RP11-680G2 map 8, WORKING DRAFT
DEFINITION
SEQUENCE, 10 unordered pieces.
AC091075
VERSION AC091075.2 GI:14336474
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197870)
Birren,B., Linton,L., Nussbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-680G2
Unpublished
2 (bases 1 to 197870)
Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavskiy,L., Boukhalter,B., Brown,A.,
Cammarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collumore,A., Cooke,P., DeArellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Laskoczek,K.,
Lamarez,R., Landers,T., Lenocky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meidrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,

TITLE
JOURNAL
COMMENT

Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 11, 2001 this sequence version replaced gi:13470191.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11753
Center clone name: 680_G_2
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 194427 bases at least Q40
Consensus quality: 195744 bases at least Q30
Consensus quality: 196367 bases at least Q20
Insert size: 200000; agarose-fp
Quality coverage: 10.7 in Q20 bases; sum-of-contigs
Quality coverage: 10.9 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.

* 1 36504: contig of 36504 bp in length
* 36505 36604: gap of 100 bp
* 36605 37316: contig of 712 bp in length
* 37317 37416: gap of 100 bp
* 37417 88008: contig of 50592 bp in length
* 88009 88108: gap of 100 bp
* 88109 89700: contig of 1592 bp in length
* 89701 89800: gap of 100 bp
* 89801 91377: contig of 1577 bp in length
* 91378 91477: gap of 100 bp
* 91478 96729: contig of 5252 bp in length
* 96730 96829: gap of 100 bp
* 96830 118877: contig of 22048 bp in length
* 118878 118977: gap of 100 bp
* 118978 146670: contig of 27693 bp in length
* 146671 146770: gap of 100 bp
* 146771 197149: contig of 50379 bp in length
* 197150 197249: gap of 100 bp
* 197250 197870: contig of 621 bp in length.

FEATURES

source
1. .197870
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"
/clone_lib="RP11-680G2"
/clone_lib="RP11-680G2"
1. .36504
/note="assembly_fragment"
clone_end:SP6
vector_side:left
36605..37316
/note="assembly_fragment"
37417..88008
/note="assembly_fragment"
88109..89700
/note="assembly_fragment"

misc_feature
/note="assembly_fragment"
118978..146670
/note="assembly_fragment"
146771..197149
/note="assembly_fragment"
197250..197870
/note="assembly_fragment"

misc_feature
36605..37316
/note="assembly_fragment"
37417..88008
/note="assembly_fragment"
88109..89700
/note="assembly_fragment"

misc_feature 89801..91377
/note="assembly_fragment"
91478..96729
/note="assembly_fragment"
96830..118877
/note="assembly_fragment"
118978..146670
/note="assembly_fragment"
146771..197149
/note="assembly_fragment"
197250..197870
/note="assembly_fragment"
clone_end:T
vector_side:right

BASE COUNT 55077 a 43169 c 43473 g 55250 t 901 others
ORIGIN

Query Match 6.4%; Score 64; DB 2; Length 197870;
Best Local Similarity 100.0%; Pred.No. 6e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 228 GGTCGGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCAC 287
|||||
Db 9986 GGTCGGGTGGCTCACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGTGGATCAC 10045
QY 288 CTGA 291
|||||
Db 10046 CTGA 10049

RESULT 34
AC019236
LOCUS
DEFINITION Homo sapiens chromosome 8 clone RP11-680G2, WORKING DRAFT SEQUENCE,
23 unordered pieces.
AC019236 199208 bp DNA linear HTG 10-SEP-2000

AC019236
VERSION AC019236.5 GI:10048101
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Waterston,R.H.
JOURNAL The sequence of Homo sapiens clone
REFERENCE 2 (bases 1 to 199208)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT
On Sep 10, 2000 this sequence version replaced gi:7235318.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0680G02
----- Summary Statistics -----
Sequencing vector: M13; 76%
Sequencing vector: plasmid; 24%
Chemistry: Dye-primer ET; 76% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 188489 bases at least Q40
Consensus quality: 191861 bases at least Q30
Insert size: 202000; agarose-fp
Insert size: 198337; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 4.08 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1
1812: contig of 1812 bp in length
1813
1912: gap of unknown length
3838: contig of 1926 bp in length
3938: gap of unknown length
3939
5889: contig of 1951 bp in length
5890
5989: gap of unknown length
5990
8667: contig of 2678 bp in length
8668
8767: gap of unknown length
8768
11541: contig of 2774 bp in length
11542
14813: contig of 3172 bp in length
14814
14913: gap of unknown length
17378: contig of 2465 bp in length
17379
17478: gap of unknown length
21197: contig of 3719 bp in length
21198
21297: gap of unknown length
26511: contig of 5214 bp in length
26512
26611: gap of unknown length
30595: contig of 3984 bp in length
30596
30695: gap of unknown length
35841: contig of 5146 bp in length
35842
35941: gap of unknown length
35942
39400: contig of 3459 bp in length
39401
39500: gap of unknown length
43746: contig of 4246 bp in length
43747
43846: gap of unknown length
49935: contig of 6089 bp in length
49936
50035: gap of unknown length
50036
54892: contig of 4857 bp in length
54893
54993: contig of 7611 bp in length
62603: contig of 7611 bp in length
62703: gap of unknown length
70543: contig of 7840 bp in length
70544
70643: gap of unknown length
79145: contig of 8502 bp in length
79146
79245: gap of unknown length
88619: contig of 9374 bp in length
88620
88719: gap of unknown length
100155: contig of 11436 bp in length
100156
100255: gap of unknown length
114403: contig of 14148 bp in length
114404
114503: gap of unknown length
114504
142767: contig of 28264 bp in length
142768
142867: gap of unknown length
199208: contig of 56341 bp in length.
142888

FEATURES

source
1. .199208
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/clone="RP11-680G2"
1. .1812
/note="assembly_name:Contig4"
1913. .3838
/note="assembly_name:Contig5"
3939. .5889
/note="assembly_name:Contig6"
5990. .8667
/note="assembly_name:Contig7"
8768. .11541
/note="assembly_name:Contig8"
11642. .14813
/note="assembly_name:Contig9"
14914. .17378

misc_feature

1913. .3838
/note="assembly_name:Contig4"
3939. .5889
/note="assembly_name:Contig5"
5990. .8667
/note="assembly_name:Contig6"
8768. .11541
/note="assembly_name:Contig7"
11642. .14813
/note="assembly_name:Contig8"
14914. .17378

misc_feature
/note="assembly_name:Contig10"
17479. .21197
/note="assembly_name:Contig11"
21298. .26511
/note="assembly_name:Contig12"
26612. .30595
/note="assembly_name:Contig13"
30696. .35841
/note="assembly_name:Contig14"
35942. .39400
/note="assembly_name:Contig15"
39501. .43746
/note="assembly_name:Contig16"
43847. .49935
/note="assembly_name:Contig17"
50036. .54892
/note="assembly_name:Contig18"
54993. .62603
/note="assembly_name:Contig19"
62704. .70543
/note="assembly_name:Contig20"
70644. .79145
/note="assembly_name:Contig21"
79246. .88619
/note="assembly_name:Contig22"
88720. .100155
/note="assembly_name:Contig23"
100256. .114403
/note="assembly_name:Contig24"
114504. .142767
/note="assembly_name:Contig25"
clone_end:SP6
vector_side:left
142868. .199208
/note="assembly_name:Contig26"
BASE COUNT 53771 a 43806 c 43167 g 56261 t 2203 others
ORIGIN

Query Match 6.4%; Score 64; DB 2; Length 199208;
Best Local Similarity 100.0%; Pred. No. 6e-26;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGCTGCTACACCTGTATCCAGCCTTTGGAGGCTGAGACGGTGGATCAC 287
|||||
Db 124488 GGGTGGGCTGCTACACCTGTATCCAGCCTTTGGAGGCTGAGACGGTGGATCAC 124547

QY 288 CTGA 291
|||||
Db 124548 CTGA 124551

RESULT 35

LOCUS AL136973 62443 bp DNA linear PRI 06-OCT-2000
DEFINITION Human DNA sequence from clone RP3-41408 on chromosome 6 Contains
ESTs, STSs and GSSs, complete sequence.
ACCESSION AL136973
VERSION AL136973.7 GI:9650520
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Smalley,C.
TITLE Direct Submission
JOURNAL Submitted (22-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
COMMENT On Aug 1, 2000 this sequence version replaced gi:9588480.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr6>
RP3-41408 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP3-41408. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-41408 is at 62443 in this sequence. The true left end of clone RP1-125E8 is at 23727 in this sequence. The true right end of clone RP4-753D5 is at 100 in this sequence.

FEATURES

	source
repeat_region	1. .62443
repeat_region	/organism="Homo sapiens"
repeat_region	/db_xref="taxon:9606"
repeat_region	/chromosome="6"
repeat_region	/clone="RP3-41408"
repeat_region	/clone_lib="RPCI-3"
repeat_region	1. .1203
repeat_region	/note="TIGGER1 repeat: matches 1204. .2417 of consensus"
repeat_region	1208. .1613
repeat_region	/note="LIMC4 repeat: matches 7432. .7738 of consensus"
repeat_region	1614. .1916
repeat_region	/note="AluSx repeat: matches 5. .304 of consensus"
repeat_region	1917. .2186
repeat_region	/note="LIMC4 repeat: matches 7155. .7432 of consensus"
repeat_region	3084. .3145
repeat_region	/note="L2 repeat: matches 2683. .2744 of consensus"
repeat_region	3253. .3418
repeat_region	/note="MER20 repeat: matches 40. .216 of consensus"
repeat_region	3433. .3493
repeat_region	/note="MIR repeat: matches 35. .95 of consensus"
repeat_region	complement(3697. .4051)
repeat_region	/note="match: GSS: Em:AQ018541"
repeat_region	4461. .4557
repeat_region	/note="MER5A repeat: matches 11. .110 of consensus"
repeat_region	5153. .5364
repeat_region	/note="MER3 repeat: matches 1. .209 of consensus"
repeat_region	5814. .6100
repeat_region	/note="AluSx repeat: matches 1. .287 of consensus"
repeat_region	6101. .6403
repeat_region	/note="AluJc repeat: matches 3. .304 of consensus"
repeat_region	7510. .7741
repeat_region	/note="MIR repeat: matches 9. .231 of consensus"
repeat_region	7962. .8043
repeat_region	/note="41 copies 2 mer ta 79% conserved"
repeat_region	8047. .8284
repeat_region	/note="MIR repeat: matches 2. .250 of consensus"
repeat_region	8915. .8973
repeat_region	/note="L2 repeat: matches 2688. .2748 of consensus"
repeat_region	9781. .9928
repeat_region	/note="MER5A repeat: matches 38. .183 of consensus"
repeat_region	complement(11696. .11949)
repeat_region	/note="match: GSS: Em:AQ079494"
repeat_region	12517. .13266
repeat_region	/note="L2 repeat: matches 1947. .2742 of consensus"

repeat_region	13351. .13626
repeat_region	/note="LIMC1 repeat: matches 6055. .6332 of consensus"
repeat_region	13800. .13972
repeat_region	/note="MER41B repeat: matches 258. .427 of consensus"
repeat_region	13974. .14271
repeat_region	/note="AluSx repeat: matches 2. .300 of consensus"
repeat_region	14503. .15494
repeat_region	/note="LIMC1 repeat: matches 5032. .6055 of consensus"
repeat_region	15499. .16381
repeat_region	/note="L2 repeat: matches 874. .1794 of consensus"
repeat_region	18235. .18540
repeat_region	/note="AluSp repeat: matches 4. .310 of consensus"
repeat_region	18783. .19092
repeat_region	/note="AluSg repeat: matches 1. .306 of consensus"
repeat_region	21018. .21135
repeat_region	/note="FIAM.A repeat: matches 1. .125 of consensus"
repeat_region	21787. .22865
repeat_region	/note="L2 repeat: matches 1597. .2748 of consensus"
repeat_region	23139. .23328
repeat_region	/note="LIPB1 repeat: matches 5962. .6155 of consensus"
repeat_region	23397. .23497
repeat_region	/note="MIR repeat: matches 3. .111 of consensus"
repeat_region	23747. .24114
repeat_region	/note="match: STS: Em:HS125B8T"
repeat_region	24914. .25044
repeat_region	/note="MIR repeat: matches 20. .155 of consensus"
repeat_region	25634. .25712
repeat_region	/note="L2 repeat: matches 2631. .2710 of consensus"
repeat_region	25984. .26110
repeat_region	/note="L2 repeat: matches 2621. .2750 of consensus"
repeat_region	26431. .26558
repeat_region	/note="MIR repeat: matches 25. .154 of consensus"
repeat_region	27082. .27282
repeat_region	/note="MLT1J repeat: matches 70. .271 of consensus"
repeat_region	27401. .27436
repeat_region	/note="18 copies 2 mer tt 91% conserved"
repeat_region	27802. .28277
repeat_region	/note="MLT1D repeat: matches 1. .496 of consensus"
repeat_region	28298. .28454
repeat_region	/note="MIR repeat: matches 81. .262 of consensus"
repeat_region	31015. .31121
repeat_region	/note="L2 repeat: matches 2632. .2736 of consensus"
repeat_region	31149. .31188
repeat_region	/note="20 copies 2 mer ga 95% conserved"
repeat_region	31193. .31367
repeat_region	/note="L2 repeat: matches 2446. .2618 of consensus"
repeat_region	31603. .31894
repeat_region	/note="AluSx repeat: matches 1. .291 of consensus"
repeat_region	32574. .32666
repeat_region	/note="LIMC/D repeat: matches 5726. .5818 of consensus"
repeat_region	32967. .33022
repeat_region	/note="LIMC1 repeat: matches 4943. .4998 of consensus"
repeat_region	33049. .33502
repeat_region	/note="LIMC1 repeat: matches 4477. .4928 of consensus"
repeat_region	34386. .34463
repeat_region	/note="MER91C repeat: matches 56. .140 of consensus"
repeat_region	35481. .35764
repeat_region	/note="AluSg repeat: matches 1. .301 of consensus"
repeat_region	complement(36545. .37035)
repeat_region	/note="match: GSS: Em:AQ792041"
repeat_region	37154. .37502
repeat_region	/note="match: GSS: Em:AQ100693"
repeat_region	37699. .37902
repeat_region	/note="HAL1 repeat: matches 707. .926 of consensus"
repeat_region	38154. .38291
repeat_region	/note="LIMM4 repeat: matches 5294. .5429 of consensus"
repeat_region	38292. .38855
repeat_region	/note="LIMM4 repeat: matches 5493. .6068 of consensus"
repeat_region	38856. .39155
repeat_region	/note="AluSg repeat: matches 11. .303 of consensus"
repeat_region	39156. .39389
repeat_region	/note="LIMM4 repeat: matches 6068. .6298 of consensus"
repeat_region	39707. .39818

```

/Note="match: GSS: Em:AQ505447"
39828..39869
/Note="21 copies 2 mer ta 76% conserved"
40072..40357
/Note="AluJo repeat: matches 1..299 of consensus"
40513..40737
/Note="MER30 repeat: matches 1..230 of consensus"
42016..42225
/Note="MIR repeat: matches 46..252 of consensus"
43759..43835
/Note="MIR repeat: matches 58..140 of consensus"
44266..44828
/Note="match: GSS: Em:AQ801525"
45767..45904
/Note="MER5A repeat: matches 27..187 of consensus"
45972..46249
/Note="MER58B repeat: matches 1..305 of consensus"
46323..46519
/Note="MIR repeat: matches 49..251 of consensus"
47083..47145
/Note="MIR repeat: matches 41..101 of consensus"
47155..47376
/Note="L1PA8 repeat: matches 5925..6163 of consensus"
47773..48171
/Note="L1R16B repeat: matches 52..464 of consensus"
48504..48843
/Note="MER44A repeat: matches 8..333 of consensus"
49794..49906
/Note="MIR repeat: matches 134..261 of consensus"
49988..50103
/Note="58 copies 2 mer aa 60% conserved"
complement(50440..50936)
/Note="match: GSS: Em:AQ664348"
50614..50736

Query Match
Best Local Similarity 100.0%; Score 63; DB 9; Length 62443;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GTCTCTACTAAATACAAAATTAGCCAGGTGGTGGGCACACGCTGTAGTCCAGCT 394
Db 14161 GTCTCTACTAAATACAAAATTAGCCAGGTGGTGGGCACACGCTGTAGTCCAGCT 14102

QY 395 ACT 397
|||
Db 14101 ACT 14099

RESULT 36
HSY237C10_3
WPCOMMENT
Sequence split into 4 fragments LOCUS HSY237C10 Accession AL031601
Fragment Name Begin End
HSY237C10_0 1 110000
HSY237C10_1 100001 210000
HSY237C10_2 200001 310000
HSY237C10_3 300001 385713
Continuation (4 of 4) of HSY237C10 from base 300001 (AL031601 Human DNA sequence from ol
zinc finger protein, a pseudogene similar to C.e1.

Query Match
Best Local Similarity 100.0%; Score 63; DB 9; Length 85713;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GTCTCTACTAAATACAAAATTAGCCAGGTGGTGGGCACACGCTGTAGTCCAGCT 394
Db 52804 GTCTCTACTAAATACAAAATTAGCCAGGTGGTGGGCACACGCTGTAGTCCAGCT 52863

QY 395 ACT 397
|||
Db 52864 ACT 52866

```

```

RESULT 37
AL844148
LOCUS
DEFINITION
Homo sapiens chromosome 1 clone RP11-104116, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
ACCESSION
AL844148
VERSION
AL844148.2 GI:22416202
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 160010)
AUTHORS
McLay,K.
TITLE
Direct Submission
JOURNAL
Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonequest@sanger.ac.uk
COMMENT
On Aug 21, 2002 this sequence version replaced gi:21912328.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA104116
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 158580 bases at least Q40
Consensus quality: 158916 bases at least Q30
Consensus quality: 159122 bases at least Q20
Insert size: 159310; sum-of-contigs
Insert size: 173409; 4.8% error; agarose-fp
Quality coverage: 6.64x in Q20 bases; sum-of-contigs Quality
coverage: 6.22x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 3853: contig of 3853 bp in length
* 3854 3953: gap of 100 bp
* 3954 24930: contig of 20977 bp in length
* 24931 25030: gap of 100 bp
* 25031 32722: contig of 7692 bp in length
* 32723 32822: gap of 100 bp
* 32823 72051: contig of 39229 bp in length
* 72052 72151: gap of 100 bp
* 72152 81625: contig of 9474 bp in length
* 81626 81725: gap of 100 bp
* 81726 103210: contig of 21485 bp in length
* 103211 103310: gap of 100 bp
* 103311 127637: contig of 24327 bp in length
* 127638 127737: gap of 100 bp
* 127738 160010: contig of 32273 bp in length.
*
* Location/Qualifiers
* 1..160010
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="1"
* /clone="RP11-104116"
* /clone_lib="RPCI-11.1"
* 1..3853
* /note="assembly_fragment:01821
* fragment_chain:1"
* 3954..24930
* /note="assembly_fragment:01665
* fragment_chain:1"

```

```

misc_feature 25031..32722
              /note="assembly_fragment:00578
              fragment_chain:1"
misc_feature 32823..72051
              /note="assembly_fragment:00760
              fragment_chain:1"
misc_feature 72152..81625
              /note="assembly_fragment:00250
              fragment_chain:1"
misc_feature 81726..103210
              /note="assembly_fragment:01744
              fragment_chain:1"
misc_feature 103311..127637
              /note="assembly_fragment:01572
              fragment_chain:1"
misc_feature 127738..160010
              /note="assembly_fragment:00210
              fragment_chain:1"
              clone_end:T7
              vector_side:right"
BASE COUNT 48388 a 32237 c 32257 g 46428 t 700 others
ORIGIN

```

```

Query Match      6.3%; Score 63; DB 2; Length 160010;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 335 GTCTCTACTATAAATACAAAATAGCCAGGTGGTGGCACACGCCGTAGTCCAGCT 394
      |||
Db 97633 GTCTCTACTATAAATACAAAATAGCCAGGTGGTGGCACACGCCGTAGTCCAGCT 97692

```

```

QY 395 ACT 397
|||
Db 97693 ACT 97695

```

```

RESULT 38
AL391479
LOCUS      AL391479          168071 bp    DNA    linear    HTG 24-JAN-2001
DEFINITION Homo sapiens chromosome 10 clone RP13-268C11, *** SEQUENCING IN
            PROGRESS ***, 8 unordered pieces.
ACCESSION  AL391479
VERSION     AL391479.3 GI:10120141
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Sims.S.
            Direct Submission
            Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
            On Sep 13, 2000 this sequence version replaced gi:9864729.
            ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: BB268C11
            ----- Summary Statistics
            Sequencing program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 164822 bases at least Q40
            Consensus quality: 166195 bases at least Q30
            Consensus quality: 166903 bases at least Q20
            Insert size: 167371; sum-of-contigs
            Insert size: 168395; 7.1% error; agarose-fp
            Quality coverage: 4.97x in Q20 bases; sum-of-contigs Quality
            coverage: 5.02x in Q20 bases; agarose-fp

```

```

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

```

```

1 6683: contig of 6683 bp in length
6684 6783: gap of 100 bp
6784 89821: contig of 83038 bp in length
89822 89921: gap of 100 bp
89922 92032: contig of 2111 bp in length
92033 92132: gap of 100 bp
92133 99119: contig of 6987 bp in length
99120 99219: gap of 100 bp
99220 105974: contig of 6755 bp in length
105975 106074: gap of 100 bp
106075 144349: contig of 38275 bp in length
144350 144449: gap of 100 bp
144450 150629: contig of 6180 bp in length
150630 150729: gap of 100 bp
150730 168071: contig of 17342 bp in length.

```

FEATURES

```

Location/Qualifiers
1..168071
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP13-268C11"
/clone_lib="RPC1-13.2"
1..6683
/note="assembly_fragment:00272
fragment_chain:1
clone_end:SP6
vector_side:left"
6784..89821
/note="assembly_fragment:01884
fragment_chain:1"
89922..92032
/note="assembly_fragment:01743
fragment_chain:1"
92133..99119
/note="assembly_fragment:00870
fragment_chain:1"
99220..105974
/note="assembly_fragment:02095
fragment_chain:1"
106075..144349
/note="assembly_fragment:00224
fragment_chain:2"
144450..150629
/note="assembly_fragment:01619
fragment_chain:2"
150730..168071
/note="assembly_fragment:01282
fragment_chain:2"
BASE COUNT 50488 a 34118 c 34260 g 48505 t 700 others
ORIGIN

```

```

Query Match      6.3%; Score 63; DB 2; Length 168071;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 335 GTCTCTACTATAAATACAAAATAGCCAGGTGGTGGCACACGCCGTAGTCCAGCT 394
      |||
Db 43567 GTCTCTACTATAAATACAAAATAGCCAGGTGGTGGCACACGCCGTAGTCCAGCT 43626

```

```

QY 395 ACT 397
|||
Db 43627 ACT 43629

```


RESULT 39

AC021761/c
 LOCUS
 DEFINITION Homo sapiens chromosome 11, clone RP11-361M6, linear PRI 22-MAR-2002
 AC021761
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE

1 (bases 1 to 182789)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Unpublished

TITLE

Homo sapiens chromosome 11, clone RP11-361M6

REFERENCE

2 (bases 1 to 182789)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Direct Submission

TITLE

Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 182789)

REFERENCE

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dudge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lakoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phukhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission

TITLE

Submitted (21-MAR-2002) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 182789)

REFERENCE

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dudge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Lakoque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,

Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phukhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission

TITLE

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome

JOURNAL

Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 21, 2002 this sequence version replaced gi:15390958.
 All repeats were identified using RepeatMasker:

COMMENT

Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RN/RepeatMasker.html

FEATURES

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L2173

Center clone name: 361_M_6

source

1. .182789

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="11"

/map="11"

/clone="RP11-361M6"

/clone.lib="Rpci-11 Human Male BAC"

complement(23..432)

/rpt_family="L1Mcb"

complement(436..751)

/rpt_family="L1Mcb"

complement(777..1261)

/rpt_family="L1M4"

complement(1291..2396)

/rpt_family="L1M4"

complement(2397..2773)

/rpt_family="MSTA"

complement(2774..4396)

/rpt_family="MSTA-int"

complement(4399..4780)

/rpt_family="MSTA"

complement(4797..4930)

/rpt_family="L1M4"

4931..4953

/rpt_family="(CAAA)n"

complement(4954..5413)

/rpt_family="L1M4"

complement(5610..6614)

/rpt_family="L1Mcb"

complement(6628..7091)

/rpt_family="L1Mca"

complement(7092..7826)

/rpt_family="LTR8"

complement(7827..8358)

/rpt_family="L1Mca"

8428..8583

/rpt_family="L1M1"

complement(8584..8890)

/rpt_family="AluSq"

8891..9083

/rpt_family="L1M1"

9179..9293

/rpt_family="L1M1"

10399..10454

```

repeat_region /rpt_family="AT-rich"
complement(10680..10828)
repeat_region /rpt_family="MIR"
11360..11388
repeat_region /rpt_family="AT-rich"
complement(11390..12899)
repeat_region /rpt_family="LIP3A"
13179..13541
/rpt_family="LIME1"
13553..13654
/rpt_family="L1MA10"
13799..14122
/rpt_family="MLT1A1"
14955..14976
/rpt_family="AT-rich"
15127..15266
/rpt_family="MIR"
15402..15578
/rpt_family="L2"
16410..16722
/rpt_family="MER58B"
17098..17292
/rpt_family="MLT1A1"
complement(18723..18931)
/rpt_family="MLT1A2"
complement(19010..19352)
/rpt_family="THE1B"
complement(19354..19392)
/rpt_family="THE1B-int"
complement(19376..20611)
/rpt_family="THE1B-int"
complement(20612..20966)
/rpt_family="THE1B"
complement(20967..21061)
/rpt_family="MLT1A2"
21122..21316
/rpt_family="MER58A"
complement(21376..21572)
/rpt_family="MER5A"
complement(21883..22035)
/rpt_family="MIR"
22330..22428
/rpt_family="L3"
complement(22475..22680)
/rpt_family="MIR"
23473..23513
/rpt_family="(TG)n"
complement(24066..24302)
/rpt_family="MIR"
complement(24586..24747)
/rpt_family="Charlier8"
25296..25316
/rpt_family="(TA)n"
27357..27378
/rpt_family="AT-rich"
27813..27944

Query Match 6.3%; Score 63; DB 9; Length 182789;
Best Local Similarity 100.0%; Pred. No. 2.3e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 TAAATACAAAATAGCCAGGTGTGGCAGCAGCTGTAGTCCAGCTACTTGGGA 402
|||||
Db 65095 TAAATACAAAATAGCCAGGTGTGGCAGCAGCTGTAGTCCAGCTACTTGGGA 65036
|||||

QY 403 GGC 405
|||
Db 65035 GGC 65033

RESULT 40
AL354975/c
LOCUS AL354975 212730 bp DNA linear HTG 11-SEP-2001

```

```

DEFINITION Homo sapiens chromosome 10 clone RP11-300L24, *** SEQUENCING IN
PROGRESS ***, 8 unordered pieces.
ACCESSION AL354975
VERSION AL354975.15 GI:15590902
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212730)
AUTHORS Phillimore,B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT requests: clonerequest@sanger.ac.uk
On Sep 12, 2001 this sequence version replaced gi:14586088.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA300L24
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 211054 bases at least Q40
Consensus quality: 211410 bases at least Q30
Consensus quality: 211660 bases at least Q20
Insert size: 212030; sum-of-contigs
Insert size: 197391; 9.1% error; agarose-fp
Quality coverage: 8.73x in Q20 bases; sum-of-contigs Quality
coverage: 9.68x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 9151: contig of 9151 bp in length
* 9152 9251: gap of 100 bp
* 9252 41384: contig of 32133 bp in length
* 41385 41484: gap of 100 bp
* 41485 54463: contig of 12979 bp in length
* 54464 54563: gap of 100 bp
* 54564 56880: contig of 2317 bp in length
* 56881 56980: gap of 100 bp
* 56981 77886: contig of 20906 bp in length
* 77887 122287: contig of 44301 bp in length
* 122288 122387: gap of 100 bp
* 122388 128570: contig of 6183 bp in length
* 128571 128670: gap of 100 bp
* 128671 212730: contig of 84060 bp in length.
FEATURES
Location/Qualifiers
1..212730
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-300L24"
/clone_lib="RPCT-11.2"
1..9151
/note="assembly_fragment:03340"
fragment_chain:1
clone_end:T7
vector_side:left"
9252..41384
/note="assembly_fragment:02020"
fragment_chain:1"
misc_feature 1..9151
/note="assembly_fragment:03340"
fragment_chain:1"
misc_feature 9252..41384
/note="assembly_fragment:02020"
fragment_chain:1"

```



```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP13-251015"
/clone_lib="RPC1-13.2"
1. 5872
/note="assembly_fragment:00817
fragment_chain:1"
5973. 11302
/note="assembly_fragment:02075
fragment_chain:1"
11403. 15003
/note="assembly_fragment:02256
fragment_chain:1"
15104. 15081
/note="assembly_fragment:00201
fragment_chain:1"
19182. 28512
/note="assembly_fragment:01282
fragment_chain:1"
28613. 36009
/note="assembly_fragment:00649
fragment_chain:2"
36110. 43831
/note="assembly_fragment:00481
fragment_chain:2"
43932. 101489
/note="assembly_fragment:01511
fragment_chain:2"
101590. 137416
/note="assembly_fragment:01201
fragment_chain:2"
137517. 150711
/note="assembly_fragment:00117
fragment_chain:3"
150812. 159076
/note="assembly_fragment:00118
fragment_chain:3"
159177. 166731
/note="assembly_fragment:01939
fragment_chain:3"
166832. 170446
/note="assembly_fragment:02774
fragment_chain:4"
170547. 183663
/note="assembly_fragment:00485
fragment_chain:4"
183764. 186875
/note="assembly_fragment:00790
fragment_chain:4"
186976. 189138
/note="assembly_fragment:01385
fragment_chain:5"
189239. 191366
/note="assembly_fragment:01448
fragment_chain:5"
191467. 193973
/note="assembly_fragment:01471
fragment_chain:6"
194074. 196413
/note="assembly_fragment:02190
fragment_chain:6"
196514. 199969
/note="assembly_fragment:00042"
200070. 203326
/note="assembly_fragment:00679"
203427. 206251
/note="assembly_fragment:01099"
206352. 208716
/note="assembly_fragment:01233"
208817. 211743
/note="assembly_fragment:01246"
211844. 214458
```

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misc_feature /note="assembly_fragment:01479"
214559. 216763
misc_feature /note="assembly_fragment:01572"
216864. 220060
misc_feature /note="assembly_fragment:01668"
220161. 223061
misc_feature /note="assembly_fragment:01866"
223162. 225305
misc_feature /note="assembly_fragment:02021"
225406. 227527
misc_feature /note="assembly_fragment:02054"
227628. 229963
misc_feature /note="assembly_fragment:02419"
230064. 232162
misc_feature /note="assembly_fragment:02818"
230064. 232162
BASE COUNT 69322 a 46531 c 42921 g 70283 t 3105 others
ORIGIN
Query Match 6.3%; Score 63; DB 2; Length 232162;
Best Local Similarity 100.0%; Pred. No. 2.4e-25;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 GTCTTACTTAAATAACAAAATTAGCCAGGTGGTGGCAGCCCTGTAGTCCAGCT 394
|||||
Db 114332 GTCTTACTTAAATAACAAAATTAGCCAGGTGGTGGCAGCCCTGTAGTCCAGCT 114391
|||||
QY 395 ACT 397
||||
Db 114392 ACT 114394

RESULT 42
AP000098/8
LOCUS Homo sapiens genomic DNA, 68122 bp DNA linear PRI 24-FEB-2000
DEFINITION LL56-APP region, complete sequence.
ACCESSION AP000098
VERSION AP000098.2 GI:7077210
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 68,122 genomic DNA of 21q21.1-q21.2
Published Only in Database (1999)
2 (bases 1 to 68122)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (24-DEC-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
COMMENT On Feb 24, 2000 this sequence version replaced gi:6997413.
FEATURES
Location/Qualifiers
source
1. 68122
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q21.1-q21.2"
/clone="B304D2"
BASE COUNT 20417 a 12290 c 13407 g 22008 t
ORIGIN
Query Match 6.2%; Score 62; DB 9; Length 68122;
Best Local Similarity 100.0%; Pred. No. 8.6e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 395
|||||
Db 21283 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 21224
|||||
QY 396 CT 397
||
Db 21223 CT 21222

RESULT 43
AC025810 71530 bp DNA linear PRI 04-JAN-2002
LOCUS Homo sapiens chromosome 16 clone CTD-2034121, complete sequence.
DEFINITION AC025810
ACCESSION AC025810
VERSION AC025810.4 GI:18057077
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 71530)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Unpublished
REFERENCE 2 (bases 1 to 71530)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (13-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 71530)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (04-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jan 4, 2002 this sequence version replaced gi:14589449.
COMMENT Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
-----
Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than
1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
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FEATURES
source Location/Qualifiers
1..71530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
/clone="CTD-2034121"
BASE COUNT 21125 a 16392 c 15391 g 18622 t
ORIGIN
Query Match 6.2%; Score 62; DB 9; Length 71530;
Best Local Similarity 100.0%; Pred. No. 8.6e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 395
|||||
Db 65905 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 65964
|||||
QY 396 CT 397

RESULT 45
AC079855 143146 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone RP11-332116 from 7, complete sequence.
DEFINITION AC079855
ACCESSION AC079855
VERSION AC079855.8 GI:14717359
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 143146)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

```

```

Db 65965 CT 65966
||
RESULT 44
AC016593 124211 bp DNA linear PRI 07-NOV-2000
LOCUS Homo sapiens chromosome 5 clone CTD-2005H4, complete sequence.
DEFINITION AC016593
ACCESSION AC016593
VERSION AC016593.5 GI:111119456
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 124211)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Unpublished
REFERENCE 2 (bases 1 to 124211)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (04-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 124211)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (07-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 7, 2000 this sequence version replaced gi:7710203.
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.igi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.sngc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.6.
FEATURES
source Location/Qualifiers
1..124211
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2005H4"
BASE COUNT 37357 a 22562 c 23975 g 40317 t
ORIGIN
Query Match 6.2%; Score 62; DB 9; Length 124211;
Best Local Similarity 100.0%; Pred. No. 8.9e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 395
|||||
Db 43273 TCTCTACTAAATAACAAAAATTAGCCAGGTGTGGTGGCACACGCGCTGTAGTCCAGCTA 43214
|||||
QY 396 CT 397
||
Db 43213 CT 43212

RESULT 45
AC079855 143146 bp DNA linear PRI 01-MAR-2002
LOCUS Homo sapiens BAC clone RP11-332116 from 7, complete sequence.
DEFINITION AC079855
ACCESSION AC079855
VERSION AC079855.8 GI:14717359
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 143146)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

```

99063792
 9847074
 2 (bases 1 to 143146)
 Mclella.M. and Kozlowski.A.
 The sequence of Homo sapiens BAC clone RP11-332L16
 Unpublished (2001)
 3 (bases 1 to 143146)
 Waterston,R.H.
 Direct Submission
 Submitted (14-SEP-2000) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 143146)
 Waterston,R.H.
 Direct Submission
 Submitted (13-JUL-2001) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 143146)
 Waterston,R.
 Direct Submission
 Submitted (01-MAR-2002) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Jul 13, 2001 this sequence version replaced gi:13794255.
 ----- Genome Center
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@watson.wustl.edu
 ----- Summary Statistics

 Center project name: H_NH0332L16

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GRB/CHR7_send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frenken,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pletter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-379F11; the clone sequenced to the right is RP5-1132H15, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-332L16; actual end is at base position 31561 of RP5-1132H15.

Data from AC024641 and AC026281 was used to finish this clone,

AC079855. Polymorphisms exist between RP11-332L16 and RP5-1132H15. The sequence between 46100-46104 is a single chemistry region.
 Location/Qualifiers
 1. 143146
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"
 /map="7"
 /clone="RP11-332L16"
 /clone_lib="RPC1-11"
 81. 434
 /rpt_family="L1"
 315. 336
 /rpt_family="AT_rich"
 437. 494
 /rpt_family="MER1_type"
 496. 793
 /rpt_family="L2"
 838. 1377
 /rpt_family="L1"
 1428. 1661
 /rpt_family="L1"
 2283. 2481
 /rpt_family="L2"
 2939. 2959
 /rpt_family="(A)n"
 3711. 3976
 /rpt_family="Alu"
 3815. 3840
 /rpt_family="AT_rich"
 4114. 4422
 /rpt_family="Alu"
 4441. 4601
 /rpt_family="L1"
 4720. 5015
 /rpt_family="L1"
 5001. 5040
 /rpt_family="AT_rich"
 5466. 5631
 /rpt_family="L1"
 6107. 6396
 /rpt_family="Alu"
 6413. 6710
 /rpt_family="Alu"
 12767. 12817
 /rpt_family="(TAAAA)n"
 12922. 13125
 /note="match to EST AL562533 (NID:gl2911047)"
 12925. 13125
 /note="match to EST AA128112 (NID:gl687996) z123g08.rl"
 12925. 13125
 /note="match to EST AA445921 (NID:g2158586) 2w57f04.rl"
 12925. 13125
 /note="match to EST AL550344 (NID:gl2887227)"
 12925. 13125
 /note="similar to Mus musculus EST W64675 (NID:gl372592) me08d02.rl"
 12925. 13097
 /note="match to EST AL523147 (NID:gl2786640)"
 12984. 13125
 /note="match to EST BG121389 (NID:gl2614898)"
 13137. 13170
 /rpt_family="AT_rich"
 13530. 13630
 /rpt_family="L1"
 14292. 14295
 /note="match to EST AA128112 (NID:gl687996) z123g08.rl"
 14325. 14422
 /rpt_family="Achobo"
 14428. 14519
 /rpt_family="MER2_type"
 14819. 15084
 /rpt_family="Alu"

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repeat_region 15063..15084
/rpt_family="(A)n"
repeat_region 15675..15801
/rpt_family="L2"
repeat_region 15912..16242
/rpt_family="MERL_type"
repeat_region 16353..16648
/rpt_family="Alu"
repeat_region 16827..16887
/rpt_family="L2"
repeat_region 17149..17356
/rpt_family="MERL_type"
repeat_region 17956..18100
/rpt_family="L1"
repeat_region 18114..18688
/rpt_family="L1"
repeat_region 18927..19255
/rpt_family="L1"
misc_feature 19300..19539
/note="similar to Homo sapiens EST B6718062
(NID:g13997249)"
misc_feature 19573..19847
/note="similar to Homo sapiens EST BF512467
(NID:g11597569)"
misc_feature 19687..19814
/note="similar to Homo sapiens EST B6718062
(NID:g13997249)"
repeat_region 20071..20704
/rpt_family="L1"
repeat_region 20826..21132
/rpt_family="Alu"
repeat_region 21191..21506
/rpt_family="L2"
repeat_region 21507..21535
/rpt_family="(T)n"
repeat_region 21771..21929
/rpt_family="L2"
repeat_region 23083..23251
/rpt_family="Alu"
repeat_region 23245..23290
/rpt_family="AT-rich"

```

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Query Match 6.2%; Score 62; DB 9; Length 143146;
Best Local Similarity 100.0%; Pred. No. 9e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTGTAATCCAGCACTTTGGAGGCTGAGACGGGTGGATCACCTGAGTCAGGAGTTCA 304
Db 136003 CCTGTAATCCAGCACTTTGGAGGCTGAGACGGGTGGATCACCTGAGTCAGGAGTTCA 135944

Qy 305 AG 306
||
Db 135943 AG 135942

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Search completed: November 24, 2002, 12:31:27
Job time : 7279 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 13:27:24 ; Search time 1549.5 seconds
(without alignments)
261.302 Million cell updates/sec

Title: US-09-784-423-124
Perfect score: 25
Sequence: 1 GCTTGCAGTACCGGAGATAAGACT 25

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 16154066 seqs, 8097743376 residues
Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- EST:*
- 1: em_estba.*
 - 2: em_esthu.*
 - 3: em_estin.*
 - 4: em_estnu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_hic.*
 - 9: gb_esti.*
 - 10: gb_est2.*
 - 11: gb_hic.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: gb_gss.*
 - 18: em_gss_hum.*
 - 19: em_gss_inv.*
 - 20: em_gss_pln.*
 - 21: em_gss_vrt.*
 - 22: em_gss_fun.*
 - 23: em_gss_man.*
 - 24: em_gss_mus.*
 - 25: em_gss_oth.*
 - 26: em_gss_pro.*
 - 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	25	100.0	337	17	AQ356083
C 2	21	84.0	166	12	BF757007
C 3	21	84.0	166	17	B85546
C 4	21	84.0	220	9	AA297398
C 5	21	84.0	281	9	AU043112
C 6	21	84.0	325	9	AA593502

C 7	21	84.0	389	14	T92723
C 8	21	84.0	397	12	BF754298
C 9	21	84.0	452	17	AQ384259
C 10	21	84.0	461	17	AQ702820
C 11	21	84.0	476	10	AW751650
C 12	21	84.0	481	10	AW265138
C 13	21	84.0	503	10	BE646402
C 14	21	84.0	509	17	AQ721912
C 15	21	84.0	514	17	B37536
C 16	21	84.0	529	17	AQ819983
C 17	21	84.0	539	17	AQ608587
C 18	21	84.0	542	13	BI494061
C 19	21	84.0	570	17	AQ708886
C 20	21	84.0	573	13	BI494060
C 21	21	84.0	575	17	AQ520887
C 22	21	84.0	649	17	AQ482581
C 23	21	84.0	666	17	AQ059093
C 24	21	84.0	668	17	AQ039496
C 25	21	84.0	882	12	BG214939
C 26	21	84.0	914	12	BF032499
C 27	20	80.0	132	12	BF837405
C 28	20	80.0	139	12	BF878448
C 29	20	80.0	144	9	AA709114
C 30	20	80.0	154	9	AI626093
C 31	20	80.0	173	9	AA046824
C 32	20	80.0	175	17	B73330
C 33	20	80.0	184	9	AA348526
C 34	20	80.0	185	14	BQ251032
C 35	20	80.0	189	14	H02828
C 36	20	80.0	191	14	R44194
C 37	20	80.0	194	9	AI241886
C 38	20	80.0	201	14	H03719
C 39	20	80.0	211	14	N73648
C 40	20	80.0	212	10	AW772536
C 41	20	80.0	231	9	AA228262
C 42	20	80.0	233	10	B261473
C 43	20	80.0	234	12	BF962750
C 44	20	80.0	237	9	AA380519
C 45	20	80.0	239	17	B87492

ALIGNMENTS

RESULT 1
AQ356083/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ356083
CITBI-EI-2534J20.TF CITBI-EI Homo sapiens genomic clone 2534J20,
DNA sequence.
AQ356083
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 337)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: CITBI-EI-2534J20.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13-21
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1..337
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2534J20"
/clone_lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 78 a 70 c 75 g 114 t

Query Match

Best Local Similarity 100.0%; Score 25; DB 17; Length 337;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAGAGT 25
|||||
Db 249 GGTTCAGTGCAGCCGAGATAGAGT 225

RESULT 2

BF757007/c

LOCUS

DEFINITION MR0-CT0451-021100-017-907 CT0451 Homo sapiens CDNA, mRNA sequence. EST 12-JAN-2001

ACCESSION BF757007

VERSION BF757007.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

DIAS Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-CT0451-021100-017-907&t3=2000-11-02&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 91.

Location/Qualifiers

1..166

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="CT0451"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source

BASE COUNT 39 a 32 c 35 g 60 t

Query Match

Best Local Similarity 84.0%; Score 21; DB 12; Length 166;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
|||||

Db 145 GGTTCAGTGCAGCCGAGATAA 125

RESULT 3

B85546/c

LOCUS

DEFINITION B85546

ACCESSION B85546

VERSION B85546.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

ADAMS,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.

Use of BAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1..166

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="RPCI-11-19J11"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT 29 a 44 c 45 g 48 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 21; DB 17; Length 166;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
|||||

Db 165 GGTTCAGTGCAGCCGAGATAA 145

RESULT 4

AA297398/c

LOCUS

DEFINITION

AA297398

EST112932 Epithelioid sarcoma Homo sapiens

EST containing Alu repeat, mRNA sequence.

220 bp mRNA linear EST 18-APR-1997

source

1. .325
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1085085"
 /clone_lib="NCI CGAP Gas1"
 /tissue_type="gastric tumor"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: stomach; Vector: Bluescript SK-; Site:1:
 scori; Site:2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. Pooled gastric tumors. 5' adaptor sequence: 5'
 GAATTCGCGCAGG 3' 3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTT 3' average insert size: 1.0 kb."
 BASE COUNT 55 a 97 c 77 g 96 t
 ORIGIN

Query Match 84.0%; Score 21; DB 9; Length 325;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 32 GGTTCAGTGCAGCGAGATAA 12

RESULT 7

T92723/c
 LOCUS T92723 389 bp mRNA linear EST 22-MAR-1995
 DEFINITION Y223c04.s1 Stragatene lung (#937210) Homo sapiens cDNA clone
 IMAGE:118566 3' similar to contains Alu repetitive element; mRNA
 sequence.
 T92723
 ACCESSION T92723
 VERSION T92723.1 GI:724636
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 389)

CHISSOE, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome res. 6 (9), 807-828 (1996)
 97044478

TITLE
 JOURNAL Contact: Wilson RK
 MEDLINE Washington University School of Medicine
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

Insert Size: 601
 High quality sequence stops: 359 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 601 Std Error: 0.00
 Seq primer: -21ml3

FEATURES

High quality sequence stop: 359.
 Location/Qualifiers
 1. .389
 /organism="Homo sapiens"
 /db_xref="GDB:486855"
 /db_xref="taxon:9606"
 /clone="IMAGE:118566"
 /clone_lib="Stragatene lung (#937210)"
 /sex="male"
 /dev_stage="72 years"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site:1: EcoRI
 ; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR

Vector; -5' adaptor sequence: 5' GAATTCGCGCAGG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3"
 BASE COUNT 75 a 113 c 92 g 99 t 10 others
 ORIGIN

Query Match 84.0%; Score 21; DB 14; Length 389;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 57 GGTTCAGTGCAGCGAGATAA 37

RESULT 8

BF754298/c
 LOCUS BF754298 397 bp mRNA linear EST 10-JAN-2001
 DEFINITION IL5-CT0519-091000-172-d02 CT0519 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF754298
 VERSION BF754298.1 GI:12081078
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 397)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663

CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&tl2=IL5-CT0519-
 091000-172-d02&tl3=2000-10-09&tl4=1)

Seq primer: puc 18 forward
 High quality sequence stop: 396.
 Location/Qualifiers
 1. .397

FEATURES

Source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CT0519"
 /dev_stage="Adult"
 /note="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No. 196
 ,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."
 BASE COUNT 76 a 92 c 76 g 153 t
 ORIGIN

Query Match 84.0%; Score 21; DB 12; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCGAGATAA 21
 |||||
 Db 33 GGTTCAGTGCAGCGAGATAA 13

```

RESULT 9
AQ384259
LOCUS
DEFINITION
  RPC111-139H18.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-139H18,
  DNA sequence.
ACCESSION
  AQ384259
VERSION
  AQ384259.1 GI:4355282
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 452)
  Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
  ,J.C.
  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
  Map Building
  Unpublished (1997)
  Other_GSSs: RPC111-139H18.TV
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbe@tigr.org
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
  http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
  Seq primer: SP6
  Class: BAC ends.
  Features:
  Location/Qualifiers
    1..452
    /organism="Homo sapiens"
    /db_xref="GDB:755317"
    /db_xref="taxon:9606"
    /clone="RPCI-11-139H18"
    /clone_lib="RPCI-11"
    /sex="Male"
    /cell_type="Lymphocytes"
    /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
    RPC111 Human Male BAC Library"
  BASE COUNT      133 a   98 c  104 g  114 t      3 others
  ORIGIN
    133 a   98 c  104 g  114 t      3 others

Query Match      84.0%; Score 21; DB 17; Length 452;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTCGAGCCGAGATAA 21
|||||
Db 322 GGTTCGAGTCGAGCCGAGATAA 342

RESULT 10
AQ702820/c
LOCUS
DEFINITION
  HS.5449.B1.H07.W7A RPCI-11 Human Male BAC Library Homo sapiens
  genomic clone Plate-1025 Col-13 Row-P, DNA sequence.
ACCESSION
  AQ702820
VERSION
  AQ702820.1 GI:5412246
KEYWORDS
  GSS.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 461)
  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
  Kellner,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
  Hood,L.
  Sequence-tagged connectors: A sequence approach to mapping and
  scanning the human genome
  Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  99380589
  Contact: Mahairas GG, Wallace JC, Hood L
  High Throughput Sequencing Center
  University of Washington
  401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Tel: (206) 616-3618
  Fax: (206) 616-3887
  Email: jwallace@u.washington.edu
  Clones are derived from the human BAC library RPCI-11. For BAC
  library availability, please contact Pieter de Jong
  (pieter@dejong.med.buffalo.edu). Clones may be purchased from
  BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
  Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
  http://www.htsc.washington.edu
  Plate: 1025 row: P column: 13
  Seq primer: T7
  Class: BAC ends
  High quality sequence stop: 461.
  Location/Qualifiers
    1..461
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="Plate-1025 Col-13 Row-P"
    /clone_lib="RPCI-11 Human Male BAC Library"
    /sex="male"
    /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
    Male blood DNA was isolated from one randomly chosen donor
    and partially digested with a combination of EcoRI and
    EcoRI Methylase. Size selected DNA was cloned into the
    pBAC3.6 vector at EcoRI sites"
  BASE COUNT      103 a  107 c  104 g  144 t      3 others
  ORIGIN
    103 a  107 c  104 g  144 t      3 others

Query Match      84.0%; Score 21; DB 17; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTCGAGCCGAGATAA 21
|||||
Db 275 GGTTCGAGTCGAGCCGAGATAA 255

RESULT 11
AW751650
LOCUS
DEFINITION
  IL0-CT0079-030899-106-e11 CT0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION
  AW751650
VERSION
  AW751650.1 GI:7666582
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 476)
  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
  Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
  Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
  Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
  ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
  Simpson,A.J.
  Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  20202663
  Contact: Simpson A.J.G
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

```

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TITLE
JOURNAL
MEDLINE
COMMENT
Kellner,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (http://bacpac.med.buffalo.edu/ordering) or from
http://www.htsc.washington.edu
Plate: 1025 row: P column: 13
Seq primer: T7
Class: BAC ends
High quality sequence stop: 461.
Location/Qualifiers
  1..461
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="Plate-1025 Col-13 Row-P"
  /clone_lib="RPCI-11 Human Male BAC Library"
  /sex="male"
  /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
  Male blood DNA was isolated from one randomly chosen donor
  and partially digested with a combination of EcoRI and
  EcoRI Methylase. Size selected DNA was cloned into the
  pBAC3.6 vector at EcoRI sites"
  BASE COUNT      103 a  107 c  104 g  144 t      3 others
  ORIGIN
    103 a  107 c  104 g  144 t      3 others

Query Match      84.0%; Score 21; DB 17; Length 461;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTCGAGCCGAGATAA 21
|||||
Db 275 GGTTCGAGTCGAGCCGAGATAA 255

RESULT 11
AW751650
LOCUS
DEFINITION
  IL0-CT0079-030899-106-e11 CT0079 Homo sapiens cDNA, mRNA sequence.
ACCESSION
  AW751650
VERSION
  AW751650.1 GI:7666582
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 476)
  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
  Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
  Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
  Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
  ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
  Simpson,A.J.
  Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  20202663
  Contact: Simpson A.J.G
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

```

Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=TL0&t2=IL0-CT0079-030899-106-ell&t3=1999-08-03&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 96

High quality sequence stop: 126.

FEATURES

SOURCE

1..476
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0079"
/dev_stage="Adult"

/note="Organ: colon; Vector: pUC18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 180 a 85 c 105 g 106 t

ORIGIN

Query Match 84.0%; Score 21; DB 10; Length 476;

Best Local Similarity 100.0%; Pred. No. 0.049;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21

|||||

Db 381 GGTCAGTGAGCCGAGATAA 401

RESULT 12

AW265138/c

LOCUS

DEFINITION xp80c10.x1 NCI_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2746674 3'

similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AW265138

VERSION AW265138.1 GI:6641954

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 481)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,

Michael R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Possible reversed clone: polyt not found

Seq primer: -400P from Gibco

High quality sequence stop: 437.

FEATURES

SOURCE

1..481

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2746674"

/clone_lib="NCI_CGAP_Ov40"

/sex="female"
/tissue_type="endometrioid ovarian metastasis"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dt priming. Non-directionally cloned into the UDG sites of PAMP10. Size-selected on agarose gel, average insert size 500 bp. Primary library; non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 95 a 138 c 104 g 144 t

ORIGIN

Query Match

Best Local Similarity 84.0%; Score 21; DB 10; Length 481;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21

|||||

Db 141 GGTTCAGTGAGCCGAGATAA 121

RESULT 13

BE646402/c

LOCUS

DEFINITION BE646402 503 bp mRNA linear EST 05-SP-2000

similar to contains Alu repetitive element; contains element PTR5 repetitive element ; mRNA sequence.

ACCESSION BE646402

VERSION BE646402.1 GI:9970713

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 503)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -400P from Gibco

High quality sequence stop: 449.

Location/Qualifiers

FEATURES

SOURCE

1..503

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3292036"

/clone_lib="NCI_CGAP_CLL1"

/tissue_type="B-cell, chronic lymphocytic leukemia"

/lab_host="DH10B"

/note="Vector: p773D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5'

TGTACCAATCTGAAGTGGAGCGCCGATTGCTTTTTTTTTTTTTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified p773 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 107 a 149 c 121 g 126 t

ORIGIN

Query Match

84.0%; Score 21; DB 10; Length 503;

Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0;

QY 1 GGTTCGAGTGGCCGAGATAA 21

Db 75 GGTTCGAGTGGCCGAGATAA 55

RESULT 14
AQ721912/C
LOCUS
DEFINITION
509 bp DNA linear GSS 14-JUL-1999
HS-5561.B2.C06.W7A.RPCI-11 Human Male BAC library Homo sapiens
genomic clone Plate-1137 Col-12 Row-F, DNA sequence.

ACCESSION
AQ721912

VERSION
AQ721912.1 GI:5481581

KEYWORDS
GSS.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 509)

Mahairas, G.S., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

Contact: Mahairas GG, Wallace JC, Hood L

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Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)

or from Resear h Genetics (info@resgen.com). BAC end web Server:

http://www.htsc.washington.edu

Plate: 1137 row: F column: 12

Seq primer: T7

Class: BAC ends

High quality sequence stop: 509.

Location/Qualifiers

1. 509

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

BASE COUNT 104 a 123 c 92 g 183 t 7 others

ORIGIN

Query Match 84.0%; Score 21; DB 17; Length 509;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTGGCCGAGATAA 21

Db 123 GGTTCGAGTGGCCGAGATAA 103

RESULT 15

B37536/c

LOCUS

DEFINITION

sapiens genomic clone Plate-CT 826 Col-21 Row-M, DNA sequence.
B37536
B37536.1 GI:2536905

KEYWORDS
GSS.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 514)

Mahairas, G.S., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,

Tralcoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.

Construction of a Characterized Clone Resource for Genomic

Sequencing: Generation and Preliminary Analysis of 20,000 Sequence

Tagged Connectors

Unpublished (1997)

Contact: Mahairas GG, Zackrone KD, Hood L

University of Washington

Seattle, WA 98195, USA

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Fax: (206) 685-7301

Email: kzackrone@u.washington.edu

Sequence Tagged Connector

Plate: CT 826 row: M column: 21

Class: BAC ends

High quality sequence stop: 514.

Location/Qualifiers

1. 514

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Plate-CT 826 Col-21 Row-M"

/clone_lib="CIT Human Genomic Sperm Library C"

/sex="M"

/note="Organ: sperm; Vector: pBelorAC11; BAC Clones in

E-Coli DH10B"

BASE COUNT 125 a 118 c 91 g 179 t 1 others

ORIGIN

Query Match 84.0%; Score 21; DB 17; Length 514;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTGGCCGAGATAA 21

Db 142 GGTTCGAGTGGCCGAGATAA 122

RESULT 16

AQ819983

LOCUS

DEFINITION

HS-5270.AL.A10.SP6E.RPCI-11 Human Male BAC library Homo sapiens

genomic clone Plate-846 Col-19 Row-A, DNA sequence.

ACCESSION
AQ819983

VERSION
AQ819983.1 GI:5782376

KEYWORDS
GSS.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 529)

Mahairas, G.S., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

99380589

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Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>) or from Research Genetics (<http://www.htsc.washington.edu>). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 846 row: A column: 19
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 529.

FEATURES

source
 Location/Qualifiers
 1..529

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-846 Col-19 Row-A"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"

BASE COUNT 146 a 125 c 120 g 133 t 5 others
 ORIGIN

Query Match 84.0%; Score 21; DB 17; Length 529;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGGCCGAGATAA 21
 |||||
 Db 424 GGTTCAGTGGCCGAGATAA 444

RESULT 17
 A0608587/c
 LOCUS
 DEFINITION HS_5411_B1_L7A RPCI-11 Human Male BAC Library GSS 10-JUN-1999
 accession A0608587 genomic clone Plate-987 Col-21 Row-D, DNA sequence.
 VERSION A0608587.1 GI:5068581
 KEYWORDS GSS.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 539)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
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 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 615-3618
 Fax: (206) 615-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>) or from Research Genetics (<http://www.htsc.washington.edu>)
 Plate: 987 row: D column: 21
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 539.

FEATURES

source
 Location/Qualifiers
 1..539

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-987 Col-21 Row-D"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACE3.6 vector at EcoRI sites"
 BASE COUNT 111 a 142 c 130 g 150 t 6 others
 ORIGIN

Query Match 84.0%; Score 21; DB 17; Length 539;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGGCCGAGATAA 21
 |||||
 Db 158 GGTTCAGTGGCCGAGATAA 138

RESULT 18
 B1494061
 LOCUS
 DEFINITION df107d10.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:2538690 5', mRNA sequence.
 ACCESSION B1494061
 VERSION B1494061.1 GI:15333405
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 542)
 AUTHORS Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.
 TITLE Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening
 JOURNAL Genomics 23, 42-50 (1994)
 MEDLINE 95130111
 COMMENT Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 PLATE: L1AM6323 row: H column: 19
 Seq primer: M13RPI reverse primer (AB1).

FEATURES

source
 Location/Qualifiers
 1..542

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2538690"
 /clone_lib="Morton Fetal Cochlea"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="organ: ear; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dt. Fetal cochlea, normal. 3% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT 160 a 110 c 126 g 126 t

ORIGIN

Query Match 84.0%; Score 21; DB 13; Length 542;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
 |||||||
 Db 479 GGTTCAGTGAGCCGAGATAA 499

RESULT 19

AQ708886/c
 LOCUS
 DEFINITION HS_2116_AL_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2116 Col-1 Row-G, DNA sequence.

ACCESSION AQ708886
 VERSION AQ708886.1 GI:5418312
 KEYWORDS GSS.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

MEDLINE

99380589

COMMENT

High throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2116 row: G column: 1
 Seq primer: M13 Reverse
 Class: BAC ends
 High quality sequence stop: 570.

FEATURES

source
 Location/Qualifiers
 1..570
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate-2116 Col-1 Row-G"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
 E-Coli DH10B"
 BASE COUNT 145 a 111 c 131 g 177 t 6 others
 ORIGIN

Query Match

84.0%; Score 21; DB 17; Length 570;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
 |||||||
 Db 264 GGTTCAGTGAGCCGAGATAA 244

RESULT 20

BI494060/c
 LOCUS
 DEFINITION df107d10.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:2538690 3', mRNA sequence.

ACCESSION BI494060
 VERSION BI494060.1 GI:15333404
 KEYWORDS EST.

SOURCE

ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 573)
 AUTHORS
 Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
 and Morton,C.C.

TITLE
 Isolation of novel and known genes from a human fetal cochlear cDNA
 library using subtractive hybridization and differential screening

JOURNAL

Genomics 23, 42-50 (1994)

MEDLINE

95130111

COMMENT

Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
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 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).

FEATURES

source
 Location/Qualifiers
 1..573
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2538690"
 /clone_lib="Morton Fetal Cochlea"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: ear; Vector: pBluescript SK-; Site:1: ECOR1;
 Site:2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
 BASE COUNT 128 a 126 c 112 g 207 t
 ORIGIN

Query Match

84.0%; Score 21; DB 13; Length 573;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
 |||||||
 Db 95 GGTTCAGTGAGCCGAGATAA 75

RESULT 21

AQ520887/c
 LOCUS
 DEFINITION HS_5218_B2_B08_T7A RPCT-11 Human Male BAC Library Homo sapiens
 genomic clone Plate-794 Col-16 Row=D, DNA sequence.

ACCESSION AQ520887
 VERSION AQ520887.1 GI:4752012
 KEYWORDS GSS.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 (bases 1 to 575)
 AUTHORS
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.

TITLE
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome

JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

93380589
 MEDLINE COMMENT
 Contact: Mahairas GG, Wallace JC, Hood L
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 University of Washington
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 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
 Plate: 794 row: D column: 16
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 575.
 Location/Qualifiers
 1..575
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="RPCI-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
 BASE COUNT 142 a 131 c 117 g 178 t 7 others
 ORIGIN
 1 GGTTCAGTGCAGCGAGATAA 21
 |||||||||||||||||||||
 126 GTTTCAGTGCAGCGAGATAA 106
 Query Match 84.0%; Score 21; DB 17; Length 575;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||||||||||||||||||
 Db 126 GTTTCAGTGCAGCGAGATAA 106
 RESULT 22
 A0482581
 LOCUS
 DEFINITION RPCI-11-243G23-TV RPCI-11 Homo sapiens genomic clone RPCI-11-243G23
 , DNA sequence.
 ACCESSION A0482581
 VERSION A0482581.1 GI:4669985
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 649)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
 Unpublished (1997)
 Other_GSSs: RPCI-11-243G23.TJ
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends

http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..649
 /organism="Homo sapiens"
 /db_xref="GDB:7593094"
 /db_xref="taxon:9606"
 /clone="RPCI-11-243G23"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
 BASE COUNT 194 a 140 c 144 g 171 t
 ORIGIN
 1 GGTTCAGTGCAGCGAGATAA 21
 |||||||||||||||||||||
 344 GTTTCAGTGCAGCGAGATAA 364
 Query Match 84.0%; Score 21; DB 17; Length 649;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTTCAGTGCAGCGAGATAA 21
 |||||||||||||||||||||
 Db 344 GTTTCAGTGCAGCGAGATAA 364
 RESULT 23
 A0039496
 LOCUS
 DEFINITION CIT-HSP-2327C9-TR CIT-HSP Homo sapiens genomic clone 2327C9, DNA sequence.
 ACCESSION A0039496
 VERSION A0039496.1 GI:3305328
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 666)
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter J.C.
 Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
 Unpublished (1998)
 Other_GSSs: CIT-HSP-2327C9.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M3 Reverse
 Class: BAC ends.
 Location/Qualifiers
 1..666
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2327C9"
 /clone_lib="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelBAC11; Site_1: HindIII; Site_2: HindIII"
 BASE COUNT 209 a 151 c 170 g 136 t
 ORIGIN
 1 GGTTCAGTGCAGCGAGATAA 21
 |||||||||||||||||||||
 136 GTTTCAGTGCAGCGAGATAA 156
 Query Match 84.0%; Score 21; DB 17; Length 666;
 Best Local Similarity 100.0%; Pred. No. 0.053;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCAGTGAGCCGAGATAA 21
 |||||
 Db 328 GGTGTCAGTGAGCCGAGATAA 348

RESULT 24
 AG050903
 LOCUS
 DEFINITION Pan troglodytes DNA, clone: PTB-031H14.F, genomic survey sequence.
 ACCESSION AG050903
 VERSION AG050903.1 GI:16587795
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
 ORGANISM
 BAC Library clone:PTB-031H14.F.
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE BAC end sequences of Library PTB
 JOURNAL Unpublished
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho,Tsuri-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chirobes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the R&D process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: -21M13

LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 FEATURES
 source
 1..668
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-031H14.F"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_lib="PTB Chimpanzee Male BAC Library"
 BASE COUNT 180 a 152 c 176 g 160 t
 ORIGIN

Query Match 84.0%; Score 21; DB 17; Length 668;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCAGTGAGCCGAGATAA 21
 |||||
 Db 489 GGTGTCAGTGAGCCGAGATAA 509

RESULT 25
 BG214939/c
 LOCUS
 DEFINITION RST34594 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
 ACCESSION BG214939
 VERSION BG214939.1 GI:13740960
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS

1 (bases 1 to 882)
 Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
 Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J.,
 Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,
 E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,
 J., Danzig,J. and Ducar,M.
 Creation of genome-wide protein expression libraries using random
 activation of gene expression
 Nat. Biotechnol. 19 (5), 440-445 (2001)
 21227151
 COMMENT
 Contact: Scott J. Cain
 Athersys, Inc.
 3201 Carnegie Ave, Cleveland, OH 44115, USA
 Tel: 216 431 9900
 Fax: 216 361 9596
 Email: scai@atersys.com
 High quality sequence stop: 441.
 Location/Qualifiers
 1..882
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Athersys RAGE Library"
 /cell_line="HT1080"
 /note="See 'Creation of Genome-wide Protein Expression
 Libraries using Random Activation of Gene Expression',
 Nature Biotechnology, in press. Note that even though the
 cell type indicated is HT1080, since a random activation
 method was used, these sequence tags are not necessarily
 expressed in HT1080 under normal circumstances."

BASE COUNT 187 a 287 c 203 g 205 t
 ORIGIN

Query Match 84.0%; Score 21; DB 12; Length 882;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCAGTGAGCCGAGATAA 21
 |||||
 Db 66 GGTGTCAGTGAGCCGAGATAA 46

RESULT 26
 BF032499
 LOCUS
 DEFINITION 601453325f1 NIH_MGC_66 Homo sapiens CDNA clone IMAGE:3856806 5',
 mRNA sequence.
 ACCESSION BF032499
 VERSION BF032499.1 GI:10740211
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LIAW9586 row: b column: 07
 High quality sequence stop: 557.
 Location/Qualifiers
 1..914
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3856806"

/clone_lib="NIH_MGC_66"
 /tissue_type="adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 BASE COUNT 280 a 228 c 241 g 165 t
 ORIGIN

Query Match 84.0%; Score 21; DB 12; Length 914;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 Db 541 GGTTCAGTGCAGCCGAGATAA 561

RESULT 27
 BF837405
 LOCUS 132 bp mRNA linear EST 13-JAN-2001
 DEFINITION PM2-HT0353-211100-007-f09 HT0353 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF837405
 VERSION BF837405.1 GI:12189600
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 132)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0353-
 211100-007-f09&t3=2000-11-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 3
 High quality sequence stop: 131.
 Location/Qualifiers
 1. 132
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0353"
 /dev_stage="Adult"
 /note="Organ: head, neck; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 54 a 30 c 34 g 14 t
 ORIGIN

Query Match 80.0%; Score 20; DB 12; Length 132;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 68 GGTTCAGTGCAGCCGAGATA 87

Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 39 GGTTCAGTGCAGCCGAGATA 58

RESULT 28
 BF878448
 LOCUS 139 bp mRNA linear EST 17-JAN-2001
 DEFINITION MR0-ET0109-191100-002-c07 ET0109 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF878448
 VERSION BF878448.1 GI:12268578
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 139)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR0&t2=MR0-ET0109-
 191100-002-c07&t3=2000-11-19&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 46
 High quality sequence stop: 138.
 Location/Qualifiers
 1. 139
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ET0109"
 /dev_stage="Adult"
 /note="Organ: lung, tumor; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 31 a 33 c 48 g 27 t
 ORIGIN

Query Match 80.0%; Score 20; DB 12; Length 139;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 68 GGTTCAGTGCAGCCGAGATA 87

RESULT 29
 AA709114/c
 LOCUS 144 bp mRNA linear EST 24-DEC-1997
 AA709114

```

DEFINITION zf92f10.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:384427 3' similar to contains Alu repetitive element;; mRNA
sequence.
ACCESSION AA709114
VERSION AA709114.1 GI:2719032
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 144)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from AmerSham.
FEATURES
Location/Qualifiers
1..144
/organism="Homo sapiens"
/db_xref="GDB:1292684"
/db_xref="taxon:9606"
/clone="IMAGE:384427"
/clone_lib="Soares_pineal_gland_N3HPG"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: pineal gland; Vector: pTZ19 (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5' TGTTACCAATCTGAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3']
; double-stranded cDNA was size selected, ligated to Eco
RI adapters (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 25 a 35 c 35 g 49 t
ORIGIN
Query Match 80.0%; Score 20; DB 9; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGCGAGTGGCCGAGATA 20
|||||
Db 82 GGTGCGAGTGGCCGAGATA 63

RESULT 30
A1626093/c
LOCUS A1626093 154 bp mRNA linear EST 23-APR-1999
DEFINITION ar87h11.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2152293 3' similar to contains Alu repetitive element
;contains element MER22 repetitive element ;, mRNA sequence.
ACCESSION A1626093
VERSION A1626093.1 GI:4662893
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 154)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.

```

```

TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 154.
FEATURES
Location/Qualifiers
1..154
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2152293"
/clone_lib="Barstead colon HPLRB7"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/note="Organ: colon; Vector: pTZ19 (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCCGCTTTTCTTTTCTTTT 3']
; double-stranded cDNA was ligated to Eco RI adapters
[5' AATTCAGTAAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pTZ19 vector. Library constructed by Bob
Barstead."
BASE COUNT 27 a 47 c 38 g 42 t
ORIGIN
Query Match 80.0%; Score 20; DB 9; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGCGAGTGGCCGAGATA 20
|||||
Db 68 GGTGCGAGTGGCCGAGATA 49

RESULT 31
AA046824
LOCUS AA046824 173 bp mRNA linear EST 01-FEB-1997
DEFINITION zfl2g10.r1 Soares_fetal_heart_NHH19W Homo sapiens cDNA clone
IMAGE:376770 5' similar to contains Alu repetitive element;; mRNA
sequence.
ACCESSION AA046824
VERSION AA046824.1 GI:1524785
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favell,A., Gish,W., Hawkins
M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevisan,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
TITLE Washington University School of Medicine
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

```

Putative full length read
The vector to vector length is 186
Insert Length: 533 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham.

FEATURES

source

1. .173
/organism="Homo sapiens"
/db_xref="GDB:1285026"
/db_xref="taxon:9606"
/clone="IMAGE:376770"
/clone_lib="Soares_fetal_heart_NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCGCATCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHH19W."

BASE COUNT 51 a 36 c 52 g 31 t 3 others
ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGAGCGGAGATA 20
|||||
Db 120 GGTTCAGTGGAGCGGAGATA 139

RESULT 32
B73330/c

LOCUS

B73330 175 bp DNA linear GSS 21-JUN-1998
CIT-HSP-712K9-TV CIT-HSP Homo sapiens genomic clone 712K9, DNA sequence.

ACCESSION

B73330

VERSION

B73330.1 GI:2712481

KEYWORDS

GSS.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 175)

AUTHORS

Kim, U.-J., Adams, M.D. and Simon, M.I.

TITLE

Determination of clone end sequences of human Bacterial Artificial Chromosomes

JOURNAL

Unpublished (1997)

COMMENT

Other_GSSs: CIT-HSP-712K9.TP

Contact:

Ung-Jin Kim

Caltech Genome Research Lab

California Institute of Technology

Division of Biology, MS 147-75, Pasadena, CA 91125, USA

Tel: 626 796 7066

Fax: 626 395 4901

Email: ung@ash.tree.caltech.edu

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1. .175

/organism="Homo sapiens"

/db_xref="GDB:550829g"

/db_xref="taxon:9606"

FEATURES

source

1. .175
/organism="Homo sapiens"
/db_xref="GDB:550829g"
/db_xref="taxon:9606"

/clone="712K9"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 36 a 47 c 28 g 64 t
ORIGIN

Query Match 80.0%; Score 20; DB 17; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGAGCGGAGATA 20
|||||

Db 158 GGTTCAGTGGAGCGGAGATA 139
|||||

RESULT 33

AA348526/c

LOCUS

AA348526

DEFINITION

ESP55073 Hippocampus II Homo sapiens cDNA 5' end similar to EST

containing Alu repeat, mRNA sequence.

ACCESSION

AA348526

VERSION

AA348526.1 GI:2000835

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 184)

AUTHORS

Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.

TITLE

Rapid cDNA sequencing (expressed sequence tags) from a directionally cloned human infant brain cDNA library

JOURNAL

Nat. Genet. 4, 373-380 (1993)

MEDLINE

94004965

COMMENT

Other_ESTs: EST55072

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavet@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M3 Reverse.

FEATURES

source

1. .184

/organism="Homo sapiens"

/db_xref="ATCC (inhost):149782"

/db_xref="taxon:9606"

/clone_lib="Hippocampus II"

/sex="male"

/tissue_type="hippocampus"

/dev_stage="adult, 74 yrs"

/note="Organ: brain; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ECORI; Site_2: XhoI"

39 a 51 c 57 g 37 t

BASE COUNT

ORIGIN

Query Match

80.0%; Score 20; DB 9; Length 184;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGAGCGGAGATA 20

|||||

Db 65 GGTTCAGTGGAGCGGAGATA 46

RESULT 34

BQ251032/c

LOCUS BQ251032 185 bp mRNA linear EST 03-MAY-2002
 DEFINITION TaE25034A06R TaE25 Triticum aestivum cDNA clone TaE25034A06R, mRNA sequence.
 ACCESSION BQ251032
 VERSION BQ251032.1 GI:20446908
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticaceae; Triticum.
 REFERENCE 1 (bases 1 to 185)
 AUTHORS Cloutier,S.
 TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Daffoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@em.agr.ca
 was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >870 bp
 Plate: 034 row: A column: 06
 Seq primer: M13 Reverse

FEATURES
 source Location/Qualifiers
 1..185

/organism="Triticum aestivum"
 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE25034A06R"
 /clone_lib="TaE25"
 /tissue_type="developing seeds"
 /dev_stage="25 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pCMV-SPORT6.0 (Invitrogen Technologies); Site_1: NotI; Site_2: XbaI; mRNA obtained from wheat seeds of cultivar Glenlea 25 days post-anthesis"
 37 a 47 c 43 g 58 t

Query Match 80.0%; Score 20; DB 14; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTTCAGTGCAGCGAGATA 20
 |||||
 Db 72 GGTTCAGTGCAGCGAGATA 53

RESULT 35
 H02828/c
 LOCUS
 DEFINITION YJ43a04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151470 3' similar to contains Alu repetitive element; contains XTR repetitive element;; mRNA sequence.
 H02828
 ACCESSION H02828.1 GI:865761
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 189)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 293
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 293 Std Error: 0.00
 Seq primer: Promega -2lm13
 High quality sequence stop: 374.

FEATURES
 source Location/Qualifiers
 1..189

/organism="Homo sapiens"
 /db_xref="GB:563571"
 /db_xref="taxon:9606"
 /clone="IMAGE:151470"
 /clone_lib="Soares placenta Nb2HP"
 /sex="Female"
 /dev_stage="placenta obtained at birth (full term)"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' ACTGGAAGAATCGCGCGCAGGATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
 35 a 54 c 44 g 56 t

Query Match 80.0%; Score 20; DB 14; Length 189;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTTCAGTGCAGCGAGATA 20
 |||||
 Db 65 GGTTCAGTGCAGCGAGATA 46

RESULT 36
 R44194/c
 LOCUS
 DEFINITION R44194 191 bp mRNA linear EST 22-MAY-1995
 YG34d02.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:34561 3' similar to contains Alu repetitive element;; mRNA sequence.
 R44194
 ACCESSION R44194.1 GI:822058
 VERSION
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 191)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT On May 9, 1995 this sequence version replaced gi:802918.
 Contact: Wilson RK
 Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 1200
 High quality sequence stops: 178 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1200 Std Error: 0.00

Seq primer: Promega -2lm13

High quality sequence stop: 178.

Location/Qualifiers

source

1. .191

/organism="Homo sapiens"

/db_xref="GB:406908"

/db_xref="taxon:9606"

/clone="IMAGE:34561"

/sex="female"

/dev_stage="73 days post natal"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: whole brain; Vector: Lfamid BA; Site.1: Not

I; Site.2: Hind III; 1st strand cDNA was primed with a Not

I - oligo(dT) primer [5'

AACTGGAAGATTCCGCCGCGAGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Hind III adaptors

(Pharmacia), digested with Not I and directionally cloned

into the Not I and Hind III sites of the Lfamid BA vector.

Library went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

46 a 53 c 46 g 44 t 2 others

BASE COUNT

ORIGIN

Query Match 80.0%; Score 20; DB 14; Length 191;

Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATA 20

|||||

Db 75 GGTTCAGTGGCGGAGATA 56

RESULT 37

LOCUS

AI241886 194 bp mRNA linear EST 04-NOV-1998

qu70g06.x1 NCI CGAP_Brn35 Homo sapiens cDNA clone IMAGE:1977466 3'

similar to contains Alu repetitive element; mRNA sequence.

AI241886

AI241886.1 GI:3837283

EST.

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194)

NCI/NINDS-CoAP <http://www.ncbi.nlm.nih.gov/ncicqap>.

National Cancer Institute / National Institute of Neurological

Disorders and Stroke, Brain Tumor Genome Anatomy Project

(CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgaps@mail.nih.gov

unknown library type

Seq primer: -40UP from Gibco

High quality sequence stop: 183.

Location/Qualifiers

1. .194

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1977466"

/clone_lib="NCI CGAP_Brn35"

/tissue_type="tumor, 5 pooled (see description)"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMV-SPORT6; Site.1: SalI;

Site.2: NotI; Cloned unidirectionally. Primer: oligo dT.

Average insert size 1.33 kb. Tumor types include:

meningioma, oligodendroglioma, astrocytoma (grade II),

medulloblastoma, astrocytoma (grade IV). Life Technologies

catalog #: 11544-012"

36 a 55 c 52 g 51 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 194;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATA 20

|||||

Db 65 GGTTCAGTGGCGGAGATA 46

RESULT 38

LOCUS

H03719

DEFINITION

Y43a04.r1 Soares placenta Nb2HP Homo sapiens cDNA clone

IMAGE:151470 5' similar to contains Alu repetitive element; contains

XTR repetitive element ; mRNA sequence.

H03719

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman

, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, L., Rohlfing, J., Soares, M., Tan, F., Trevisan, E., Waterston

, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Willson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 293

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 293 Std Error: 0.00

Seq primer: M13RPI

High quality sequence stop: 321.

Location/Qualifiers

1. .201

/organism="Homo sapiens"

/db_xref="GB:563571"

/db_xref="taxon:9606"

/clone="IMAGE:151470"

/clone_lib="Soares placenta Nb2HP"

/sex="Female"

/dev_stage="placenta obtained at birth (full term)"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: placenta; Vector: pT73D (Pharmacia) with a

modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer [5'

AACTGGAGAAATTCGCCGCGAGAAATTTTTTTTTTTT 3'];

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo.

60 a 44 c 61 g 35 t

BASE COUNT

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 14; Length 201;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATA 20

|||||

Db 151 GGTTCAGTGGCGGAGATA 170

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert length: 521 Std Error: 0.00
 Seq primer: -28ml3 rev1 ET from AmerSham
 High quality sequence stop: 225.

FEATURES

source

```

Location/Qualifiers
1..231
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1010380"
/dev_stage="Male"
/lab_host="DHI10B"
/notes="Vector: PAMP10; Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from 5,000-10
,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
BASE COUNT      43 a  65 c  55 g  68 t
ORIGIN

```

Query Match 80.0%; Score 20; DB 9; Length 231;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGTTCAGTGGCCGAGATA 20
      |||||
Db 67 GGTTCAGTGGCCGAGATA 48

```

RESULT 42

BE261473

LOCUS

601148613f1 NTH_MGC_19 Homo sapiens cDNA clone IMAGE:3163875 5',
 mRNA sequence. EST 26-OCT-2000

ACCESSION BE261473

VERSION BE261473.1 GI:9133661

KEYWORDS EST

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM125 row: j column: 04

High quality sequence stop: 233.

Location/Qualifiers

1..233

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3163875"

/clone_lib="NIH_MGC_19"

/tissue_type="neuroblastoma"

/lab_host="DHI10B (phage-resistant)"

/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: This is a NIH_MGC Library."

BASE COUNT

ORIGIN

```

59 a  64 c  70 g  40 t

```

Query Match

Best Local Similarity 100.0%; Score 20; DB 10; Length 233;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATA 20

|||||

Db 165 GGTTCAGTGGCCGAGATA 184

RESULT 43

BF962750

LOCUS

QV2-NN0045-181200-560-d05 NN0045 Homo sapiens cDNA, mRNA sequence. EST 22-JAN-2001

ACCESSION BF962750

VERSION BF962750.1 GI:12380025

KEYWORDS EST..

SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 234)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

[http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-](http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NN0045-181200-560-d05&t3=2000-12-18&t4=1)

181200-560-d05&t3=2000-12-18&t4=1

Seq primer: puc 18 forward

High quality sequence stop: 234.

Location/Qualifiers

1..234

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NN0045"

/dev_stage="Adult"

/note="Organ: nervous_normal; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 87 a 39 c 62 g 46 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 20; DB 12; Length 234;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||
 Db 44 GGTTCAGTGAGCCGAGATA 63

RESULT 44
 AA380519/C

LOCUS
 DEFINITION EST93513 Supt cells Homo sapiens cDNA 5' end similar to EST
 containing Alu repeat, mRNA sequence.

ACCESSION
 VERSION AA380519
 KEYWORDS EST
 SOURCE human.

ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
 , C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
 , O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
 L.M., Fitzhugh, W.M., Fritchman, J.D., Geoghagen, N.S., Glodek, A.,
 Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
 Kelley, J.C., Liu, L.-L., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
 Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
 , M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
 Venter, J.C.

TITLE
 JOURNAL Initial assessment of human gene diversity and expression patterns
 MEDLINE based upon 83 million nucleotides of cDNA sequence
 COMMENT Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 1..237
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):184934"
 /db_xref="taxon:9606"
 /clone_lib="Supt cells"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 44 a 69 c 55 g 69 t
 ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 237;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||
 Db 119 GGTTCAGTGAGCCGAGATA 100

LOCUS
 DEFINITION EST93513 Supt cells Homo sapiens cDNA 5' end similar to EST
 containing Alu repeat, mRNA sequence.

ACCESSION
 VERSION AA380519
 KEYWORDS EST
 SOURCE human.

ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult
 , C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White
 , O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
 L.M., Fitzhugh, W.M., Fritchman, J.D., Geoghagen, N.S., Glodek, A.,
 Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,
 Kelley, J.C., Liu, L.-L., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,
 Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon
 , M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
 Venter, J.C.

TITLE
 JOURNAL Initial assessment of human gene diversity and expression patterns
 MEDLINE based upon 83 million nucleotides of cDNA sequence
 COMMENT Nature 377 (6547 Suppl), 3-174 (1995)
 96026280
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tldb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 1..237
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):184934"
 /db_xref="taxon:9606"
 /clone_lib="Supt cells"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 44 a 69 c 55 g 69 t
 ORIGIN

Query Match 80.0%; Score 20; DB 9; Length 237;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||
 Db 119 GGTTCAGTGAGCCGAGATA 100

RESULT 45
 B87492

LOCUS
 DEFINITION RPC111-29B18.TV RPC1-11 Homo sapiens genomic clone RPC1-11-29B18,
 DNA sequence.

ACCESSION
 VERSION B87492
 KEYWORDS GSS.
 SOURCE human.

ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 239)
 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
 Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
 Venter, J.C.

TITLE
 JOURNAL Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 COMMENT Unpublished (1998)
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mda@amstetgr.org

Clones are derived from the human BAC library RPC1-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (<http://resgen.com>). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 1..239
 /organism="Homo sapiens"
 /db_xref="GDB:7510793"
 /db_xref="taxon:9606"
 /clone="RPC1-11-29B18"
 /clone_lib="RPC1-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPC111 Human Male BAC Library"

BASE COUNT 80 a 50 c 57 g 52 t
 ORIGIN

Query Match 80.0%; Score 20; DB 17; Length 239;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||
 Db 62 GGTTCAGTGAGCCGAGATA 81

LOCUS
 DEFINITION RPC111-29B18.TV RPC1-11 Homo sapiens genomic clone RPC1-11-29B18,
 DNA sequence.

ACCESSION
 VERSION B87492
 KEYWORDS GSS.
 SOURCE human.

ORGANISM
 Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 239)
 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
 Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
 Venter, J.C.

TITLE
 JOURNAL Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 COMMENT Unpublished (1998)
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mda@amstetgr.org

Clones are derived from the human BAC library RPC1-11. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (<http://resgen.com>). BAC end search page:
http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html
 Seq primer: T7
 Class: BAC ends.

FEATURES
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 /sex="Male"
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 /note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPC111 Human Male BAC Library"

BASE COUNT 80 a 50 c 57 g 52 t
 ORIGIN

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QY 1 GGTTCAGTGAGCCGAGATA 20
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 Db 62 GGTTCAGTGAGCCGAGATA 81

Search completed: November 24, 2002, 15:01:44
 Job time: 1554.5 secs

GenCore version 5.1.3
 Copyright (c) 1993 - 2002 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: November 24, 2002, 12:19:18 ; Search time 211.5 Seconds
 (without alignments)
 266.194 Million cell updates/sec
 Title: US-09-784-423-124
 Perfect score: 25
 Sequence: 1 GGTTCAGTGCAGCCGATAGAGT 25
 Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0
 Searched: 2185239 seqs, 112599159 residues
 Word size : 0
 Total number of hits satisfying chosen parameters: 4370478
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
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Database : N_Geneseq_101002.*
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 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
 24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	20	AAZ27824
2	25	100.0	1000	20	AAZ27732
3	21	84.0	325	22	ABAI7408
4	21	84.0	355	22	AAI65697
5	21	84.0	608	24	ABN65341
6	21	84.0	946	22	AAK70967
7	21	84.0	1242	22	AAH48569
8	21	84.0	1714	24	ABA92605
9	21	84.0	2150	23	ABV22677

10	21	84.0	2150	23	ABV28503	Human prostate exp
11	21	84.0	2843	22	AAH48582	Human fascin DNA f
12	21	84.0	5537	22	AAK84869	Human immune/haema
13	21	84.0	11674	22	AAK70965	Human immune/haema
14	21	84.0	13055	22	AAH48621	Human fascin DNA f
15	21	84.0	16951	22	AAH48620	Human fascin DNA f
16	21	84.0	16951	22	AAH48622	Human fascin DNA f
17	21	84.0	19286	22	AAI03002	Human fascin DNA f
18	21	84.0	19286	22	ABN57349	Human reproductive
19	21	84.0	28149	22	ABAI7961	Human testicular a
20	21	84.0	30360	22	AAK62759	Human nervous syst
21	21	84.0	32192	22	ABAI7963	Human immune/haema
22	21	84.0	38258	24	AAI5906	Human nervous syst
23	21	84.0	49999	20	AAI23903	DNA encoding Colon
24	20	80.0	95	21	AAI15906	Human LOBO homolog
25	20	80.0	171	22	AAK81714	Human secreted pro
26	20	80.0	172	22	AAK83823	Human immune/haema
27	20	80.0	180	21	AAI11950	Human immune/haema
28	20	80.0	193	21	AAI04572	Human secreted pro
29	20	80.0	205	24	AAI68895	Human secreted pro
30	20	80.0	236	21	AAI32484	Activated T-cell d
31	20	80.0	304	21	AAK04849	Human secreted pro
32	20	80.0	320	22	AAH68890	Human cervical can
33	20	80.0	329	22	AAH70549	Human polyneuroti
34	20	80.0	335	22	AAI87614	Human polyneuroti
35	20	80.0	384	24	ABN79179	Human ovarian can
36	20	80.0	388	22	AAI82847	Human polyneuroti
37	20	80.0	425	23	ABV16660	Human prostate exp
38	20	80.0	428	22	AAI83705	Human polyneuroti
39	20	80.0	436	23	ABV49562	Human prostate exp
40	20	80.0	436	24	ABQ89507	Human prostate exp
41	20	80.0	451	22	AAK62995	Human immune/haema
42	20	80.0	459	23	ABV45555	Human prostate exp
43	20	80.0	472	23	ABV47512	Human prostate exp
44	20	80.0	485	23	ABV46458	Human prostate exp
45	20	80.0	533	23	ABV42598	Human prostate exp

ALIGNMENTS

RESULT 1
 ID AAZ27824 standard; DNA; 25 BP.
 AC AAZ27824;
 DT 23-DEC-1999 (first entry)
 DE PCR primer for human DNA marker clone SL32.
 XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
 XX IIR sequence; pentanucleotide tandem repeat; stutter artifact;
 KW DNA typing; DNA profiling; linkage analysis; criminal justice;
 KW paternity testing; animal lineage analysis; microsatellite loci;
 KW polymorphism detection; PCR primer; ss.
 OS Synthetic.
 OS Homo sapiens.
 XX WO9940194-A1.
 XX 12-AUG-1999.
 PD 04-FEB-1999; 99WO-US02345.
 XX 04-FEB-1998; 98US-0018584.
 XX (PROM-) PROMEGA CORP.
 PA Schumm JW, Bachner JW;
 PI WPI; 1999-590696/50.

```

XX Isolating DNA containing intermediate tandem repeat sequences, useful
PT in DNA profiling
XX
XX Claim 30: Page 21; 111pp; English.
XX
XX This sequence is a PCR primer for a human DNA marker clone used in the
CC method of the invention. The method is for isolating a fragment of DNA
CC containing an intermediate tandem repeat (ITR) sequence using
CC hybridization selection, and comprises: (a) providing several DNA
CC fragments, at least one of which contains an ITR sequence, a region of
CC the DNA fragment which contains at least one repeat unit consisting of a
CC sequence of five, six or seven bases repeated in tandem at least two
CC times; (b) providing a stationary support having at least one
CC oligonucleotide associated with it, where the oligonucleotide includes a
CC sequence of nucleotides which is complementary to a portion of the ITR
CC sequence; and (c) combining the DNA fragments with the support under
CC conditions where the DNA fragments including the DNA fragment containing
CC the ITR sequence hybridize to the support. The method is particularly
CC used to isolate DNA containing pentanucleotide tandem repeat sequences as
CC well as to detect target ITR DNA sequences having a low incidence of
CC stutter artifacts (no more than 2.4%). The method is useful in DNA
CC profiling for linkage analysis, criminal justice, paternity testing and
CC other forensic and medical uses. DNA typing is also useful for confirming
CC the lineage of horses, dogs and other prize animals. The invention
CC overcomes problems related to the use of microsatellite loci in DNA
CC profiling. The method can detect polymorphisms with a low incidence of
CC stutter artifacts, which has previously been a problem in interpreting
CC allelic content of loci. The development of markers based on larger
CC repeat units, enables easier separation of the fragments on larger
CC electrophoretic gels. This allows the simultaneous analysis of more loci.
XX
XX Sequence 25 BP; 7 A; 3 C; 10 G; 5 T; 0 other;
SQ

```

Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
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Db 1 GGTTCGAGTGAGCCGAGATAAGAGT 25

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RESULT 2
AAZ27732
ID AAZ27732 standard; DNA; 1000 BP.
XX
XX AAZ27732;
XX
XX 23-DEC-1999 (first entry)
XX Human DNA marker clone s132.
XX
XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
XX ITR sequence; pentanucleotide tandem repeat; stutter artifact;
XX DNA typing; DNA profiling; linkage analysis; criminal justice;
XX paternity testing; animal lineage analysis; microsatellite loci;
XX polymorphism detection; ds.
XX
XX Homo sapiens.
XX
XX WC9940194-A1.
XX
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US02345.
XX
XX 04-FEB-1998; 98US-0018584.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Schumm JW, Bacher JW;
XX

```

DR WPI; 1999-590696/50.
XX Isolating DNA containing intermediate tandem repeat sequences, useful
PT in DNA profiling
XX
XX Claim 22: Page 78; 111pp; English.
XX
XX This sequence represents a human DNA marker clone used in the method of
CC the invention. The method is for isolating a fragment of DNA containing
CC an intermediate tandem repeat (ITR) sequence using hybridization
CC selection, and comprises: (a) providing several DNA fragments, at least
CC one of which contains an ITR sequence, a region of the DNA fragment which
CC contains at least one repeat unit consisting of a sequence of five, six
CC or seven bases repeated in tandem at least two times; (b) providing a
CC stationary support having at least one oligonucleotide associated with
CC it, where the oligonucleotide includes a sequence of nucleotides which is
CC complementary to a portion of the ITR sequence; and (c) combining the DNA
CC fragments with the support under conditions where the DNA fragments
CC including the DNA fragment containing the ITR sequence hybridize to the
CC support. The method is particularly used to isolate DNA containing
CC pentanucleotide tandem repeat sequences as well as to detect target ITR
CC DNA sequences having a low incidence of stutter artifacts (no more than
CC 2.4%). The method is useful in DNA profiling for linkage analysis,
CC criminal justice, paternity testing and other forensic and medical uses.
CC DNA typing is also useful for confirming the lineage of horses, dogs and
CC other prize animals. The invention overcomes problems related to the use
CC of microsatellite loci in DNA profiling. The method can detect
CC polymorphisms with a low incidence of stutter artifacts, which has
CC previously been a problem in interpreting allelic content of loci. The
CC development of markers based on larger repeat units, enables easier
CC separation of the fragments on electrophoretic gels. This allows the
CC simultaneous analysis of more loci.
XX
XX Sequence 1000 BP; 302 A; 240 C; 231 G; 226 T; 1 other;
SQ

```

Query Match 100.0%; Score 25; DB 20; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||
Db 441 GGTTCGAGTGAGCCGAGATAAGAGT 465

```

RESULT 3
ABAL7408/c
ID ABAL7408 standard; DNA; 325 BP.
XX
XX ABAL7408;
XX
XX 23-JAN-2002 (first entry)
XX Human nervous system related polynucleotide SEQ ID NO 9739.
XX
XX Human; neutropic; neuroprotective; cytostatic; dermatological; virucide;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
XX antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
XX Homo sapiens.
XX
XX WC0200159063-A2.
XX
XX 16-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
XX
XX 04-FEB-2000; 2000US-0180626.
XX
XX 24-FEB-2000; 2000US-0184664.
XX

02-MAR-2000; 2000US-0186350.
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 08-DEC-2000; 2000US-0251989.
 11-DEC-2000; 2000US-0251990.
 05-JAN-2001; 2000US-0254097.
 05-JAN-2001; 2000US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 useful for preventing, diagnosing and/or treating nervous system
 cancers and metastases -
 Disclosure; SEQ ID NO 9739; 1701pp + Sequence Listing; English.

CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (AB114578-AB118001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune;
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

Sequence 325 BP; 55 A; 97 C; 77 G; 96 T; 0 other;
 Query Match 84.0%; Score 21; DB 22; Length 325;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
 Db 32 GGTTCAGTGCAGCCGAGATAA 12
 |||||

RESULT 4

AAF65697/c
 ID AAF65697 standard; cDNA; 355 BP.

AC AAF65697;

DT 09-APR-2001 (first entry)

DE Novel human polynucleotide, SEQ ID NO: 1453.

KW Human; cytostatic; gene therapy; colon cancer; prostate cancer;
 breast cancer; lung cancer; cancer detection; ss.

OS Homo sapiens.

XX WO200102568-A2.

XX 11-JAN-2001.

XX 30-JUN-2000; 2000WO-US18374.

XX 02-JUL-1999; 99US-0142310.

XX 02-JUL-1999; 99US-0142311.

PA (CHIR) CHIRON CORP.

PA (HYSE-) HYSEQ INC.

XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
 PI Reinhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Crixenjakov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 XX WPI; 2001-091805/10.

XX Library of polynucleotides for diagnosing a cancerous state of a

PT mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX

PS Claim 9; Page 752; 1046pp; English.

XX The present sequence is one of 3351 sequences in a library of human
 CC polynucleotides. The library is used to detect differentially expressed
 CC genes correlated with a cancerous state of a mammalian cell and can

CC detect colon, prostate, breast and lung cancer. The library can be used
 CC to produce probes for detection of mRNA and to produce additional copies
 CC of the polynucleotides. The probes can be used for chromosome mapping of
 CC the polynucleotide and for detection of transcription levels. Ribozymes
 CC or antisense oligonucleotides can be generated. The polynucleotides and
 CC their gene products are used as genetic or biochemical markers (e.g. in
 CC blood or tissues) that will detect the earliest changes along the
 CC carcinogenesis pathway and/or monitor the efficacy of therapies and
 CC preventive interventions. The polynucleotides, polypeptides and
 CC antibodies against them can be used in pharmaceutical compositions to
 CC treat the cancers and proliferative disorders such as neoplasia,
 CC dysplasia and hyperplasia.

XX Sequence 355 BP; 87 A; 94 C; 72 G; 102 T; 0 other;

Query Match 84.0%; Score 21; DB 22; Length 355;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
 Db 60 GGTTCAGTGCAGCCGAGATAA 40
 |||||

RESULT 5

ABN65341/c
 ID ABN65341 standard; cDNA; 608 BP.

XX AC ABN65341;

XX 28-JUN-2002 (first entry)

DE Human cancer related polynucleotide SEQ ID NO 5308.

KW Human; cytostatic; gene expression; gene mapping; tissue profiling;
 gene therapy; cancer; tumour; gene; ss.

XX Homo sapiens.

XX WO200214500-A2.

XX 21-FEB-2002.

XX 16-AUG-2001; 2001WO-US25840.

XX 16-AUG-2000; 2000US-226326P.

XX (CHIR) CHIRON CORP.

XX (HYSE-) HYSEQ INC.

PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;
 PI Lamson G, Scott EM, Zhang G, Kassam A, Pot D, Labat I;
 XX WPI; 2002-241905/29.

XX New nucleic acid for producing a polypeptide, detecting differentially
 PT expressed genes correlated with a cancerous state of a mammalian cell,
 PT and inhibiting tumor growth -
 XX

PS Claim 1; SEQ ID NO 5308; 883pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (ABN27253-ABN33262)
 CC with cytostatic activity. The polynucleotide is used to produce a
 CC polypeptide, to detect differentially expressed genes correlated with a
 CC cancerous state of a mammalian cell and to inhibit tumour growth. The
 CC polynucleotide is used as a probe in mapping and tissue profiling. The
 CC encoded polypeptide and antibodies to the polypeptide can also be used
 CC for therapeutic and diagnostic purposes. The polynucleotide is useful for
 CC gene therapy.

XX Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

```
SQ Sequence 608 BP; 153 A; 126 C; 114 G; 215 T; 0 other;
Query Match      84.0%; Score 21; DB 24; Length 608;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGAGCCGAGTAA 21
   |||||
Db 501 GGTTCAGTGGAGCCGAGTAA 481

RESULT 6
AAK70967/c
ID AAK70967 standard; DNA; 946 BP.
XX
AC AAK70967;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25779.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226661.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231142.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
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PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246533.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
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PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249219.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 03-JAN-2001; 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.
 XX
 XX Disclosure; SEQ ID NO 25779; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 XX Sequence 946 BP; 235 A; 243 C; 206 G; 262 T; 0 other;
 SQ
 Query Match 84.0%; Score 21; DB 22; Length 946;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATAA 21
 Db 899 GGTTCAGTGCAGCCGAGATAA 879
 ||||||||||||||||||||
 RESULT 7
 AAH48569/c
 ID AAH48569 standard; DNA; 1242 BP.
 XX
 XX AAH48569;
 AC
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human fascin DNA fragment SEQ ID 19.

XX
 KW Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
 KW antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
 KW immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
 KW Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
 KW autoimmune disease; transplant rejection; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200151631-A2.
 XX
 XX 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-EP00362.
 XX
 PR 13-JAN-2000; 2000DE-1001169.
 PR 02-MAR-2000; 2000DE-1010188.
 XX
 XX (RESK/) RESKE-KUNZ A.
 PA (ROSS/) ROSS X.
 PA (ROSS/) ROSS R.
 PA (BROS/) BROS M.
 XX
 XX Reske-Kunz A, Ross X, Ross R, Bros M;
 PI WPI; 2001-451859/48.
 XX
 XX New regulatory sequences from the fascin gene, useful for providing
 PT dendritic cell-specific expression of e.g. antigens, e.g. for
 PT vaccination against tumors and infections
 XX
 XX Claim 2a; Page 91; 117pp; German.
 XX
 CC This invention describes novel regulatory sequences (A) derived from
 CC human fascin that provide specific expression in dendritic cells (DC) and
 CC which have antiviral, antibacterial, antifungal, antiparasitic,
 CC anti-allergic, neurological, immunomodulatory and apoptotic activity.
 CC (A) are used to regulate expression of antigens, immunoregulators,
 CC antisense sequences etc. in DC-specific fashion. Recombinant DNA, vectors
 CC and host cells that contain (A) are useful: (i) in vaccines against
 CC viruses, bacteria, fungi, parasites, tumors, allergens and plaques in
 CC Creutzfeld-Jakob and Alzheimer's disease; and (ii) for gene therapy of
 CC tumors, allergies, infections, autoimmune diseases and transplant
 CC rejection. They can also provide specific expression of antigens and
 CC immunoregulators in DC; for isolation and identification of cell factors
 CC and cis-elements from regulatory sequences that mediate DC-specific
 CC expression; to determine the degree of maturity of DC and to block
 CC transfection factors, by providing binding sites in DC. (A) provide
 CC DC-specific expression of nucleic acid under their control, allowing a
 CC more specific regulation of the immune response and eliminating the long
 CC and laborious purification of DC (since a complete leucocyte population
 CC may be transformed), including transformation in vitro. This sequence
 CC represents a DNA fragment of human fascin which is described in the
 CC invention.
 XX
 XX Sequence 1242 BP; 230 A; 330 C; 387 G; 295 T; 0 other;
 SQ
 Query Match 84.0%; Score 21; DB 22; Length 1242;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATAA 21
 Db 522 GGTTCAGTGCAGCCGAGATAA 502
 ||||||||||||||||||||
 RESULT 8
 ABA92605
 ID ABA92605 standard; cDNA; 1714 BP.
 XX
 XX ABA92605;
 AC
 XX
 DT 21-MAR-2002 (first entry)

PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (WILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WO, Monahan JE;
 XX WPI: 2001-662795/76.
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 XX Claim 1; Page 5955; 11750pp; English.
 XX
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2150 BP; 580 A; 515 C; 567 G; 485 T; 3 other;

Query Match 84.0%; Score 21; DB 23; Length 2150;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 ||||||||||||||||||
 Db 1777 GGTTCAGTGCAGCGAGATAA 1797

RESULT 11
 ID AAH48582/C
 AC AAH48582;
 DT 20-SEP-2001 (first entry)
 XX Human fascin DNA fragment SEQ ID 34.
 DE
 XX Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
 KW antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
 KW immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
 KW Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
 KW autoimmune disease; transplant rejection; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200151631-A2.
 PN
 XX 19-JUL-2001.
 PD
 XX
 XX 12-JAN-2001; 2001WO-BP00362.
 PF
 XX 13-JAN-2000; 2000DE-1001169.
 PR
 XX 02-MAR-2000; 2000DE-1010188.
 XX
 XX (RESK/) RESKE-KUNZ A.
 PA (ROSS/) ROSS X.

PA (ROSS/) ROSS R.
 PA (BROS/) BROS M.
 XX
 XX Reske-Kunz A, Ross X, Ross R, Bros M;
 XX WPI: 2001-451858/48.
 DR
 XX
 XX New regulatory sequences from the fascin gene, useful for providing
 PT dendritic cell-specific expression of e.g. antigens, e.g. for
 PT vaccination against tumors and infections -
 XX
 XX Example 1; Page 103-104; 117pp; German.
 PS
 XX This invention describes novel regulatory sequences (A) derived from
 CC human fascin that provide specific expression in dendritic cells (DC) and
 CC which have antiviral, antibacterial, antifungal, antiparasitic,
 CC anti-allergic, neurological, immunomodulatory and apoptotic activity.
 CC (A) are used to regulate expression of antigens, immunoregulators,
 CC antisense sequences etc. in DC-specific fashion. Recombinant DNA, vectors
 CC and host cells that contain (A) are useful: (i) in vaccines against
 CC viruses, bacteria, fungi, parasites, tumors, allergens and plaques in
 CC Creutzfeld-Jakob and Alzheimer's disease; and (ii) for gene therapy of
 CC tumors, allergies, infections, autoimmune diseases and transplant
 CC rejection. They can also be provide specific expression of antigens and
 CC immunoregulators in DC; for isolation and identification of cell factors
 CC and cis-elements from regulatory sequences that mediate DC-specific
 CC expression; to determine the degree of maturity of DC and to block
 CC transcription factors; by providing binding sites in DC. (A) provide
 CC DC-specific expression of nucleic acid under their control, allowing a
 CC more specific regulation of the immune response and eliminating the long
 CC and laborious purification of DC (since a complete leucocyte population
 CC may be transformed), including transformation in vitro. This sequence
 CC represents a DNA fragment of human fascin which is described in the
 CC invention.
 XX
 SQ Sequence 2843 BP; 499 A; 909 C; 827 G; 608 T; 0 other;

Query Match 84.0%; Score 21; DB 22; Length 2843;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
 ||||||||||||||||||
 Db 1607 GGTTCAGTGCAGCGAGATAA 1587

RESULT 12
 ID AAK84869
 AC AAK84869 standard; DNA; 5537 BP.
 XX
 XX AAK84869;
 DT 07-NOV-2001 (first entry)
 XX
 XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39681.
 DE
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ds.
 KW
 XX Homo sapiens.
 OS
 XX WO200157182-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX
 XX 17-JAN-2001; 2001WO-US01354.
 PF
 XX 31-JAN-2000; 2000US-0179065.
 PR
 XX 04-FEB-2000; 2000US-0180628.
 PR
 XX 24-FEB-2000; 2000US-0184664.
 PR
 XX 02-MAR-2000; 2000US-0186350.
 PR
 XX 16-MAR-2000; 2000US-0189874.
 PR
 XX 17-MAR-2000; 2000US-0190076.

PR	18-APR-2000;	2000US-0198123.	PR	20-OCT-2000;	2000US-0240960.
PR	19-MAY-2000;	2000US-0205515.	PR	20-OCT-2000;	2000US-0241221.
PR	07-JUN-2000;	2000US-0209467.	PR	20-OCT-2000;	2000US-0241785.
PR	28-JUN-2000;	2000US-0214886.	PR	20-OCT-2000;	2000US-0241786.
PR	30-JUN-2000;	2000US-0215135.	PR	20-OCT-2000;	2000US-0241787.
PR	07-JUL-2000;	2000US-0216647.	PR	20-OCT-2000;	2000US-0241808.
PR	07-JUL-2000;	2000US-0216880.	PR	20-OCT-2000;	2000US-0241809.
PR	11-JUL-2000;	2000US-0217487.	PR	20-OCT-2000;	2000US-0241826.
PR	11-JUL-2000;	2000US-0217496.	PR	01-NOV-2000;	2000US-024617.
PR	14-JUL-2000;	2000US-0218290.	PR	08-NOV-2000;	2000US-0246474.
PR	26-JUL-2000;	2000US-0220963.	PR	08-NOV-2000;	2000US-0246475.
PR	26-JUL-2000;	2000US-0220964.	PR	08-NOV-2000;	2000US-0246477.
PR	14-AUG-2000;	2000US-0224518.	PR	08-NOV-2000;	2000US-0246478.
PR	14-AUG-2000;	2000US-0224519.	PR	08-NOV-2000;	2000US-0246523.
PR	14-AUG-2000;	2000US-0225213.	PR	08-NOV-2000;	2000US-0246524.
PR	14-AUG-2000;	2000US-0225214.	PR	08-NOV-2000;	2000US-0246525.
PR	14-AUG-2000;	2000US-0225266.	PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000;	2000US-0225267.	PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000;	2000US-0225268.	PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000;	2000US-0225270.	PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000;	2000US-0225270.	PR	08-NOV-2000;	2000US-0246609.
PR	14-AUG-2000;	2000US-0225447.	PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000;	2000US-0225757.	PR	08-NOV-2000;	2000US-0246611.
PR	14-AUG-2000;	2000US-0225758.	PR	08-NOV-2000;	2000US-0246613.
PR	14-AUG-2000;	2000US-0225759.	PR	17-NOV-2000;	2000US-0249207.
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PR	22-AUG-2000;	2000US-0226688.	PR	17-NOV-2000;	2000US-0249210.
PR	22-AUG-2000;	2000US-0227182.	PR	17-NOV-2000;	2000US-0249211.
PR	23-AUG-2000;	2000US-0227009.	PR	17-NOV-2000;	2000US-0249212.
PR	30-AUG-2000;	2000US-0228924.	PR	17-NOV-2000;	2000US-0249213.
PR	01-SEP-2000;	2000US-0229287.	PR	17-NOV-2000;	2000US-0249214.
PR	01-SEP-2000;	2000US-0229343.	PR	17-NOV-2000;	2000US-0249215.
PR	01-SEP-2000;	2000US-0229344.	PR	17-NOV-2000;	2000US-0249216.
PR	01-SEP-2000;	2000US-0229345.	PR	17-NOV-2000;	2000US-0249217.
PR	05-SEP-2000;	2000US-0229509.	PR	17-NOV-2000;	2000US-0249218.
PR	05-SEP-2000;	2000US-0229513.	PR	17-NOV-2000;	2000US-0249244.
PR	06-SEP-2000;	2000US-0230437.	PR	17-NOV-2000;	2000US-0249245.
PR	06-SEP-2000;	2000US-0230438.	PR	17-NOV-2000;	2000US-0249246.
PR	08-SEP-2000;	2000US-0231242.	PR	17-NOV-2000;	2000US-0249265.
PR	08-SEP-2000;	2000US-0231243.	PR	17-NOV-2000;	2000US-0249297.
PR	08-SEP-2000;	2000US-0231244.	PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000;	2000US-0231413.	PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000;	2000US-0231414.	PR	01-DEC-2000;	2000US-0250160.
PR	08-SEP-2000;	2000US-0232080.	PR	01-DEC-2000;	2000US-0250391.
PR	08-SEP-2000;	2000US-0232081.	PR	05-DEC-2000;	2000US-0251030.
PR	12-SEP-2000;	2000US-0231968.	PR	05-DEC-2000;	2000US-0251988.
PR	14-SEP-2000;	2000US-0232397.	PR	05-DEC-2000;	2000US-0251989.
PR	14-SEP-2000;	2000US-0232398.	PR	06-DEC-2000;	2000US-0251990.
PR	14-SEP-2000;	2000US-0232399.	PR	06-DEC-2000;	2000US-0251997.
PR	14-SEP-2000;	2000US-0232400.	PR	08-DEC-2000;	2000US-0251868.
PR	14-SEP-2000;	2000US-0232401.	PR	08-DEC-2000;	2000US-0251869.
PR	14-SEP-2000;	2000US-0233063.	PR	08-DEC-2000;	2000US-0251869.
PR	14-SEP-2000;	2000US-0233064.	PR	08-DEC-2000;	2000US-0251989.
PR	21-SEP-2000;	2000US-0233065.	PR	11-DEC-2000;	2000US-0251990.
PR	21-SEP-2000;	2000US-0234223.	PR	05-JAN-2001;	2001US-0259678.
PR	25-SEP-2000;	2000US-0234274.	PR	(HUMA-) HUMAN GENOME SCI INC.	
PR	25-SEP-2000;	2000US-0234997.	PR	Rosen CA, Barash SC, Ruben SM;	
PR	26-SEP-2000;	2000US-0234998.	PR	WPI; 2001-483426/52.	
PR	27-SEP-2000;	2000US-0235484.	PR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PR	27-SEP-2000;	2000US-0235834.	PR	useful for preventing, diagnosing and/or treating cancers and	
PR	27-SEP-2000;	2000US-0235836.	PR	metastasis -	
PR	29-SEP-2000;	2000US-0236327.	PR	Disclosure; SEQ ID NO 39681; 3071pp + Sequence Listing; English.	
PR	29-SEP-2000;	2000US-0236367.	PR	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)	
PR	29-SEP-2000;	2000US-0236368.	PR	amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic	
PR	29-SEP-2000;	2000US-0236369.	PR	activity, and can be used in gene therapy and vaccine production. (I)	
PR	29-SEP-2000;	2000US-0236370.	PR		
PR	02-OCT-2000;	2000US-0236370.	PR		
PR	02-OCT-2000;	2000US-0236802.	PR		
PR	02-OCT-2000;	2000US-0237037.	PR		
PR	02-OCT-2000;	2000US-0237038.	PR		
PR	02-OCT-2000;	2000US-0237039.	PR		
PR	02-OCT-2000;	2000US-0237039.	PR		
PR	13-OCT-2000;	2000US-0237040.	PR		
PR	13-OCT-2000;	2000US-0239935.	PR		
PR	13-OCT-2000;	2000US-0239937.	PR		

CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients' own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 5537 BP; 1451 A; 1204 C; 1400 G; 1482 T; 0 other;

Query Match 84.0%; Score 21; DB 22; Length 5537;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTGCAGTGCACCCAGATAA 21
 |||||
 Db 4565 GGTTGCAGTGCACCCAGATAA 4585

RESULT 13
 AAK70965/c
 ID AAK70965 standard; DNA; 11674 BP.
 AC AAK70965;
 DT 06-NOV-2001 (first entry)
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25777.
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytotstatic; gene therapy; vaccine; metastasis; ds.
 XX Homo sapiens.
 OS
 XX WO200157182-A2.
 PN
 XX 09-AUG-2001.
 PD
 XX
 XX 17-JAN-2001; 2001WO-US01354.
 XX
 XX 31-JAN-2000; 2000US-0179065.
 XX 04-FEB-2000; 2000US-0180628.
 XX 24-FEB-2000; 2000US-0184664.
 XX 02-MAR-2000; 2000US-0186350.
 XX 16-MAR-2000; 2000US-0189874.
 XX 17-MAR-2000; 2000US-0190076.
 XX 18-APR-2000; 2000US-0198123.
 XX 19-MAY-2000; 2000US-0205515.
 XX 07-JUN-2000; 2000US-0209467.
 XX 28-JUN-2000; 2000US-0214886.
 XX 30-JUN-2000; 2000US-0215135.
 XX 07-JUL-2000; 2000US-0216847.
 XX 07-JUL-2000; 2000US-0216980.
 XX 11-JUL-2000; 2000US-0217487.
 XX 11-JUL-2000; 2000US-0217496.
 XX 14-JUL-2000; 2000US-0218290.
 XX 26-JUL-2000; 2000US-0220963.
 XX 26-JUL-2000; 2000US-0220964.
 XX 14-AUG-2000; 2000US-0224518.
 XX 14-AUG-2000; 2000US-0224519.
 XX 14-AUG-2000; 2000US-0225213.
 XX 14-AUG-2000; 2000US-0225214.
 XX 14-AUG-2000; 2000US-0225266.
 XX 14-AUG-2000; 2000US-0225267.
 XX 14-AUG-2000; 2000US-0225268.
 XX 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 05-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 06-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 25-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 29-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 20-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 08-NOV-2000; 2000US-024617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.

08-NOV-2000; 2000US-0245532.
 08-NOV-2000; 2000US-0246609.
 08-NOV-2000; 2000US-0246610.
 08-NOV-2000; 2000US-0246611.
 08-NOV-2000; 2000US-0246613.
 17-NOV-2000; 2000US-0249207.
 17-NOV-2000; 2000US-0249208.
 17-NOV-2000; 2000US-0249209.
 17-NOV-2000; 2000US-0249210.
 17-NOV-2000; 2000US-0249211.
 17-NOV-2000; 2000US-0249212.
 17-NOV-2000; 2000US-0249213.
 17-NOV-2000; 2000US-0249214.
 17-NOV-2000; 2000US-0249215.
 17-NOV-2000; 2000US-0249216.
 17-NOV-2000; 2000US-0249217.
 17-NOV-2000; 2000US-0249218.
 17-NOV-2000; 2000US-0249244.
 17-NOV-2000; 2000US-0249245.
 17-NOV-2000; 2000US-0249264.
 17-NOV-2000; 2000US-0249265.
 17-NOV-2000; 2000US-0249297.
 17-NOV-2000; 2000US-0249299.
 01-DEC-2000; 2000US-0249300.
 01-DEC-2000; 2000US-0250160.
 01-DEC-2000; 2000US-0250391.
 05-DEC-2000; 2000US-0251030.
 05-DEC-2000; 2000US-0251988.
 06-DEC-2000; 2000US-0256719.
 08-DEC-2000; 2000US-0251479.
 08-DEC-2000; 2000US-0251856.
 08-DEC-2000; 2000US-0251868.
 08-DEC-2000; 2000US-0251869.
 08-DEC-2000; 2000US-0251989.
 11-DEC-2000; 2000US-0251990.
 05-JAN-2001; 2000US-0254097.
 2001US-0259678.
 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-483426/52.
 Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 useful for preventing, diagnosing and/or treating cancers and
 metastasis -
 Disclosure; SEQ ID NO 25777; 3071pp + Sequence Listing; English.
 AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
 activity, and can be used in gene therapy and vaccine production. (I)
 proteins and polynucleotides may be used in the prevention, diagnosis and
 treatment of diseases associated with inappropriate (I) expression. For
 example, they may be used to treat disorders associated with decreased
 expression by rectifying mutations or deletions in a patient's genome
 that affect the activity of (I) by expressing inactive proteins or to
 supplement the patients own production of (I). Additionally, (I)
 polynucleotides may be used to produce the secreted (I), by inserting
 the nucleic acids into a host cell and culturing the cell to express the
 protein. (I) proteins and polynucleotides may be used to prevent,
 diagnose and treat immune/hematopoietic-related diseases, especially
 cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 to AAK87694 represent human immune/hematopoietic antigen genomic
 sequences from the present invention. AAK54942 to AAK54950 and AAK62169
 represent sequences used in the exemplification of the present invention.
 Sequence 11674 BP; 3026 A; 2800 C; 2616 G; 3232 T; 0 other;
 Query Match 84.0%; Score 21; DB 22; Length 11674;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 DB 899 GGTTCAGTGCAGCCGAGATAA 879
 RESULT 14
 AAH48621/C
 ID AAH48621 standard; DNA; 13055 BP.
 XX
 AC AAH48621;
 XX
 DT 20-SEP-2001 (first entry)
 XX
 DE Human fascin DNA fragment #1.
 XX
 KW Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
 KW antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
 KW immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
 KW Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
 KW autoimmune disease; transplant rejection; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200151631-A2.
 XX
 PD 19-JUL-2001.
 XX
 XX
 PF 12-JAN-2001; 2001WO-EP00362.
 XX
 PR 13-JAN-2000; 2000DE-1001169.
 PR 02-MAR-2000; 2000DE-1010188.
 XX
 PA (RESK/) RESKE-KUNZ A.
 PA (ROSS/) ROSS X.
 PA (ROSS/) ROSS R.
 PA (BROS/) BROS M.
 XX
 PI Reske-Kunz A, Ross X, Ross R, Bros M;
 XX
 DR WPI; 2001-451858/48.
 XX
 PT New regulatory sequences from the fascin gene, useful for providing
 PT dendritic cell-specific expression of e.g. antigens, e.g. for
 PT vaccination against tumors and infections
 XX
 PS Example 1; Fig 2; 117pp; German.
 XX
 CC This invention describes novel regulatory sequences (A) derived from
 CC human fascin that provide specific expression in dendritic cells (DC) and
 CC which have antiviral, antibacterial, antifungal, antiparasitic,
 CC anti-allergic, neurological, immunomodulatory and apoptotic activity.
 CC (A) are used to regulate expression of antigens, immunoregulators,
 CC antisense sequences etc. in DC-specific fashion. Recombinant DNA, vectors
 CC and host cells that contain (A) are useful: (i) in vaccines against
 CC Creutzfeld-Jakob and Alzheimer's disease; and (ii) for gene therapy of
 CC tumors, allergies, infections, autoimmune diseases and transplant
 CC rejection. They can also be provide specific expression of antigens and
 CC immunoregulators in DC; for isolation and identification of antigens and
 CC expression; to determine the degree of maturity of DC and to block
 CC transcription factors, by providing binding sites in DC. (A) provide
 CC DC-specific expression of nucleic acid under their control, allowing a
 CC more specific regulation of the immune response and eliminating the long
 CC and laborious purification of DC (since a complete leucocyte population
 CC may be transformed), including transformation in vitro. This sequence
 CC represents a DNA fragment of human fascin which is described in the
 CC invention.
 XX
 SQ Sequence 13055 BP; 2372 A; 3903 C; 4097 G; 2683 T; 0 other;
 Query Match 84.0%; Score 21; DB 22; Length 13055;

Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCGGAGATAA 21
|||||

Db 10885 GGTTCAGTGGCGGAGATAA 10865

RESULT 15

AAH48620/c
ID AAH48620 standard; DNA; 16951 BP.

XX AAH48620;

XX 20-SEP-2001 (first entry)

DE Human fascin DNA fragment SEQ ID 72.

XX Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
KW antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
KW immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
KW Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
KW autoimmune disease; transplant rejection; ds.

XX Homo sapiens.

XX W0200151631-A2.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-EP00362.

XX 13-JAN-2000; 2000DE-1001169.

PR 02-MAR-2000; 2000DE-1010188.

XX (RESK/) RESKE-KUNZ A.

PA (ROSS/) ROSS X.

PA (ROSS/) ROSS R.

PA (BROS/) BROS M.

XX Reske-Kunz A, Ross X, Ross R, Bros M;

XX WPI; 2001-451858/48.

XX New regulatory sequences from the fascin gene, useful for providing
PT dendritic cell-specific expression of e.g. antigens, e.g. for
PT vaccination against tumors and infections

PS Claim 1a; Page 112-117; 117pp; German.

XX This invention describes novel regulatory sequences (A) derived from
CC human fascin that provide specific expression in dendritic cells (DC) and
CC which have antiviral, antibacterial, antifungal, antiparasitic,
CC anti-allergic, neurological, immunomodulatory and apoptotic activity.
CC (A) are used to regulate expression of antigens, immunoregulators,
CC antisense sequences etc. in DC-specific fashion. Recombinant DNA, vectors
CC and host cells that contain (A) are useful: (i) in vaccines against
CC viruses, bacteria, fungi, parasites, tumors, allergens and plaques in
CC Creutzfeld-Jakob and Alzheimer's disease; and (ii) for gene therapy of
CC tumors, allergies, infections, autoimmune diseases and transplant
CC rejection. They can also be provide specific expression of antigens and
CC immunoregulators in DC; for isolation and identification of cell factors
CC and cis-elements from regulatory sequences that mediate DC-specific
CC expression; to determine the degree of maturity of DC and to block
CC transcription factors, by providing binding sites in DC. (A) provide
CC DC-specific expression of nucleic acid under their control, allowing a
CC more specific regulation of the immune response and eliminating the long
CC and laborious purification of DC (since a complete leucocyte population
CC may be transformed), including transformation in vitro. This sequence
CC represents a DNA fragment of human fascin which is described in the
CC invention.

XX Sequence 16951 BP; 3224 A; 4928 C; 5200 G; 3599 T; 0 other;

Query Match 84.0%; Score 21; DB 22; Length 16951;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCGGAGATAA 21
|||||

Db 14594 GGTTCAGTGGCGGAGATAA 14674

RESULT 16

AAH48622/c

ID AAH48622 standard; DNA; 16951 BP.

XX AAH48622;

XX 20-SEP-2001 (first entry)

DE Human fascin DNA fragment #2.

XX Fascin; regulatory sequence; human; dendritic cell; antiviral; tumor;
KW antibacterial; antifungal; antiparasitic; anti-allergic; neurological;
KW immunomodulatory; apoptotic; expression regulator; vaccine; allergen;
KW Creutzfeld-Jakob disease; Alzheimer's disease; gene therapy;
KW autoimmune disease; transplant rejection; ds.

XX Homo sapiens.

XX W0200151631-A2.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-EP00362.

XX 13-JAN-2000; 2000DE-1001169.

PR 02-MAR-2000; 2000DE-1010188.

XX (RESK/) RESKE-KUNZ A.

PA (ROSS/) ROSS X.

PA (ROSS/) ROSS R.

PA (BROS/) BROS M.

XX Reske-Kunz A, Ross X, Ross R, Bros M;

XX WPI; 2001-451858/48.

XX New regulatory sequences from the fascin gene, useful for providing
PT dendritic cell-specific expression of e.g. antigens, e.g. for
PT vaccination against tumors and infections

PS Disclosure; Fig 9; 117pp; German.

XX This invention describes novel regulatory sequences (A) derived from
CC human fascin that provide specific expression in dendritic cells (DC) and
CC which have antiviral, antibacterial, antifungal, antiparasitic,
CC anti-allergic, neurological, immunomodulatory and apoptotic activity.
CC (A) are used to regulate expression of antigens, immunoregulators,
CC antisense sequences etc. in DC-specific fashion. Recombinant DNA, vectors
CC and host cells that contain (A) are useful: (i) in vaccines against
CC viruses, bacteria, fungi, parasites, tumors, allergens and plaques in
CC Creutzfeld-Jakob and Alzheimer's disease; and (ii) for gene therapy of
CC tumors, allergies, infections, autoimmune diseases and transplant
CC rejection. They can also be provide specific expression of antigens and
CC immunoregulators in DC; for isolation and identification of cell factors
CC and cis-elements from regulatory sequences that mediate DC-specific
CC expression; to determine the degree of maturity of DC and to block
CC transcription factors, by providing binding sites in DC. (A) provide
CC DC-specific expression of nucleic acid under their control, allowing a
CC more specific regulation of the immune response and eliminating the long
CC and laborious purification of DC (since a complete leucocyte population
CC may be transformed), including transformation in vitro. This sequence
CC represents a DNA fragment of human fascin which is described in the
CC invention.

```
XX SQ Sequence 16951 BP; 3224 A; 4928 C; 5200 G; 3599 T; 0 other;
Query Match      84.0%; Score 21; DB 22; Length 16951;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGAGCGAGATAA 21
   |||||
Db 14694 GGTTCAGTGGAGCGAGATAA 14674

RESULT 17
AL03002
ID AAL03002 standard; DNA; 19286 BP.
XX AC AAL03002;
XX DT 21-NOV-2001 (first entry)
XX DE Human reproductive system related antigen DNA SEQ ID NO: 5690.
XX KW Human; reproductive system related antigen; reproductive system disorder;
XX KW cancer; gene therapy; ds.
XX OS Homo sapiens.
XX PN W0200155320-A2.
XX PD 02-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01339.
XX PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249210.
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PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
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PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 02-OCT-2000; 2000US-0237038.
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PR 13-OCT-2000; 2000US-0239935.
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PR 20-OCT-2000; 2000US-0240960.
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PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
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PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
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PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
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PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
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PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
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PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 05-DEC-2000; 2000US-0250391.
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PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483232/52.

Nucleic acids encoding 973 human testicular antigen polypeptides,

PT useful for preventing, diagnosing and/or treating testicular cancer -
XX Disclosure; SEQ ID NO 2001; 766pp; English.
XX
CC The present invention provides the protein and coding sequences of 973
CC human testicular antigens, and fragments of their genomic sequences. The
CC sequences can be used in the treatment of cardiovascular, urinary system,
CC reproductive system, immune, respiratory, neurological and
CC gastrointestinal disorders, infections, and particularly cancer,
CC especially testicular cancers. The present sequence is a DNA encoding a
CC protein fragment of the invention.
XX
SQ Sequence 19286 BP; 4918 A; 4223 C; 4758 G; 5387 T; 0 other;

Query Match 84.0%; Score 21; DB 23; Length 19286;
Best Local Similarity 100.0%; Pred. NO. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCGGAGATAA 21
Db 5393 GGTTCAGTGGCGGAGATAA 5413
|||||

RESULT 19
ABAL7961
ID ABAL7961 standard; DNA; 26149 BP.
XX
AC ABAL7961;

DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polynucleotide SEQ ID NO 10292.
XX

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
antiparasitic; cardiac; immune disorder; cardiovascular disorder;
neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.

OS Homo sapiens.
XX
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.

17-JAN-2001; 2001WO-US01334.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
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PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 14-AUG-2000; 2000US-0224518.
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 PR 02-OCT-2000; 2000US-0237040.
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 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
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 PR 08-NOV-2000; 2000US-0246526.

PR 08-NOV-2000; 2000US-0246527.
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 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250391.
 PR 01-DEC-2000; 2000US-0251160.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 XX 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 WPI; 2001-541565/60.
 DR Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 XX Disclosure; SEQ ID NO 10292; 1701pp + Sequence Listing; English.
 PS The invention relates to novel genes (ABA11004-ABA21534) and proteins
 XX (AB14678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 28149 BP; 7151 A; 6467 C; 6967 G; 7564 T; 0 other;

Query Match 84.0%; Score 21; DB 22; Length 28149;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
 Db 2876 GGTTCAGTGGCCGAGATAA 2896

RESULT 20
 AAK82759/c

ID AAK82759 standard; DNA; 30360 BP.

XX AC AAK82759;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37571.
 DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytotatic; gene therapy; vaccine; metastasis; ds.
 XX OS Homo sapiens.

XX WO200157182-A2.

PN 09-AUG-2001.

PD 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
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 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
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 PR 25-SEP-2000; 2000US-0234997.
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 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 13-OCT-2000; 2000US-0237040.
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 PR 20-OCT-2000; 2000US-0239937.
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 PR 20-OCT-2000; 2000US-0241221.
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 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 08-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
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 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
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PR 17-NOV-2000; 2000US-0249244.
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 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
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 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
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 PR 08-DEC-2000; 2000US-0251868.
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 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0254097.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 PI
 XX WPI; 2001-483426/52.
 DR
 XX
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.
 XX
 PS Disclosure; SEQ ID NO 37571; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 XX
 SQ Sequence 30360 BP; 8943 A; 5665 C; 6045 G; 9707 T; 0 other;
 Query Match 84.0%; Score 21; DB 22; Length 30360;
 Best Local Similarity 100.0%; Pred. No. 0.0051;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGGCCGAGATAA 21
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 Db 14433 GGTTCAGTGGCCGAGATAA 14413
 RESULT 21
 ABAL7963
 ID ABAL7963 standard; DNA; 32192 BP.
 XX
 AC
 AC ABAL7963;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Human nervous system related polynucleotide SEQ ID NO 10294.
 XX
 XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;

KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulneryary;
 KW antiparkinsonian; antispickling; antianaemic; antiarthritis; cancer;
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200159063-A2.
 PN
 PN
 XX
 PD 16-AUG-2001.
 XX
 XX
 PF 17-JAN-2001; 2001WO-US01334.
 XX

PR 31-JAN-2000; 2000US-0179065.
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PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
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PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.

PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX
PS Disclosure; SEQ ID NO 10294; 1701pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB14678-AB18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 32192 BP; 7965 A; 7802 C; 8055 G; 8370 T; 0 other;
Query Match 84.0%; Score 21; DB 22; Length 32192;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
|||||
Db 2876 GGTTCAGTGGCCGAGATAA 2896

RESULT 22
AAS98633
ID AAS98633 standard; DNA; 38258 BP.
XX
AC AAS98633;
XX
DT 26-MAR-2002 (first entry)
XX
DE DNA encoding Colony stimulating factor 1 receptor (CSF1R).
XX
KW Colony stimulating factor 1 receptor; CSF1R; polymorphic variant;
KW cytosolic; gene therapy; malignant histiocytosis; isogene;
KW myeloid malignancy; inflammatory disorder; transgenic animal;
XX haplotype; genotype; human; chromosome 5q33-35; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation 867
FT /*tag= a
FT /standard_name= "Single nucleotide polymorphism"
FT variation 875
FT /*tag= b
FT /standard_name= "Single nucleotide polymorphism"
FT variation 1022

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FT      /*tag= c
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FT      /tag= d
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FT      1591
FT      /tag= g
FT      /standard_name= "Single nucleotide polymorphism"
FT      1617
FT      /tag= h
FT      /standard_name= "Single nucleotide polymorphism"
FT      1810
FT      /tag= i
FT      /standard_name= "Single nucleotide polymorphism"
FT      1916..34258
FT      /tag= j
FT      /standard_name= "Single nucleotide polymorphism"
FT      /product= "CSFIR"
FT      /note= "Colony stimulating factor 1 receptor. Coding
FT      sequence is specifically claimed in claim 24."
FT      1916..1964
FT      /tag= k
FT      /number= 1
FT      1965..7315
FT      /tag= l
FT      /number= 1
FT      2015
FT      /tag= m
FT      /standard_name= "Single nucleotide polymorphism"
FT      2043
FT      /tag= n
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /number= 2
FT      7348
FT      /tag= p
FT      /standard_name= "Single nucleotide polymorphism"
FT      7532
FT      /tag= q
FT      /standard_name= "Single nucleotide polymorphism"
FT      7546
FT      /tag= r
FT      /standard_name= "Single nucleotide polymorphism"
FT      7558
FT      /tag= s
FT      /standard_name= "Single nucleotide polymorphism"
FT      7572..8001
FT      /tag= t
FT      /number= 2
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FT      /tag= u
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FT      8062
FT      /tag= v
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= w
FT      /standard_name= "Single nucleotide polymorphism"
FT      8287..10089
FT      /tag= x
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FT      8327
FT      /tag= y
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /standard_name= "Single nucleotide polymorphism"
FT      1060
FT      /tag= aa
FT      /standard_name= "Single nucleotide polymorphism"
FT      10082
FT      /tag= ab
FT      /standard_name= "Single nucleotide polymorphism"
FT      10090..10226
FT      /tag= ac
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FT      10218
FT      /tag= ad
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= ae
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= ai
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FT      /standard_name= "Single nucleotide polymorphism"
FT      11207
FT      /tag= ao
FT      /standard_name= "Single nucleotide polymorphism"
FT      14843..15035
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FT      /number= 6
FT      15036..17765
FT      /tag= aq
FT      /number= 6
FT      15068
FT      /tag= ar
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= at
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= av
FT      /number= 7
FT      17768
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FT      /standard_name= "Single nucleotide polymorphism"
FT      17882..18034
FT      /tag= ax
FT      /number= 7
FT      18035..18155

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FT      /*tag= ba
FT      intron 18465..20006
FT      /*tag= bb
FT      exon   20007..20122
FT      /*tag= bc
FT      intron 20123..26477
FT      /*tag= bd
FT      /number= 10
FT      variation 20125
FT      /*tag= be
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation 20129
FT      /*tag= bf
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation 20134
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FT      /standard_name= "Single nucleotide polymorphism"
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FT      variation 20272
FT      /*tag= bi

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Query Match      84.0%; Score 21; DB 24; Length 38258;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGTTCAGTGAGCCGAGATAA 21
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Db 37789 GGTTCAGTGAGCCGAGATAA 37809

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RESULT 23
AAZ23903
ID AAZ23903 standard; DNA; 49999 BP.
XX AC
XX AAZ23903;
XX
XX 25-JAN-2000 (first entry)
XX Human LOBO homologue genomic DNA fragment 5.
XX
XX LOBO; long bones; bone development; bone extension; skull; osteopathic;
XX diagnostic; pharmaceutical; gene therapy; transgenic animal; disease;
XX spondyloepiphyseal dysplasia; achondroplasia; human; ds.
XX
XX Homo sapiens.
XX
XX WO9950284-A2.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-EP02055.
XX
XX 27-MAR-1998; 98DE-1013799.
XX
XX (ROSE/) ROSENTHAL A.
XX
XX Rosenthal A, Rump A, Hess J, Aigner T, Wirth J;
XX WPI; 1999-601320/51.
XX
XX Nucleic acids encoding proteins which influence bone development,
XX useful for treating and studying bone disorders -

```

```

XX
PS Example 3; Page 328-356; 391pp; German.
XX
CC This invention describes novel nucleic acids (I; designated LOBO (long
CC bones)) encoding proteins influencing bone development in mammals. The
CC proteins of the invention reduce and/or inactivate bone extension (i.e.
CC development), with exception of the skull and have osteopathic activity.
CC The nucleic acid molecules, proteins and antibodies can be used in
CC diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods
CC and nucleic acid molecules, etc. are useful for production of transgenic
CC animals, especially a transgenic mouse for the study of diseases
CC associated with bone development, e.g. spondyloepiphyseal dysplasia and
CC achondroplasia. This sequence encodes a human LOBO protein described
CC in the method of the invention.
XX
SQ Sequence 49999 BP; 10983 A; 13723 C; 13439 G; 11854 T; 0 other;

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Query Match      84.0%; Score 21; DB 20; Length 49999;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGTTCAGTGAGCCGAGATAA 21
    |||||
Db 30972 GGTTCAGTGAGCCGAGATAA 30992

```

```

RESULT 24
AAC15906/c
ID AAC15906 standard; cDNA; 95 BP.
XX AC
XX AAC15906;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 19981.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-0200610.
XX
XX 26-FEB-1999; 99US-0122487.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 1; SEQ ID 19981; 71pp + CD-ROM; English.

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XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX in diagnostic, forensic, gene therapy and chromosome mapping procedures.

```

CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.

SQ Sequence 95 BP; 11 A; 29 C; 21 G; 34 T; 0 other;

Query Match 80.0%; Score 20; DB 21; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCGAGTGCAGGAGATA 20
|||||
Db 90 GGTTCGAGTGCAGGAGATA 71

RESULT 25

AAK81714/C
ID AAK81714 standard: DNA; 171 BP.

XX AAK81714;

XX 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36526.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosstatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

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XX 28-JUN-2000; 2000US-0214886.

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XX 07-JUL-2000; 2000US-0216880.

XX 11-JUL-2000; 2000US-0217487.

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XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

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XX 14-AUG-2000; 2000US-0225214.

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XX 14-AUG-2000; 2000US-0225758.

XX 18-AUG-2000; 2000US-0225759.

XX 22-AUG-2000; 2000US-0226279.

XX 22-AUG-2000; 2000US-0226681.

XX 22-AUG-2000; 2000US-0226868.

XX 23-AUG-2000; 2000US-0227182.

XX 30-AUG-2000; 2000US-0227009.

XX 01-SEP-2000; 2000US-0228924.

XX 01-SEP-2000; 2000US-0229287.

XX 01-SEP-2000; 2000US-0229343.

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PR 01-NOV-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-0244617.
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 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249284.
 PR 17-NOV-2000; 2000US-0249285.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 08-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Disclosure; SEQ ID NO 36526; 3071pp + Sequence Listing; English.
 PS
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC the nucleic acids may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to prevent
 CC protein. (I) proteins and polynucleotides may be used to prevent
 CC cancers and treat immune/hematopoietic-related diseases, especially
 CC to AAK67694 represent human immune/hematopoietic-derived cells. AAK64703
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 171 BP; 28 A; 52 C; 39 G; 52 T; 0 other;

Query Match 80.0%; Score 20; DB 22; Length 171;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCAGTGGCGGAGATAA 21
 |||||
 Db 79 GTTCAGTGGCGGAGATAA 60

RESULT 26
 AAK83823
 ID AAK83823 standard; DNA; 172 BP.
 XX
 AC AAK83823;
 XX

DT 07-NOV-2001 (first entry)
 XX Human immune/hematopoietic antigen genomic sequence SEQ ID NO:38635.
 DE Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;
 XX cytostatic; gene therapy; vaccine; metastasis; ds.
 KW Homo sapiens.
 KW
 OS WO200157182-A2.
 XX
 PN 09-AUG-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01354.
 XX 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.

PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0241826.
PR 08-NOV-2000; 2000US-024617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249267.
PR 17-NOV-2000; 2000US-0249268.
PR 17-NOV-2000; 2000US-0249269.
PR 17-NOV-2000; 2000US-0249270.
PR 17-NOV-2000; 2000US-0249271.
PR 17-NOV-2000; 2000US-0249272.
PR 17-NOV-2000; 2000US-0249273.
PR 17-NOV-2000; 2000US-0249274.
PR 17-NOV-2000; 2000US-0249275.
PR 17-NOV-2000; 2000US-0249276.
PR 17-NOV-2000; 2000US-0249277.
PR 17-NOV-2000; 2000US-0249278.
PR 17-NOV-2000; 2000US-0249279.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251368.
PR 05-DEC-2000; 2000US-0251369.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and
XX metastasis.
XX Disclosure; SEQ ID NO 38635; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting
XX the nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK34942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention.
XX SQ Sequence 172 BP; 56 A; 38 C; 49 G; 29 T; 0 other;
Query Match 80.0%; Score 20; DB 22; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGCAGCCGAGATA 20
Db 81 GGTTCAGTGCAGCCGAGATA 100
RESULT 27
AAC11950/c
ID AAC11950 standard; cDNA; 180 BP.
XX AAC11950;
XX AAC11950;
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 16025.
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX EP1033401-A2.
XX 06-SEP-2000.
XX 21-FEB-2000; 2000EP-0200610.
XX 26-FEB-1999; 99US-0122487.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI

XX WPI; 2000-500381/45.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 16025; 71pp + CD-ROM; English.
 XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX Sequence 180 BP; 42 A; 59 C; 52 G; 27 T; 0 other;
 SQ
 Query Match 80.0%; Score 20; DB 21; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 83 GGTTCAGTGCAGCCGAGATA 64
 RESULT 28
 AAC04572/c
 ID AAC04572 standard; cDNA; 193 BP.
 XX AAC04572;
 AC
 XX 06-OCT-2000 (first entry)
 DE Human secreted protein 5' EST, SEQ ID NO: 8647.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 FN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-0200610.
 PF
 XX 26-FEB-1999; 99US-0122487.
 PR
 XX (GEST) GENSET.
 PA
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 8647; 71pp + CD-ROM; English.
 XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from

CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX Sequence 193 BP; 37 A; 41 C; 50 G; 65 T; 0 other;
 SQ
 Query Match 80.0%; Score 20; DB 21; Length 193;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 155 GGTTCAGTGCAGCCGAGATA 136
 RESULT 29
 AAI68895/c
 ID AAI68895 standard; DNA; 205 BP.
 XX AAI68895;
 AC
 XX 29-JAN-2002 (first entry)
 DT
 XX Activated T-cell derived DNA fragment #31.
 DE
 XX Activated T-cell; immunosuppressive; immunostimulant; antiinflammatory;
 KW cytostatic; gene therapy; vaccine; allergen; transplant rejection;
 KW guest versus host disease; malignant disease; ds.
 XX Homo sapiens.
 OS
 XX DE10021834-A1.
 FN
 XX 15-NOV-2001.
 PD
 XX 06-MAY-2000; 2000DE-1021834.
 PF
 XX 06-MAY-2000; 2000DE-1021834.
 PR
 XX (LYNX-) LYNX THERAPEUTICS GMBH.
 PA
 XX Kramer MD, Winter H, Reinartz J;
 PI WPI; 2002-027320/04.
 DR
 XX New mRNA indicative of T cell activation and functional status, useful
 PT for diagnosis and therapy e.g. of autoimmunity or transplant rejection
 PT
 XX Claim 1; Page 17; 94pp; German.
 XX
 XX This sequence represents a novel messenger RNA, (mRNA), (I), for use as
 CC indicator of the activation and functional status of T cells, that have
 CC increased or reduced expression, and are present at higher or lower
 CC concentration, in activated T cells, relative to normal or resting cells,
 CC where (I) hybridizes to any of 334 sequences, reproduced, or their
 CC derivatives, complements or fragments. The products of the invention
 CC have immunosuppressive, immunostimulant, antiinflammatory and cytostatic
 CC activity and can be used for gene therapy. The polynucleotides of the
 CC invention are used: (i) as reagent for detecting activation/functional
 CC status of T cells, for diagnosis, therapy, modulation or control of the
 CC status, in cases of (auto)immunity (against microorganisms, vaccines or
 CC allergens); transplant rejection; immunologically-related inflammation;
 CC immunosuppression; immune deficiency; guest versus host disease, and
 CC malignant diseases of the immune system; (ii) for identifying agents,

CC potential pharmaceuticals, that bind to (II) or derived polypeptides
 CC (III); (iii) to prepare kits for measuring gene expression profiles in
 CC isolated immune, especially T, cells; (iv) to raise antibodies (Ab)
 CC directed against (III); and (v) to prepare binding molecules (IV)
 CC specific for (II). Ab and (IV) are also useful for detecting and
 CC modulating the activation and functional status of T cells.
 CC AAI6865-AA169198 represent the activated T-cell derived polynucleotide
 CC fragments described in the method of the invention.

XX SQ Sequence 205 BP; 37 A; 54 C; 55 G; 59 T; 0 other;

Query Match 80.0%; Score 20; DB 24; Length 205;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 64 GGTTCAGTGCAGCCGAGATA 45

RESULT 30

AAC32484/c
 ID AAC32484 standard; cDNA; 236 BP.

XX AAC32484;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 36559.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 36559; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

SQ Sequence 236 BP; 58 A; 47 C; 55 G; 76 T; 0 other;

Query Match 80.0%; Score 20; DB 21; Length 236;

Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 96 GGTTCAGTGCAGCCGAGATA 77

RESULT 31

AAC04849/c

ID AAC04849 standard; cDNA; 304 BP.

XX AAC04849;

DT 06-OCT-2000 (first entry)

DE Human secreted protein 5' EST, SEQ ID NO: 8924.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

PF 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 8924; 71pp + CD-ROM; English.

XX The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.

SQ Sequence 304 BP; 45 A; 80 C; 77 G; 90 T; 12 other;

Query Match 80.0%; Score 20; DB 21; Length 304;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
 |||||
 Db 87 GGTTCAGTGCAGCCGAGATA 68

RESULT 32

AAH68890

ID AAH68890 standard; cDNA; 320 BP.

XX

```

AC AAH68890;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human cervical cancer marker nucleic acid 164.
XX
KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200142467-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US33312.
XX
PR 08-DEC-1999; 99US-0169681.
XX
PR 21-DEC-1999; 99US-0171350.
XX
PR 14-MAR-2000; 2000US-0189315.
XX
PR 12-MAY-2000; 2000US-0203791.
XX
PR 09-JUN-2000; 2000US-0210600.
XX
PR 21-JUL-2000; 2000US-0220114.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Deeds J, Berger A, Zhao X;
XX
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer
PT and for assessing and detecting compounds for treating the cancer -
XX
PS Claim 1; Page 131; 1051pp; English.
XX
CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.
XX
SQ Sequence 320 BP; 96 A; 67 C; 86 G; 71 T; 0 other;

Query Match 80.0%; Score 20; DB 22; Length 320;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
    |||||
Db 226 GGTTCAGTGCAGCCGAGATA 245

RESULT 33
AAH70549
ID AAH70549 standard; cDNA; 329 BP.
XX
AC AAH70549;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human cervical cancer marker nucleic acid 1823.
XX
KW Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200142467-A2.
XX
PD 14-JUN-2001.
XX
PF 08-DEC-2000; 2000WO-US33312.

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XX
PR 08-DEC-1999; 99US-0169681.
PR 21-DEC-1999; 99US-0171350.
PR 14-MAR-2000; 2000US-0189315.
PR 12-MAY-2000; 2000US-0203791.
PR 09-JUN-2000; 2000US-0210600.
PR 21-JUL-2000; 2000US-0220114.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Deeds J, Berger A, Zhao X;
XX
XX WPI; 2001-375006/39.
XX
XX New isolated nucleic acid for diagnosing and treating cervical cancer
PT and for assessing and detecting compounds for treating the cancer -
XX
PS Claim 1; Page 394; 1051pp; English.
XX
CC The invention relates to novel genes (AAH68727-AAH73383) associated with
CC cervical cancer with cytostatic activity. The nucleic acids and encoded
CC polypeptides are useful: to assess if a patient is afflicted with
CC cervical cancer or has a pre-malignant condition; to monitor the
CC progression of cervical cancer or a premalignant condition in a patient;
CC and to select and/or assess the efficacy of a compound or therapy for
CC inhibiting cervical cancer in a patient. The nucleic acids may also be
CC useful for gene therapy.
XX
SQ Sequence 329 BP; 99 A; 68 C; 88 G; 74 T; 0 other;

Query Match 80.0%; Score 20; DB 22; Length 329;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
    |||||
Db 235 GGTTCAGTGCAGCCGAGATA 254

RESULT 34
AAH87614
ID AAH87614 standard; cDNA; 335 BP.
XX
AC AAH87614;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 7674.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
XX
XX P-PSDB; AAO07683.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing

```

PT diagnosing and treating e.g. leukaemia, inflammation and immune
 XX disorders -
 PS Claim 1; SEQ ID NO 7674; 1399pp + Sequence Listing; English.
 XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 335 BP; 117 A; 54 C; 84 G; 79 T; 1 other;

Query Match 80.0%; Score 20; DB 22; Length 335;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 11 GGTTCAGTGCAGCCGAGATA 30
 |||

RESULT 35
 ABL79179/c
 ID ABL79179 standard; cDNA; 384 BP.

XX
 AC ABL79179;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human ovarian cancer related cDNA clone SEQ ID NO:2157.
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 PN WO200192581-A2.
 XX
 PD 06-DEC-2001.

XX
 PF 29-MAY-2001; 2001WO-US17756.
 XX
 PR 26-MAY-2000; 2000US-207484P.
 XX
 PA (CORI-) CORIXA CORP.

PI Algate PA, Harlocker SL, Jones R;
 XX
 DR WPI: 2002-122075/16.
 XX

PT Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 XX polypeptide -

PS Claim 1; SEQ ID 2157; 489pp; English.

XX
 CC The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence
 CC (SI) from the 10912 nucleotide sequences as given in ABL77023 to
 CC ABL87934, (III) encoding (II) having a sequence (S2), a T cell
 CC population of (II), or antigen presenting cells that express (II).
 CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to

CC (SI) can be used for detecting ovarian cancer in a patient's biological
 CC sample preferably serum or ovarian tissue. The method comprises
 CC contacting a biological sample from a patient with (IV), detecting the
 CC amount of polynucleotide hybridising to (IV) and comparing the amount to
 CC a predetermined cutoff value and thereby detecting ovarian cancer in the
 CC patient, where the amount of polynucleotide hybridising to (IV) is
 CC detected preferably by polymerase chain reaction (PCR). (I) comprising
 CC (III) and/or (II) is useful for stimulating and/or expanding T cells
 CC specific for an ovarian tumour protein comprising contacting T cells
 CC with (III) or (II). (III) is useful in design and preparation of
 CC ribozyme molecules for inhibiting expression of the tumour polypeptides
 CC and proteins in tumour cells; and to isolate a full length gene from a
 CC suitable library e.g., a tumour cDNA library using well known
 CC techniques.

XX
 SQ Sequence 384 BP; 90 A; 102 C; 89 G; 100 T; 3 other;

Query Match 80.0%; Score 20; DB 24; Length 384;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 70 GGTTCAGTGCAGCCGAGATA 51
 |||

RESULT 36
 AAI82847
 ID AAI82847 standard; cDNA; 388 BP.

XX
 AC AAI82847;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 2907.

XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation; ss.

OS Homo sapiens.
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.

XX
 PF 26-FEB-2001; 2001WO-US04927.

XX
 PR 28-FEB-2000; 2000US-0515126.
 XX
 PR 18-MAY-2000; 2000US-0577409.

XX
 PA (HYSE-) HYSEQ INC.

XX
 PI Tang YT, Liu C, Drmanac RT;

XX
 DR WPI: 2001-514838/56.
 XX
 DR P-PSDB; AAO2916.

XX
 PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX
 PS Claim 1; SEQ ID NO 2907; 1399pp + Sequence Listing; English.

XX
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and

CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 388 BP; 94 A; 52 C; 63 G; 179 T; 0 other;

Query Match 80.0%; Score 20; DB 22; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATA 20
|||||
DB 55 GGTTCAGTGCAGCGAGATA 74

RESULT 37

ABV16660
ID ABV16660 standard; cDNA; 425 BP.

XX AC ABV16660;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 16651.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.

XX OS Homo sapiens.

XX PN WO200160860-A2.

XX PD 23-AUG-2001.

XX PF 20-FEB-2001; 2001WO-US05171.

XX PR 17-FEB-2000; 2000US-183319P.

XX PR 16-MAR-2000; 2000US-189862P.

XX PR 25-MAY-2000; 2000US-207454P.

XX PR 09-JUN-2000; 2000US-211314P.

XX PR 18-JUL-2000; 2000US-219007P.

XX PR 13-DEC-2000; 2000US-255281P.

XX FA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Schlegel R, Endege WO, Monahan JE;

XX PS WPI; 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -

XX Claim 1; Page 2775; 11/750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:

CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or incidence of prostate cancer in a
CC patient;

CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX SQ Sequence 425 BP; 150 A; 96 C; 92 G; 87 T; 0 other;

Query Match 80.0%; Score 20; DB 23; Length 425;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATA 20
|||||
DB 198 GGTTCAGTGCAGCGAGATA 217

RESULT 38

AAI83705

ID AAI83705 standard; cDNA; 428 BP.

XX AC AAI83705;

XX DT 06-NOV-2001 (first entry)

XX DE Human polynucleotide SEQ ID NO 3765.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR P-PSDB; AAO03774.

XX PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -

XX PS Claim 1; SEQ ID NO 3765; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.

XX CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 428 BP; 108 A; 102 C; 130 G; 86 T; 2 other;

Query Match 80.0%; Score 20; DB 22; Length 428;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATA 20

```

Db      34  GGTTCAGTGGCCGAGATA 53
|||||
RESULT 39
ABV49562
ID      ABV49562 standard; cDNA; 436 BP.
XX
XX
XX
XX      ABV49562;
AC
DT      17-SEP-2002 (first entry)
XX
XX      Human prostate expression marker cDNA 49553.
DE
XX
XX
XX      Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW      pharmacogenomic marker; gene; ss.
XX
XX      Homo sapiens.
OS
XX      WO200160860-A2.
PN
XX      23-AUG-2001.
PD
XX      20-FEB-2001; 2001WO-US05171.
PF
XX      17-FEB-2000; 2000US-183319P.
PR
XX      16-MAR-2000; 2000US-189862P.
PR
XX      25-MAY-2000; 2000US-207454P.
PR
XX      09-JUN-2000; 2000US-211314P.
PR
XX      18-JUL-2000; 2000US-219007P.
PR
XX      13-DEC-2000; 2000US-255281P.
XX
XX      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
XX      Schlegel R, Endege WO, Monahan JE;
PI
XX      WPI; 2001-662795/76.
DR
XX
XX      Novel isolated nucleic acid molecule associated with cancerous state of
PT      prostate cells and correlating with presence of prostate cancer, useful
PT      for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX      Claim 1; Page 9674; 11750pp; English.
CC
CC      The invention relates to an isolated nucleic acid molecule (I) comprising
CC      a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC      specification or its complement. (I) is useful for:
CC      (a) assessing whether a patient is afflicted with prostate cancer;
CC      (b) monitoring the progression of prostate cancer in a patient;
CC      (c) assessing the efficacy of a test compound to inhibit prostate
CC      cancer in a patient;
CC      (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC      in a patient;
CC      (e) selecting a composition for inhibiting prostate cancer in a patient;
CC      (f) assessing the prostate cell carcinogenic potential of a compound;
CC      (g) determining whether prostate cancer has metastasized in a patient;
CC      (h) assessing the aggressiveness or indolence of prostate cancer in a
CC      patient;
CC      (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX      Sequence 436 BP; 138 A; 102 C; 122 G; 74 T; 0 other;
SQ
Query Match      80.0%; Score 20; DB 23; Length 436;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTTCAGTGGCCGAGATA 20
|||||
Db      232  GGTTCAGTGGCCGAGATA 251
|||||
RESULT 40
ABQ89507/c
ID      AAK62995 standard; cDNA; 451 BP.
XX
XX      AAK62995;
AC
XX
XX      06-NOV-2001 (first entry)
DT
XX
XX      Human immune/hematopoietic antigen encoding cDNA SEQ ID NO:8055.
DE

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```

ID      ABQ89507 standard; cDNA; 436 BP.
XX
XX      ABQ89507;
AC
XX      27-SEP-2002 (first entry)
DT
XX
XX      Human prostate expressed polynucleotide SEQ ID NO 763.
DE
XX      Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy;
KW      gene; ss.
XX
XX      Homo sapiens.
OS
XX      WO200255700-A2.
PN
XX      18-JUL-2002.
PD
XX      07-DEC-2001; 2001WO-US47349.
PF
XX      07-DEC-2000; 2000US-254648P.
PR
XX      13-MAR-2001; 2001US-275688P.
PR
XX      (CHIR ) CHIRON CORP.
PA      (HYSE-) HYSEQ INC.
XX
XX      Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
PI      Ctkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D;
PI      Kita D, Garcia V, Jones WL, Stache-Crain B, Scott EM;
XX      WPI; 2002-557824/59.
DR
XX
XX      New genes and gene products isolated from human prostate, useful for
PT      treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
PT      cancer), or as vaccines for treating or preventing these diseases.
XX
XX      Claim 1; SEQ ID NO 763; 186pp + Sequence Listing; English.
CC
CC      The invention relates to an isolated polynucleotide comprising any of
CC      1477 sequences or its fragment, degenerate variant, antisense or
CC      complement. The polynucleotides and gene products are useful for treating
CC      or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer,
CC      lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs,
CC      cats, rabbits, horse or human). The polynucleotides and polypeptides are
CC      also useful as vaccines for treating or preventing these diseases. The
CC      polynucleotides are useful for gene therapy. The present sequence is that
CC      of one of a group of polynucleotides (ABQ88745-ABQ90015) disclosed
CC      electronically as sequences of the invention. However only 1271
CC      polynucleotide sequences are given, whereas 1477 polynucleotides and 91
CC      proteins are claimed.
CC      Note: The sequence data for this patent did not form part of the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequence.
XX
XX      Sequence 436 BP; 92 A; 89 C; 93 G; 129 T; 33 other;
SQ
Query Match      80.0%; Score 20; DB 24; Length 436;
Best Local Similarity 100.0%; Pred. NO. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GGTTCAGTGGCCGAGATA 20
|||||
Db      278  GGTTCAGTGGCCGAGATA 259
|||||
RESULT 41
AAK62995/c
ID      AAK62995 standard; cDNA; 451 BP.
XX
XX      AAK62995;
AC
XX
XX      06-NOV-2001 (first entry)
DT
XX
XX      Human immune/hematopoietic antigen encoding cDNA SEQ ID NO:8055.
DE

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XX	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;	PR	21-SEP-2000; 2000US-0234274.
KW	cytostatic; gene therapy; vaccine; metastasis; ss.	PR	25-SEP-2000; 2000US-0234997.
KW	Homo sapiens.	PR	25-SEP-2000; 2000US-0234998.
OS		PR	26-SEP-2000; 2000US-0235484.
PN		PR	27-SEP-2000; 2000US-0235834.
XX		PR	27-SEP-2000; 2000US-0235836.
XX		PR	29-SEP-2000; 2000US-0236327.
PD		PR	29-SEP-2000; 2000US-0236367.
XX		PR	29-SEP-2000; 2000US-0236368.
XX		PR	29-SEP-2000; 2000US-0236369.
XX		PR	29-SEP-2000; 2000US-0236370.
PF		PR	02-OCT-2000; 2000US-0236802.
XX		PR	02-OCT-2000; 2000US-0237037.
PR		PR	02-OCT-2000; 2000US-0237038.
PR		PR	02-OCT-2000; 2000US-0237039.
PR		PR	02-OCT-2000; 2000US-0237040.
PR		PR	13-OCT-2000; 2000US-0239935.
PR		PR	13-OCT-2000; 2000US-0239937.
PR		PR	20-OCT-2000; 2000US-0240960.
PR		PR	20-OCT-2000; 2000US-0241221.
PR		PR	20-OCT-2000; 2000US-0241785.
PR		PR	20-OCT-2000; 2000US-0241786.
PR		PR	20-OCT-2000; 2000US-0241787.
PR		PR	20-OCT-2000; 2000US-0241808.
PR		PR	20-OCT-2000; 2000US-0241809.
PR		PR	20-OCT-2000; 2000US-0241826.
PR		PR	01-NOV-2000; 2000US-0244617.
PR		PR	08-NOV-2000; 2000US-0246474.
PR		PR	08-NOV-2000; 2000US-0246475.
PR		PR	08-NOV-2000; 2000US-0246476.
PR		PR	08-NOV-2000; 2000US-0246477.
PR		PR	08-NOV-2000; 2000US-0246478.
PR		PR	08-NOV-2000; 2000US-0246523.
PR		PR	08-NOV-2000; 2000US-0246524.
PR		PR	08-NOV-2000; 2000US-0246525.
PR		PR	08-NOV-2000; 2000US-0246526.
PR		PR	08-NOV-2000; 2000US-0246527.
PR		PR	08-NOV-2000; 2000US-0246528.
PR		PR	08-NOV-2000; 2000US-0246532.
PR		PR	08-NOV-2000; 2000US-0246609.
PR		PR	08-NOV-2000; 2000US-0246610.
PR		PR	08-NOV-2000; 2000US-0246611.
PR		PR	08-NOV-2000; 2000US-0246613.
PR		PR	17-NOV-2000; 2000US-0249207.
PR		PR	17-NOV-2000; 2000US-0249208.
PR		PR	17-NOV-2000; 2000US-0249209.
PR		PR	17-NOV-2000; 2000US-0249210.
PR		PR	17-NOV-2000; 2000US-0249211.
PR		PR	17-NOV-2000; 2000US-0249212.
PR		PR	17-NOV-2000; 2000US-0249213.
PR		PR	17-NOV-2000; 2000US-0249214.
PR		PR	17-NOV-2000; 2000US-0249215.
PR		PR	17-NOV-2000; 2000US-0249216.
PR		PR	17-NOV-2000; 2000US-0249217.
PR		PR	17-NOV-2000; 2000US-0249218.
PR		PR	17-NOV-2000; 2000US-0249244.
PR		PR	17-NOV-2000; 2000US-0249245.
PR		PR	17-NOV-2000; 2000US-0249264.
PR		PR	17-NOV-2000; 2000US-0249265.
PR		PR	17-NOV-2000; 2000US-0249297.
PR		PR	17-NOV-2000; 2000US-0249299.
PR		PR	17-NOV-2000; 2000US-0249300.
PR		PR	01-DEC-2000; 2000US-0250160.
PR		PR	01-DEC-2000; 2000US-0250391.
PR		PR	05-DEC-2000; 2000US-0251030.
PR		PR	05-DEC-2000; 2000US-0251988.
PR		PR	05-DEC-2000; 2000US-0256719.
PR		PR	06-DEC-2000; 2000US-0251479.
PR		PR	08-DEC-2000; 2000US-0251856.
PR		PR	08-DEC-2000; 2000US-0251868.
PR		PR	08-DEC-2000; 2000US-0251869.
PR		PR	08-DEC-2000; 2000US-0251989.
PR		PR	08-DEC-2000; 2000US-0251990.

PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI: 2001-483426/52.
 DR P-PSDB; AAM90214.
 XX
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 XX
 PS Claim 1; SEQ ID NO 8055; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 451 BP; 91 A; 93 C; 107 G; 154 T; 6 other;

Query Match 80.0%; Score 20; DB 22; Length 451;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 284 GGTTCAGTGCAGCCGAGATA 265
 XXXXXXXXXXXXXXXXXXXXXXX

RESULT 42
 ABV45555/C
 ID ABV45555 standard; cDNA; 459 BP.
 XX
 AC ABV45555;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 45546.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 9009; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 459 BP; 98 A; 113 C; 113 G; 135 T; 0 other;

Query Match 80.0%; Score 20; DB 23; Length 459;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCAGTGCAGCCGAGATA 20
 DB 158 GGTTCAGTGCAGCCGAGATA 139
 XXXXXXXXXXXXXXXXXXXXXXX

RESULT 43
 ABV47512
 ID ABV47512 standard; cDNA; 472 BP.
 XX
 AC ABV47512;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 47503.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX

PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 9340-9341; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 472 BP; 157 A; 116 C; 103 G; 96 T; 0 other;

Query Match 80.0%; Score 20; DB 23; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
Db 153 GGTTCAGTGAGCCGAGATA 172
|||||
RESULT 44
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ID ABV46458 standard; cDNA; 486 BP.
XX
AC ABV46458;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 46449.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
PT WPI; 2001-662795/76.
XX
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 9166; 11750pp; English.
XX

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 486 BP; 167 A; 116 C; 108 G; 95 T; 0 other;

Query Match 80.0%; Score 20; DB 23; Length 486;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
Db 257 GGTTCAGTGAGCCGAGATA 276
|||||
RESULT 45
ABV42598
ID ABV42598 standard; cDNA; 533 BP.
XX
AC ABV42598;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 42589.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
PT WPI; 2001-662795/76.
XX
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8524; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate

CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX

SQ Sequence 533 BP; 142 A; 127 C; 134 G; 129 T; 1 other;

Query Match 80.0%; Score 20; DB 23; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCAGATA 20
 |||||
 Db 418 GGTTCAGTGCAGCAGATA 437

Search completed: November 24, 2002, 13:16:32
 Job time : 254.5 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 12:31:33 ; Search time 1611.5 Seconds
(without alignments)
451.486 Million cell updates/sec

Title: US-09-784-423-124
Perfect score: 25
Sequence: 1 GGTTCAGTGCAGCCGAGATAAGAGT 25

Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_pro.*

36: em_htg_rnd.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	25	100.0	25	6	AR154074	AR154074 Sequence
2	25	100.0	1000	6	AR153982	AR153982 Sequence
3	25	100.0	69964	9	HS496C20	Z83847 Human DNA s
4	25	100.0	138459	2	AC090795	AC090795 Homo sapi
5	23	92.0	99035	9	HS90012	AL031506 Human DNA
6	22	88.0	65613	9	AL391644	AL391644 Human DNA
7	22	88.0	117824	9	AL389886	AL389886 Human DNA
8	22	88.0	126482	9	AL137220	AL137220 Human DNA
9	22	88.0	148396	9	AL157400	AL157400 Human DNA
10	22	88.0	148623	2	AC068582	AC068582 Homo sapi
11	22	88.0	164857	9	AL161448	AL161448 Human DNA
12	22	88.0	173645	2	AC010770	AC010770 Homo sapi
13	22	88.0	180315	2	AC068460	AC068460 Homo sapi
14	22	88.0	195068	9	AL354499	AL354499 Human DNA
15	22	88.0	198141	9	AL512373	AL512373 Homo sapi
16	22	88.0	209790	2	AX070981	AX070981 Sequence
17	21	84.0	355	6	HSPA27G11	Z79279 H.sapiens f
18	21	84.0	520	9	AX390380	AX390380 Sequence
19	21	84.0	608	6	AX195315	AX195315 Sequence
20	21	84.0	1242	6	AX195315	MI2036 Human tyros
21	21	84.0	1838	9	HOMHER2B	AX195330 Sequence
22	21	84.0	2843	6	AX195330	AC000981 Homo sapi
23	21	84.0	3761	9	HSAC000981	AX193668 Sequence
24	21	84.0	16951	6	AX195368	AY044229 Homo sapi
25	21	84.0	16952	9	AY044229	AC092149 Homo sapi
26	21	84.0	24144	2	AC092149	Z68225 Human DNA s
27	21	84.0	25889	9	HSU112A12	AC108170 Homo sapi
28	21	84.0	26913	9	AC108170	AL354801 Human DNA
29	21	84.0	31163	9	AL354801	AC005331 Homo sapi
30	21	84.0	35581	9	AC005331	AC006138 Homo sapi
31	21	84.0	37448	9	AC005331	AC000035 Homo sapi
32	21	84.0	38429	9	AC000035	Z82254 Human DNA s
33	21	84.0	38540	9	HSU46H11	AC093236 Homo sapi
34	21	84.0	38634	9	AC093236	AC011516 Homo sapi
35	21	84.0	40014	9	AC011516	Z75890 Human DNA s
36	21	84.0	40943	9	HSR42B1	AL355881 Human DNA
37	21	84.0	42304	9	AL355881	U63963 Human CSF-1
38	21	84.0	42874	9	HSU63963	AL357952 Human DNA
39	21	84.0	43456	9	AL357952	AC068187 Homo sapi
40	21	84.0	44986	2	AC068187	AC005387 Homo sapi
41	21	84.0	46213	9	AC005387	AB065918 Homo sapi
42	21	84.0	49228	9	AB065918	AX015916 Sequence
43	21	84.0	49999	6	AX015916	AC068390 Homo sapi
44	21	84.0	52687	2	AC068390	AC091585 Homo sapi
45	21	84.0	59305	2	AC091585	

ALIGNMENTS

RESULT 1
AR154074
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AR154074
Sequence 124 from patent US 6238863.
AR154074
AR154074.1 GI:15122127
Unknown.
Unclassified.
1 (bases 1 to 25)
Schumm,J.W. and Bacher,J.W.
Materials and methods for indentifying and analyzing intermediate
tandem repeat DNA markers
Patent: US 6238863-A 124 29-MAY-2001;

25 bp DNA linear PAT 08-AUG-2001


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repeat_region /note="MER5A repeat: matches 57. .185 of consensus"  
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13046. .13314  
repeat_region /note="AlusX repeat: matches 28. .305 of consensus"  
13527. .13983  
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13984. .14293  
repeat_region /note="AlusQ repeat: matches 1. .310 of consensus"  
14294. .14347  
repeat_region /note="L1MA8 repeat: matches 5340. .5393 of consensus"  
14348. .14649  
repeat_region /note="AlusX repeat: matches 2. .304 of consensus"  
14651. .14966  
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14967. .15007  
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repeat_region /note="L1M4 repeat: matches 3784. .5097 of consensus"  
16413. .16611  
repeat_region /note="L1 repeat: matches 3186. .3382 of consensus"  
16662. .16875  
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16891. .17310  
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17137. .17686  
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17359. .17438  
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17825. .18044  
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18046. .18357  
repeat_region /note="AlusG repeat: matches 1. .309 of consensus"  
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repeat_region /note="AlusQ repeat: matches 1. .313 of consensus"  
18830. .18897  
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19044. .19080  
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23209. .23725  
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34944. .35243  
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35351. .35551  
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36460. .36544  
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37861. .38188  
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Query Match 100.0%; Score 25; DB 9; Length 69964;  
Best Local Similarity 100.0%; Pred. No. 9.6e-06;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGTTCAGTCAGCCGAGATAAGACT 25

Db 6244 GGTTCAGTCAGCCGAGATAAGACT 6220

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RESULT 4  
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LOCUS 138459 bp DNA linear HTG 11-JUN-2001  
DEFINITION Homo sapiens chromosome 8 clone RP11-254K5 map 8, WORKING DRAFT  
SEQUENCE, 12 unordered pieces.  
AC090795  
AC090795.2 GI:14336499  
HTG: HTGS-PHASE1; HTGS_DRAFT; HTGS_FULLTOP.  
KEYWORDS Homo sapiens.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 138459)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
Homo sapiens chromosome 8, clone RP11-254K5  
Unpublished  
REFERENCE 2 (bases 1 to 138459)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,  
Barn,N., Bastien,V., Boguslavsky,L., Bouckhalter,B., Brown,A.,  
Camarata,J., Campiano,A., Choepel,Y., Colangelo,M., Collins,S.,  
Collamore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,  
Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,  
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
Jones,C., Karatas,A., LaRoque,K., Lamazares,R., Landers,T.,  
Lenczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,  
McPeeters,R., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,  
Murphy,T., Naylor,J., Meneus,L., Mihova,T., Mlenga,V.,  
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
Phunkiang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,  
Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,  
Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S., Severy,P.,  
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
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Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A., and Zody, M.

TITLE JOURNAL

COMMENT

Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 11, 2001 this sequence version replaced gi:13270664.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L12790

Center clone name: 254_K_5

----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 133567 bases at least Q40

Consensus quality: 135811 bases at least Q30

Consensus quality: 136678 bases at least Q20

Insert size: 139000; agarose-fp

Quality coverage: 137359; sum-of-contigs

Quality coverage: 6.5 in Q20 bases; agarose-fp

Quality coverage: 6.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1411: contig of 1411 bp in length
1412 1511: gap of 100 bp
1512 2165: contig of 654 bp in length
2166 2265: gap of 100 bp
2266 3074: contig of 809 bp in length
3075 3174: gap of 100 bp
3175 4763: contig of 1589 bp in length
4764 4863: gap of 100 bp
4864 6161: contig of 1298 bp in length
6162 6261: gap of 100 bp
6262 8601: contig of 2340 bp in length
8602 8701: gap of 100 bp
8702 13139: contig of 4438 bp in length
13140 13239: gap of 100 bp
13240 17613: contig of 4374 bp in length
17614 17713: gap of 100 bp
17714 30894: contig of 13181 bp in length
30895 30994: gap of 100 bp
30995 40051: contig of 9057 bp in length
40052 40151: gap of 100 bp
40152 95859: contig of 55708 bp in length
95860 95959: gap of 100 bp
95960 138459: contig of 42500 bp in length.

FEATURES source

Location/Qualifiers
1..138459
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
/map="8"

misc_feature
1..1411
/clone="RP11-254K5"
/clone_lib="RPC1-11 Human Male BAC"
/note="assembly_fragment
clone_end:SP6
vector_side:left"

misc_feature 1512..2165
/note="assembly_fragment"
2266..3074
/note="assembly_fragment"
3175..4763
/note="assembly_fragment"
4864..6161
/note="assembly_fragment"
6262..8601
/note="assembly_fragment"
8702..13139
/note="assembly_fragment"
13240..17613
/note="assembly_fragment"
17714..30894
/note="assembly_fragment"
30995..40051
/note="assembly_fragment"
40152..95859
/note="assembly_fragment"
95960..138459
/note="assembly_fragment
clone_end:T7
vector_side:right"
BASE COUNT 38140 a 31260 c 30041 g 37914 t 1104 others
ORIGIN

Query Match 100.0%; Score 25; DB 2; Length 138459;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTACCCGAGATAAGACT 25
|||||

Db 33960 GGTTCAGTACCCGAGATAAGACT 33984
|||||

RESULT 5

HS90012/c

LOCUS

DEFINITION

Human DNA sequence from clone 90012 on chromosome 6p24.1-25.1.

Contains STSs and GSSs, complete sequence.

AL031906

ACCESSION

AL031906.1 GI:3766282

KEYWORDS

HTG.

SOURCE

Homo sapiens.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 99035)

AUTHORS

Phillips, S

TITLE

Direct Submission

JOURNAL

Submitted (03-NOV-1998) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

requests: clonerequest@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with

only a small overlap as described above.

IMPORTANT: This sequence is not the entire insert of clone 90012.

It may be shorter because we only sequence overlapping sections

once, or longer because we arrange for a small overlap between

neighbouring submissions.

The true left end of clone 103M22 (AL031904) is at 98936 in this

sequence.

This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems,

such as compressions and repeats, but not necessarily within known

annotated human repeat sequence elements (e.g. Alu). Where the

sequence is ambiguous, there is an annotation using the 'unsure'

feature key.

This sequence was generated from part of bacterial clone contigs of

human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr6>
 90012 is from the library RPC11 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/VECTOR:PCYPAC2>.

FEATURES

Source
 1..99035
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /map="p24.1-25.1"
 /clone="RP1-90012"
 /clone_lib="RPC1-1"
 1..272
 /note="L1MA9 repeat: matches 5727..5999 of consensus"
 repeat_region
 641..888
 /note="MLT1C repeat: matches 219..466 of consensus"
 repeat_region
 893..1047
 /note="L2 repeat: matches 2213..2363 of consensus"
 repeat_region
 1048..1553
 /note="MER44B repeat: matches 40..533 of consensus"
 repeat_region
 1570..1918
 /note="L2 repeat: matches 2375..2750 of consensus"
 repeat_region
 1844..1990
 /note="MIR repeat: matches 100..262 of consensus"
 repeat_region
 2561..2586
 /note="L3 copies 2 mer aa 92% conserved"
 repeat_region
 2591..2707
 /note="FLAM_A repeat: matches 1..117 of consensus"
 repeat_region
 2817..3122
 /note="AluX repeat: matches 1..306 of consensus"
 repeat_region
 3870..4087
 /note="L2 repeat: matches 2410..2656 of consensus"
 repeat_region
 4731..5046
 /note="AluYb8 repeat: matches 1..310 of consensus"
 repeat_region
 5556..5865
 /note="AluX repeat: matches 1..310 of consensus"
 repeat_region
 5911..6209
 /note="AluY repeat: matches 1..299 of consensus"
 repeat_region
 6534..6834
 /note="AluSq repeat: matches 1..311 of consensus"
 repeat_region
 7502..7541
 /note="L20 copies 2 mer tt 80% conserved"
 repeat_region
 8939..8983
 /note="L15 copies 3 mer tct 91% conserved"
 repeat_region
 9212..9514
 /note="AluSq repeat: matches 1..311 of consensus"
 repeat_region
 10567..10654
 /note="MIR repeat: matches 78..170 of consensus"
 repeat_region
 10680..10719
 /note="L10 copies 4 mer tgtg 88% conserved"
 repeat_region
 10680..10717
 /note="L9 copies 2 mer tg 90% conserved"
 repeat_region
 10900..11200
 /note="AluSq repeat: matches 3..303 of consensus"
 repeat_region
 11900..12156
 /note="AluYb repeat: matches 63..307 of consensus"
 repeat_region
 12197..12740
 /note="L2 repeat: matches 1811..2419 of consensus"
 repeat_region
 14423..14470
 /note="L24 copies 2 mer tg 88% conserved"
 repeat_region
 15868..16027
 /note="MIR repeat: matches 53..212 of consensus"
 misc_feature
 18445..18878
 /note="match: GSSs AQ124934 AQ064640"
 repeat_region
 20722..20783
 /note="L31 copies 2 mer ta 74% conserved"
 repeat_region
 20722..20781
 /note="L15 copies 4 mer tata 73% conserved"
 misc_feature
 complement(21988..22391)
 /note="match: GSS AQ030463"
 repeat_region
 22517..22625

/note="L1M4 repeat: matches -5..103 of consensus"
 23263..23549
 /note="AluYb repeat: matches 3..296 of consensus"
 repeat_region
 24442..24732
 /note="AluYb repeat: matches 17..304 of consensus"
 repeat_region
 25195..25233
 /note="L1PA7 repeat: matches 6107..6163 of consensus"
 repeat_region
 27460..27736
 /note="AluSc repeat: matches 1..291 of consensus"
 repeat_region
 28336..28518
 /note="L2 repeat: matches 2549..2750 of consensus"
 repeat_region
 30201..30248
 /note="L24 copies 2 mer ta 81% conserved"
 repeat_region
 30259..30310
 /note="L26 copies 2 mer ac 77% conserved"
 repeat_region
 31062..31097
 /note="L9 copies 4 mer ataa 83% conserved"
 repeat_region
 31099..31208
 /note="MIR repeat: matches 1..115 of consensus"
 repeat_region
 31752..31855
 /note="L52 copies 2 mer aa 63% conserved"
 repeat_region
 31887..32169
 /note="AluY repeat: matches 1..283 of consensus"
 repeat_region
 32431..32603
 /note="L1M4 repeat: matches 5114..5298 of consensus"
 repeat_region
 33650..34808
 /note="L2 repeat: matches 408..1636 of consensus"
 repeat_region
 34822..35129
 /note="MLT1A1 repeat: matches 1..307 of consensus"
 repeat_region
 35138..36578
 /note="L1PA2 repeat: matches 4712..6146 of consensus"
 repeat_region
 37487..37671
 /note="MLT11 repeat: matches 167..352 of consensus"
 repeat_region
 37793..38386
 /note="L2 repeat: matches 1911..2527 of consensus"
 repeat_region
 39061..39184
 /note="L1M4 repeat: matches 2876..2991 of consensus"
 repeat_region
 39577..39762
 /note="MER58A repeat: matches 7..207 of consensus"
 repeat_region
 42238..43218
 /note="L2 repeat: matches 1326..2404 of consensus"
 repeat_region
 43305..43446
 /note="L2 repeat: matches 2550..2735 of consensus"
 misc_feature
 complement(44389..44852)
 /note="match: GSS AQ170695"
 misc_feature
 complement(45574..46231)
 /note="match: GSS B49432"
 repeat_region
 46399..46690
 /note="AluYb repeat: matches 3..308 of consensus"
 repeat_region
 47337..47612
 /note="AluSc repeat: matches 1..277 of consensus"
 misc_feature
 47427..47862
 /note="match: SRS AL031017"
 repeat_region
 47863..47980
 /note="MIR repeat: matches 74..185 of consensus"
 repeat_region
 47981..48423
 /note="MLT1C repeat: matches 1..464 of consensus"
 repeat_region
 48424..48464
 /note="MIR repeat: matches 33..74 of consensus"
 repeat_region
 49974..50286
 /note="AluX repeat: matches 1..311 of consensus"
 misc_feature
 complement(50053..50357)
 /note="match: GSS AQ082392"
 repeat_region
 51121..51355
 /note="AluSq repeat: matches 1..236 of consensus"
 repeat_region
 52036..52753
 /note="L1PA2 repeat: matches 5430..6146 of consensus"
 repeat_region
 52795..52854
 /note="HAL1 repeat: matches 1552..1605 of consensus"
 repeat_region
 54067..54128
 /note="MER9A repeat: matches 66..131 of consensus"
 repeat_region
 54129..54420
 /note="AluYb repeat: matches 6..298 of consensus"

```

repeat_region 54421..54498
/note="MER94 repeat: matches 1..66 of consensus"
55613..55675
/note="9 copies 7 mer aatatat 76% conserved"
55809..55990
/note="26 copies 7 mer attatat 64% conserved"
56456..56626
/note="FRAM repeat: matches -6..163 of consensus"
57248..57293
/note="MER70A repeat: matches 544..585 of consensus"
57294..57570
/note="AluX repeat: matches 17..299 of consensus"
57571..57945
/note="MER70A repeat: matches 134..544 of consensus"
59109..59411
/note="AluX repeat: matches 1..304 of consensus"
60599..60628
/note="15 copies 2 mer tt 100% conserved"
62412..62449

Query Match 92.0%; Score 23; DB 9; Length 99035;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCGAGATAAGA 23
|||||
Db 51139 GGTTCAGTGCAGCGAGATAAGA 51117

RESULT 6
AL391644
LOCUS
DEFINITION Human DNA sequence from clone RP11-535F17 on chromosome 6 Contains
part of a KH domain protein; similar to mammalian Sam68, E6ts and
GSSs, complete sequence.
ACCESSION AL391644
VERSION AL391644.12 GI:11229206
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bates, K.
Direct Submission
Submitted (09-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Nov 20, 2000 this sequence version replaced gi:11190597.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
IMPORTANT: This sequence is not the entire insert of clone
RP11-535F17. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP3-522D12 is at 65514 in this sequence.
The true right end of clone RP1-240B8 is at 100 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such

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as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP11-535F17 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6.

FEATURES	Location/Qualifiers
source	1..65613
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="6"
	/clone="RP11-535F17"
	/clone_lib="RPCI-11.2"
	739..1206
repeat_region	/note="L2 repeat: matches 2266..2745 of consensus"
repeat_region	2904..3068
misc_feature	/note="MIR repeat: matches 80..259 of consensus"
	3900..4345
misc_feature	/note="match: GSS: Em:AQ731895"
	3904..4430
misc_feature	/note="match: GSS: Em:AQ489033"
	3908..4305
repeat_region	/note="match: GSS: Em:AQ566108"
	4438..4626
repeat_region	/note="L2 repeat: matches 2273..2470 of consensus"
	4794..4938
misc_feature	/note="MER5A repeat: matches 29..182 of consensus"
	5354..5758
repeat_region	/note="match: GSS: Em:B37233"
	6506..6709
repeat_region	/note="MIR repeat: matches 31..262 of consensus"
	6831..7153
repeat_region	/note="MER46C repeat: matches 1..337 of consensus"
	7475..7602
repeat_region	/note="L1PB3 repeat: matches 4636..4756 of consensus"
	7592..8952
repeat_region	/note="L1PB3 repeat: matches 4748..6244 of consensus"
	9957..10037
repeat_region	/note="MLT1F repeat: matches 83..163 of consensus"
	10008..10435
repeat_region	/note="MLT1F repeat: matches 122..535 of consensus"
	complement(10824..11284)
misc_feature	/note="match: GSS: Em:AQ784097"
repeat_region	11909..12105
repeat_region	/note="MIR repeat: matches 49..261 of consensus"
	12406..12626
repeat_region	/note="LTR33 repeat: matches 1..228 of consensus"
	13729..16230
repeat_region	/note="L1PA3 repeat: matches 3643..6146 of consensus"
	16152..16296
repeat_region	/note="match: GSS: Em:AQ078529"
	16652..16943
repeat_region	/note="AluX repeat: matches 8..299 of consensus"
	16945..17436
repeat_region	/note="L1PA11 repeat: matches 773..1252 of consensus"
	17451..17510
repeat_region	/note="AluX repeat: matches 240..299 of consensus"
	17525..22399
repeat_region	/note="L1PA11 repeat: matches 1246..6164 of consensus"
	22792..22825
repeat_region	/note="L1PA13 repeat: matches 6111..6144 of consensus"
	22827..23369
repeat_region	/note="L1PA12 repeat: matches 5550..6100 of consensus"
	23371..23909
repeat_region	/note="L1ME repeat: matches 5132..5668 of consensus"
	24061..24150
repeat_region	/note="L2 repeat: matches 2620..2710 of consensus"
	24570..24687
repeat_region	/note="L2 repeat: matches 2373..2489 of consensus"
	25807..26027
repeat_region	/note="L1MC4 repeat: matches 5861..6116 of consensus"
	complement(26624..26706)

gene

```

CDS
/gene="bA535F17.1"
complement(<26624..>26706)
/gene="bA535F17.1"
/note="match: cDNAs: Em:AF069681 Em:AF098796 Em:AF051321
match: ESTs: Em:AN003449 Em:BE864957
match: proteins: Tr:Q9JULP1 Tr:Q9WU01 Tr:O75525 Tr:O88624"
/codon_start=1
/revidence=not_experimental
/product="bA535F17.1 (KH domain protein; similar to
mammalian Sam68)"
/db_xref="GI:13016537"
/translation="GIDGCGGYDQTYETDYSYATQIQ"
2751..27538
/repeat_region
/note="AluSg repeat: matches 1..303 of consensus"
28503..28934
/repeat_region
/note="HAL1 repeat: matches 963..1403 of consensus"
29078..29676
/repeat_region
/note="L1MC4 repeat: matches 7368..7977 of consensus"
29892..30124
/repeat_region
/note="HAL1 repeat: matches 345..816 of consensus"
29826..30277
/repeat_region
/note="match: GSS: Em:AQ711793"
30155..30194
/repeat_region
/note="20 copies 2 mer ca 95% conserved"
31309..31392
/repeat_region
/note="42 copies 2 mer at 63% conserved"
32915..33102
/repeat_region
/note="MER63C repeat: matches 1..195 of consensus"
33213..33445
/repeat_region
/note="MER63C repeat: matches 244..477 of consensus"
33458..33968
/repeat_region
/note="MER63 repeat: matches 511..1048 of consensus"
34184..34442
/repeat_region
/note="L2 repeat: matches 2143..2413 of consensus"
34774..34855
/repeat_region
/note="L2 repeat: matches 1653..1738 of consensus"
35416..35550
/repeat_region
/note="L1PA16 repeat: matches 6023..6157 of consensus"
37582..38030
/repeat_region
/note="L1PA4 repeat: matches 5696..6146 of consensus"
38050..38354
/repeat_region
/note="LTR40b repeat: matches 128..462 of consensus"
40016..40112
/repeat_region
/note="L1PA8 repeat: matches 6067..6163 of consensus"
40189..40642
/repeat_region
/note="L1PA8 repeat: matches 5607..6066 of consensus"
40667..41086
/repeat_region
/note="L1P repeat: matches 4988..5401 of consensus"
41942..42228
/repeat_region
/note="AluSg repeat: matches 3..289 of consensus"
42757..42924
/repeat_region
/note="MER3 repeat: matches 2..170 of consensus"
42944..43254
/repeat_region
/note="AluY repeat: matches 1..310 of consensus"
43255..43311
/repeat_region
/note="MER3 repeat: matches 144..203 of consensus"
45663..46083
/repeat_region
/note="MLT1B repeat: matches 3..389 of consensus"
complement(46439..46918)
/misc_feature
/note="match: GSS: Em:AQ117757"
42944..43254
/misc_feature
complement(46532..46912)
/repeat_region
/note="match: GSS: Em:AQ824979"
46547..46842
/misc_feature
/note="L2 repeat: matches 2465..2745 of consensus"
complement(46786..47251)
/misc_feature
/note="match: GSS: Em:AQ789636"
complement(46991..47202)
/repeat_region
/note="match: GSS: Em:B98928"
47670..48112
/misc_feature
/note="MLT1C repeat: matches 1..466 of consensus"
complement(48857..49387)
/note="match: GSS: Em:AQ317058"

```

complement(48879..49387)
 /note="match: GSS: Em:AQ240593"
 repeat_region
 /note="MER3B repeat: matches 1..118 of consensus"
 49472..49759
 repeat_region
 /note="AluSg repeat: matches 1..298 of consensus"
 50203..50501
 repeat_region
 /note="AluX repeat: matches 1..296 of consensus"
 50637..51048
 repeat_region
 /note="L1MEL repeat: matches 5756..6274 of consensus"
 51047..51281
 /note="L1M4 repeat: matches 2467..2709 of consensus"

Query Match 88.0%; Score 22; DB 9; Length 65613;
 Best Local Similarity 100.0%; Pred. NO. 0.00084;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTCAGCCGAGATAAG 22
 |||||
 Db 49677 GGTTCAGTCAGCCGAGATAAG 49698

RESULT 7
 AL389886/c
 LOCUS
 DEFINITION Human DNA sequence from clone RPl-237C24 on chromosome 20. Contains the 3' end of the SLC23A1 gene encoding solute carrier family 23 (nucleobase transporters) member 1, ESTs, STSS and GSSs, complete sequence.
 ACCESSION AL389886
 VERSION AL389886.10 GI:10086152
 KEYWORDS HTG; nucleobase transporter; SLC23A1.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 117824)
 AUTHORS Kay,M.
 TITLE Direct Submission
 JOURNAL Submitted (26-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 COMMENT On Sep 11, 2000 this sequence version replaced gi:9801155. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TREMBL; Wp; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C/elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20 This sequence is the entire insert of clone RPl-237C24 The true left end of clone RP5-826118 is at 30591 in this sequence. The true right end of clone RP4-571110 is at 5147 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPl-237C24 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: PCYPAC2. Location/Qualifiers

```

source
1..117824
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RPI-237C24"
/clone_lib="RPCI-1"
1..65
/note="AluSc repeat: matches 232..296 of consensus"
/note="L1 repeat: matches 4731..4854 of consensus"
346..641
/note="AluSx repeat: matches 1..308 of consensus"
978..1271
/note="AluJb repeat: matches 1..289 of consensus"
1273..1382
/note="Tandem repeat. Tandem repeat shows differences
between individual subclones. Overall assembly consistent
with restriction digest."
1275..1379
/note="3 copies 35 mer 78% conserved"
1276..1381
/note="53 copies 2 mer 99 67% conserved"
1288..1386
/note="3 copies 33 mer 78% conserved"
1629..1845
/note="AluJb repeat: matches 2..219 of consensus"
2306..2407
/note="L1Pall1 repeat: matches 6064..6164 of consensus"
2654..2727
/note="L1M2 repeat: matches 5539..5594 of consensus"
2728..3037
/note="AluSx repeat: matches 1..310 of consensus"
3038..3088
/note="L1M2 repeat: matches 5594..5649 of consensus"
4213..4471
/note="MER46A repeat: matches 1..236 of consensus"
4484..4649
/note="Tigger3(Golem) repeat: matches 2833..3028 of
consensus"
4650..5005
/note="MER1B repeat: matches 1..337 of consensus"
5006..5039
/note="Tigger3(Golem) repeat: matches 2804..2833 of
consensus"
5040..5228
/note="AluJb repeat: matches 113..301 of consensus"
5313..5633
/note="AluJb repeat: matches 5..308 of consensus"
6563..6864
/note="AluJ repeat: matches 1..301 of consensus"
7151..7256
/note="MER30 repeat: matches 3..96 of consensus"
7257..7563
/note="AluSg repeat: matches 1..308 of consensus"
7564..7661
/note="MER30 repeat: matches 96..230 of consensus"
8150..8215
/note="MER2 repeat: matches 268..342 of consensus"
8246..8373
/note="MER2 repeat: matches 88..210 of consensus"
8414..8715
/note="AluJo repeat: matches 1..294 of consensus"
8717..8811
/note="MER2 repeat: matches 2..97 of consensus"
complement(8858..89217)
/gene="SLC23A1"
complement(join(8858..13705,15790..15885,18449..18586,
19279..19408,24271..24376,26407..26554,30437..30593,
31077..31197,40143..40324,41254..41324,42322..42410,
56056..56213,58943..59059,69381..69479,88956..89217))
/gene="SLC23A1"
/product="dj237C24.1 (Solute carrier family 23 (nucleobase
transporters), member 1 (KIAA0238))"

polyA_site
/gene="SLC23A1"
complement(8875..8880)
/gene="SLC23A1"
10892..10917
/note="13 copies 2 mer 91 100% conserved"
complement(join(13473..13705,15790..15885,18449..18586,
19279..19408,24271..24376,26407..26554,30437..30593,
31077..31197,40143..40324,41254..41324,42322..42410,
56056..56213,58943..59059,69381..69479,88956..89063))
/gene="SLC23A1"
/note="match; proteins: Tr:Q9Z2J0 Tr:Q9UI39 Tr:Q9UHI7
Tr:Q95191 Tr:Q9WTW8 Tr:Q9WTW7"
/codon_start=1
/evidence=not_experimental
/product="dj237C24.1 (Solute carrier family 23 (nucleobase
transporters), member 1 (KIAA0238))"
/protein_id="CAC16126.1"
/db_xref="GI:12314277"
/translation="MMGIGKNTTSKMEAGSTGEKYEAKHPAFFTPVWINGGAT
SSGQDNDETELMAIYTGIAEKSLAETLDSTGSLDPQSDMIYITEDVPPWYLC
IFLQGHVYFCFSGTIAVPELLADAMCVGDOWATSLIGTIFFCVGLITLLOTFCG
RLPQAFAPFATAPARAILSLDKWCTNTDVSANGTABELLTHEINWPRIRIQGA
IIMSLLEVIGLIGPALLKIGLITTPVVALIGLSFGQAGERAGKRWGJAMITD
IFVLFSOYARNVKPELPITYKSKGTAKQLQKMFPIALILVSWLLCFITFTVD
VPPDSTKGFARTADQGVLPWFVKPYPPFOWGLPTVSAAGVIGMLSAVVASTI
ESIDYFACARLSCAPPPHAINRGIFVEGLSCVLDGIFGTNGSTSSNIGVLGI
TKGSRVTCQCALMALMGKGFALPDPVLGALFCTFLGMITAVGLSNLOF
IDLNSRNLFVLGFIFFGLPSYLRONPLVTGITGIDQVLNLLTAMFVGCVAF
FLDNTPTGPEERGIKWKGVKGNKSLDMESYNLPFGWNIIRKRCFSYLPISPT
FVGWTKGLRKSDNSRSDSDSQTG"
13776..13837
/note="31 copies 2 mer ca 96% conserved"
13779..13846
/note="2 copies 34 mer 91% conserved"
14150..14460
/note="AluSx repeat: matches 1..311 of consensus"
14471..14538
/note="2 copies 34 mer 92% conserved"
16112..16830
/note="match; GSS: Em:AQ319998"
16466..16649
/note="L1MB5 repeat: matches 5482..5667 of consensus"
16674..17043
/note="MER82 repeat: matches 228..641 of consensus"
17040..17129
/note="MER82 repeat: matches 1..97 of consensus"
17138..17259
/note="L1MB5 repeat: matches 5705..5822 of consensus"
17260..17552
/note="AluSx repeat: matches 1..289 of consensus"
17553..17873
/note="L1MB5 repeat: matches 5822..6161 of consensus"
19877..20061
/note="MIR repeat: matches 28..238 of consensus"
21206..21582
/note="match; GSS: Em:AQ603395"
21270..21381
/note="L2 repeat: matches 2337..2459 of consensus"
21901..21977
/note="L2 repeat: matches 2675..2750 of consensus"
21920..21986
/note="MIR repeat: matches 184..251 of consensus"

```

```

repeat_region 22173..22329
/note="MER2 repeat: matches 1..171 of consensus"
repeat_region 22330..22633
/note="AluX repeat: matches 1..304 of consensus"
repeat_region 22634..22854

Query Match 88.0%; Score 22; DB 9; Length 117824;
Best Local Similarity 100.0%; Pred.No.0.00079;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGAGTACCGAGATAAG 22
|||||
Db 48770 GGTGCGAGTACCGAGATAAG 48749

RESULT 8
AL137220/c
LOCUS
DEFINITION
Human DNA sequence from clone RP11-354I10 on chromosome 6 Contains
GSSs and STSs, complete sequence.
ACCESSION
AL137220
VERSION
AL137220.8 GI:9367921
KEYWORDS
HTG.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126482)
Tromans,A.
Direct Submission
Submitted (07-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clonerequests@sanger.ac.uk
On Jul 22, 2000 this sequence version replaced gi:9366903.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em', EMBL; Sw', SWISSPROT; Tr', TREMBL; Wp', WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-354I10 is from the library RPII-11.2 constructed at the
Roswell Park Cancer Institute by the group of Pieter de Jong. For
further details see http://bacpac.med.buffalo.edu/
VECTOR: pBAC3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-354I10 it may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-354I10 is at 126482 in this
sequence. The true left end of clone RP1-246P14 is at 103489 in
this sequence. The true right end of clone RP1-133H11 is at 100 in
this sequence.

FEATURES
source
i..126482
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-354I10"
/clone_lib="RPII-11.2"

```

```

repeat_region 10..103
/note="MSTD repeat: matches 76..194 of consensus"
153..280
/note="MSTD repeat: matches 283..393 of consensus"
767..1065
/note="AluJo repeat: matches 1..310 of consensus"
1123..1225
/note="L2 repeat: matches 2636..2750 of consensus"
1981..2306
/note="AluSp repeat: matches 1..313 of consensus"
2483..2843
/note="L2 repeat: matches 10..410 of consensus"
2871..3017
/note="AluSg/x repeat: matches 166..312 of consensus"
3018..4467
/note="PTRS repeat: matches 743..2438 of consensus"
3046..3514
/note="CpG island"
/evidence=not_experimental
4800..5290
repeat_region
/note="MLTIF repeat: matches 3..534 of consensus"
5426..5597
repeat_region
/note="L2 repeat: matches 1282..1453 of consensus"
5624..5834
/note="L1PB2 repeat: matches 5938..6155 of consensus"
5835..6125
/note="AluSp repeat: matches 1..294 of consensus"
complement(6533..6889)
/note="match: GSS: Em:AQ726655"
6572..6650
/note="AluSg/x repeat: matches 210..288 of consensus"
8860..9098
/note="L2 repeat: matches 2455..2697 of consensus"
9501..9549
repeat_region
/note="MIR repeat: matches 91..139 of consensus"
9570..9875
/note="AluJb repeat: matches 1..308 of consensus"
complement(9694..10158)
/note="match: GSS: Em:B92811"
10254..10534
/note="MLT1B repeat: matches 152..390 of consensus"
10535..10844
/note="AluSg repeat: matches 1..309 of consensus"
10845..10974
/note="MLT1B repeat: matches 24..153 of consensus"
11330..11420
/note="MIR repeat: matches 72..176 of consensus"
11483..11767
/note="AluSc repeat: matches 1..285 of consensus"
14000..14186
/note="L1PAL6 repeat: matches 5967..6157 of consensus"
15407..15460
/note="MIR repeat: matches 77..139 of consensus"
16339..17122
/note="L1PAL3 repeat: matches 5372..6155 of consensus"
18620..18716
/note="L1 repeat: matches 3632..3722 of consensus"
18794..19034
/note="MIR repeat: matches 13..251 of consensus"
19102..19439
/note="LTR16A repeat: matches 92..445 of consensus"
20045..20483
/note="match: GSS: Em:AQ735574"
21172..21325
/note="L2 repeat: matches 2596..2750 of consensus"
22699..23307
/note="L1MBC repeat: matches 2063..2354 of consensus"
23381..23596
/note="L1M1 repeat: matches 1411..1613 of consensus"
23912..25032
/note="L1M1 repeat: matches 272..1418 of consensus"
24730..25141
/note="match: GSS: Em:AQ115747"

```

```

repeat_region 25372..25631
/note="AluI repeat: matches 38..299 of consensus"
27712..27759
/note="12 copies 4 mer taca 95% conserved"
27803..28296
/note="L2 repeat: matches 2059..2582 of consensus"
28379..28579
/note="MER46C repeat: matches 3..220 of consensus"
28863..29163
/note="AluSg repeat: matches 1..311 of consensus"
30914..31284
/note="MLT1B repeat: matches 1..387 of consensus"
31397..31464
/note="34 copies 2 mer tg 91% conserved"
complement(31554..32145)
/note="match: GSS: Em:AQ470977"
33808..34126
/note="MER7A repeat: matches 1..334 of consensus"
36084..36393
/note="AluSg repeat: matches 2..307 of consensus"
37452..37491
/note="L1M4c repeat: matches 1877..1918 of consensus"
37492..37801
/note="AluY repeat: matches 1..311 of consensus"
37802..37914
/note="L1M4c repeat: matches 1776..1877 of consensus"
38063..38724
/note="L1M4c repeat: matches 1037..1697 of consensus"
38722..38899
/note="L1MD repeat: matches 8..171 of consensus"
38996..39201
/note="L1M4 repeat: matches 2148..2362 of consensus"
39342..39525
/note="92 copies 2 mer ta 67% conserved"
39346..39525
/note="30 copies 6 mer tatata 67% conserved"
39721..39812
/note="46 copies 2 mer tt 62% conserved"
41159..41390
/note="AluSg repeat: matches 1..234 of consensus"
41966..42075
/note="45 copies 2 mer tt 62% conserved"
complement(42516..42963)
/note="match: GSS: Em:AQ813487"
42837..42972
/note="match: SRS: Em:HSGDSTS9"
42972..43671
/note="match: GSS: Em:AQ626117"
44171..44206
/note="9 copies 4 mer tgtg 83% conserved"
45154..45250
/note="LTR29 repeat: matches 4..100 of consensus"
45346..45908
/note="Tigger4(Zombi) repeat: matches 2167..2731 of consensus"
45909..46008
/note="50 copies 2 mer ac 78% conserved"
46009..46298
/note="AluJb repeat: matches 5..302 of consensus"
46740..46828
/note="MER39b repeat: matches 483..568 of consensus"
46810..46882
/note="LTR29 repeat: matches 555..617 of consensus"
48034..48168
/note="MIR repeat: matches 134..262 of consensus"
48891..49394
/note="match: GSS: Em:AQ720319"
50724..50791
/note="17 copies 4 mer tctc 73% conserved"
50893..50958
/note="MIR repeat: matches 62..145 of consensus"

```

Query Match

88.0%; Score 22; DB 9; Length 126482;

```

Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGGCCGAGATAAG 22
|||||
Db 41177 GGTTCAGTGGCCGAGATAAG 41156
|||||

```

```

RESULT 9
AL157400/c
LOCUS Human DNA sequence from clone RP11-80H5 on chromosome 10, complete
sequence.
DEFINITION AL157400
ACCESSION AL157400
VERSION AL157400.8 GI:14596274
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148396)
Direct Submission
Submitted (03-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 4, 2001 this sequence version replaced gi:14529754.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em.: EMBL; Sw.:
SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence is the entire insert of clone RP11-80H5. The true left
end of clone RP11-248C1 is at 129612 in this sequence. The true
right end of clone RP11-9C23 is at 17504 in this sequence.

```

COMMENT

```

REFERENCE
AUTHORS
TITLE
JOURNAL

```

FEATURES

source

Location/Qualifiers

```

1..148396
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-80H5"
/clone_lib="RPCI-11.1"
7..156

```

repeat_region

/note="L1M3 repeat: matches 7575..7738 of consensus"

repeat_region

799..981

/note="MER5B repeat: matches 1..154 of consensus"

repeat_region

1346..1471

/note="L2 repeat: matches 2577..2748 of consensus"

repeat_region

3580..3926

/note="MER1B repeat: matches 1..336 of consensus"

repeat_region

4157..4454

/note="AluJd repeat: matches 1..292 of consensus"

repeat_region 4493..4609
/note="FIAM_A repeat: matches 11..126 of consensus"
5205..5373
/note="MER5A repeat: matches 8..179 of consensus"
5712..6009
/note="AluX repeat: matches 1..296 of consensus"
6279..6483
/note="AluB repeat: matches 38..256 of consensus"
6722..7032
/note="AluX repeat: matches 1..309 of consensus"
7526..7837
/note="AluY repeat: matches 3..311 of consensus"
8440..8740
/note="AluY repeat: matches 2..308 of consensus"
10302..12532
/note="TIGGER1 repeat: matches 26..2352 of consensus"
12541..13173
/note="L1MB8 repeat: matches 5499..6158 of consensus"
13172..13391
/note="HALL repeat: matches 704..924 of consensus"
14180..14401
/note="L2 repeat: matches 2514..2734 of consensus"
14825..15123
/note="L2 repeat: matches 2170..2486 of consensus"
15180..15572
/note="L2 repeat: matches 2246..2681 of consensus"
15829..15882
/note="MER46C repeat: matches 280..334 of consensus"
15885..16187
/note="AluY repeat: matches 1..309 of consensus"
16578..16707
/note="MIR repeat: matches 19..156 of consensus"
19115..19162
/note="MIR repeat: matches 183..231 of consensus"
19495..19861
/note="MT1A1 repeat: matches 1..365 of consensus"
19994..20170
/note="MIR repeat: matches 67..251 of consensus"
20703..20745
/note="MER53 repeat: matches 1..43 of consensus"
21233..21612
/note="AluX repeat: matches 5..298 of consensus"
22283..22903
/note="L1MA7 repeat: matches 5542..6279 of consensus"
23700..23756
/note="L2 repeat: matches 2641..2701 of consensus"
24503..24602
/note="50 copies 2 mer aa 68% conserved"
24889..25028
/note="L1ME repeat: matches 5509..5651 of consensus"
25288..25392
/note="L1MC5 repeat: matches 7711..7809 of consensus"
26800..26938
/note="L1ME3A repeat: matches 6000..6145 of consensus"
29645..29947
/note="AluX repeat: matches 3..301 of consensus"
30012..30308
/note="AluX repeat: matches 1..300 of consensus"
30309..30412
/note="4 copies 26 mer 76% conserved"
32503..32614
/note="MER20 repeat: matches 97..218 of consensus"
34233..34676
/note="MIR repeat: matches 1..464 of consensus"
34886..35055
/note="MIR repeat: matches 97..259 of consensus"
35362..35517
/note="MIR repeat: matches 72..261 of consensus"
35671..35972
/note="AluB repeat: matches 5..300 of consensus"
37601..37801
/note="MER63A repeat: matches 5..210 of consensus"
37986..38081

repeat_region
/note="MIR repeat: matches 70..164 of consensus"
38177..38258
/note="MER5A repeat: matches 109..189 of consensus"
38765..38887
/note="TIGGER1 repeat: matches 2295..2418 of consensus"
38888..39187
/note="AluX repeat: matches 4..303 of consensus"
39188..39236
/note="TIGGER1 repeat: matches 2247..2295 of consensus"
39237..39524
/note="AluY repeat: matches 1..287 of consensus"
39525..40995
/note="TIGGER1 repeat: matches 823..2247 of consensus"
40996..41297
/note="AluB repeat: matches 1..302 of consensus"
41298..42061
/note="TIGGER1 repeat: matches 48..823 of consensus"
42505..42804
/note="AluY repeat: matches 1..300 of consensus"
43354..43546
/note="L2 repeat: matches 2364..2534 of consensus"
43547..43838
/note="AluX repeat: matches 1..292 of consensus"
43839..43953
/note="L2 repeat: matches 2534..2707 of consensus"
44660..44762
/note="MIR repeat: matches 47..149 of consensus"
45925..46088
/note="MIR repeat: matches 75..261 of consensus"
47234..47399
/note="MER5B repeat: matches 1..177 of consensus"
48990..49282
/note="AluB repeat: matches 1..292 of consensus"
50066..50149
/note="AluB repeat: matches 23..111 of consensus"
50966..51115
/note="FAM repeat: matches 20..169 of consensus"
51118..51401
/note="AluSg repeat: matches 4..287 of consensus"
51558..51697
/note="MT1I repeat: matches 291..408 of consensus"
53048..53454
/note="MIR repeat: matches 8..410 of consensus"
54338..55405
/note="MER1C repeat: matches 1..1071 of consensus"
55494..55792
/note="AluSP repeat: matches 1..299 of consensus"
55976..56049
/note="MIR repeat: matches 63..139 of consensus"
56206..56487
/note="AluX repeat: matches 1..282 of consensus"
57028..57324
/note="AluY repeat: matches 1..295 of consensus"
57685..57996
/note="AluY repeat: matches 1..310 of consensus"
58688..58938
/note="ORSL repeat: matches 222..472 of consensus"
59164..59333
/note="MER5A repeat: matches 2..186 of consensus"
59378..59674
/note="AluB repeat: matches 1..297 of consensus"
60778..61062
/note="AluY repeat: matches 16..300 of consensus"
61641..61965

Query Match 88.0%; Score 22; DB 9; Length 148396;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAAG 22
|||||
Db 96484 GGTTCAGTGGCCGAGATAAG 96463

RESULT 10

AC068582/c

LOCUS

DEFINITION

AC068582 Homo sapiens clone RP11-27C24, WORKING DRAFT SEQUENCE, 22 unordered

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Unpublished

2 (bases 1 to 148623)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,

Boguslavskiy,L., Boukhalter,B., Brown,A., Burkett,G.,

Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,

Galagan,J., Gardyna,S., Ginde,S., Govette,M., Graham,L.,

Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,

Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,

Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczy,J.,

Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,

Meldrum,J., Meneus,L., Mihova,T., Miranda,C., Miengra,V., Morrow,J.,

Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,

Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,

Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,

Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,

Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,

Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (04-MAY-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 25, 2000 this sequence version replaced gi:7705139.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence.submissions@genome.wi.mit.edu

----- Project Information

Center project name: L4683

Center clone name: 27_C_24

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 136479 bases at least Q40

Consensus quality: 142634 bases at least Q30

Consensus quality: 144995 bases at least Q20

Insert size: 167000; agarose-ff

Insert size: 146523; sum-of-contigs

Quality coverage: 4.2 in Q20 bases; agarose-ff

Quality coverage: 4.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

```

* be preserved.
*
* 1594: contig of 1594 bp in length
* 1595 1694: gap of 100 bp
* 1695 2745: contig of 1051 bp in length
* 2746 2845: gap of 100 bp
* 2846 5356: contig of 2511 bp in length
* 5357 5456: gap of 100 bp
* 5457 8179: contig of 2723 bp in length
* 8180 8279: gap of 100 bp
* 8280 11291: contig of 3012 bp in length
* 11292 11391: gap of 100 bp
* 11392 13945: contig of 2554 bp in length
* 13946 14045: gap of 100 bp
* 14046 17830: contig of 3785 bp in length
* 17831 17930: gap of 100 bp
* 17931 21469: contig of 3539 bp in length
* 21470 21569: gap of 100 bp
* 21570 24779: contig of 3210 bp in length
* 24780 24879: gap of 100 bp
* 24880 27330: contig of 2451 bp in length
* 27331 27430: gap of 100 bp
* 27431 30523: contig of 3093 bp in length
* 30524 30623: gap of 100 bp
* 30624 34816: contig of 4193 bp in length
* 34817 34916: gap of 100 bp
* 34917 39866: contig of 4950 bp in length
* 39867 39966: gap of 100 bp
* 39967 45579: contig of 6613 bp in length
* 45580 46679: gap of 100 bp
* 46680 52861: contig of 6182 bp in length
* 52862 52961: gap of 100 bp
* 52962 61332: contig of 8371 bp in length
* 61333 61432: gap of 100 bp
* 61433 65239: contig of 7807 bp in length
* 65240 69339: gap of 100 bp
* 69340 82363: contig of 13024 bp in length
* 82364 82463: gap of 100 bp
* 82464 94321: contig of 11858 bp in length
* 94322 94421: gap of 100 bp
* 94422 108651: contig of 14230 bp in length
* 108652 108751: gap of 100 bp
* 108752 128711: contig of 19960 bp in length
* 128712 128811: gap of 100 bp
* 128812 148623: contig of 19812 bp in length.
*
* Location/Qualifiers
*   1..148623
*     /organism="Homo sapiens"
*     /db_xref="taxon:9606"
*     /clone_lib="RP11-27C24"
*     /clone_lib="RP11-27C24"
*     1..1594
*       /note="assembly_fragment"
*     1695..2745
*       /note="assembly_fragment"
*     clone_end:77
*     vector_side:right
*     2846..5356
*       /note="assembly_fragment"
*     5457..8179
*       /note="assembly_fragment"
*     8280..11291
*       /note="assembly_fragment"
*     11392..13945
*       /note="assembly_fragment"
*     14046..17830
*       /note="assembly_fragment"
*     17931..21469
*       /note="assembly_fragment"
*     21570..24779
*       /note="assembly_fragment"
*     24880..27330
*       /note="assembly_fragment"
*     27431..30523

```


misc_feature 30624..34816 /note="assembly_fragment"
 misc_feature 34917..39866 /note="assembly_fragment"
 misc_feature 39967..46579 /note="assembly_fragment"
 misc_feature 46680..52861 /note="assembly_fragment"
 misc_feature 52962..61332 /note="assembly_fragment"
 misc_feature 61433..69239 /note="assembly_fragment"
 misc_feature 69340..82363 /note="assembly_fragment"
 misc_feature 82464..94321 /note="assembly_fragment"
 misc_feature 94422..108651 /note="assembly_fragment"
 misc_feature 108752..128711 /note="assembly_fragment"
 misc_feature 128812..148623 /note="assembly_fragment"
 BASE COUNT 42327 a 33848 c 32549 g 37797 t 2102 others
 ORIGIN

Query Match 88.0%; Score 22; DB 2; Length 148623;
 Best Local Similarity 100.0%; Pred. No. 0.00077;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTGCAGTGAGCGGAGATAAG 22
 |||||
 Db 134898 GTTGCAGTGAGCGGAGATAAG 134877

RESULT 11
 AC010770
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-381H12 on chromosome 9, complete sequence.
 ACCESSION AL161448
 VERSION AL161448.16 GI:18491317
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Tronans, A.
 Direct Submission
 Submitted (01-FEB-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Feb 4, 2002 this sequence version replaced gi:119339694.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/Chr9
 RP11-381H12 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
 http://www.chori.org/bacpac/home.htm
 VECTOR: pBac3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-381H12. It may be shorter because we sequence overlapping sections only once, except for a short overlap.
 The true right end of clone RP11-381H12 is at 164857 in this sequence. The true left end of clone RP11-310F24 is at 148729 in this sequence. The true right end of clone RP11-376F21 is at 2000 in this sequence.

FEATURES
 Source
 1..164857
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="9"
 /clone="RP11-381H12"
 /clone_lib="RPCI-11.2"
 BASE COUNT 42782 a 40111 c 39202 g 42762 t
 ORIGIN

Query Match 88.0%; Score 22; DB 9; Length 164857;
 Best Local Similarity 100.0%; Pred. No. 0.00076;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTTGCAGTGAGCGGAGATAAGA 23
 |||||
 Db 56802 GTTGCAGTGAGCGGAGATAAGA 56823

RESULT 12
 AC010770
 LOCUS
 DEFINITION Homo sapiens clone RP11-127P14, WORKING DRAFT SEQUENCE, 28 unordered pieces.
 ACCESSION AC010770
 VERSION AC010770.4 GI:8096907
 KEYWORDS HTG; HTGS-PHASE1; HTGS-DRAFT.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome, clone RP11-127P14
 Unpublished
 2 (bases 1 to 173645)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Bouckhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A., Cooke, P., Dearlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrel, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gage, M., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J., Lechoczy, J., Lie, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 26, 2000 this sequence version replaced gi:6479114.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

```
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L2315
Center clone name: L27_P14
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 126351 bases at least Q40
Consensus quality: 148388 bases at least Q30
Consensus quality: 162029 bases at least Q20
Insert size: 178000; agarose-fp
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1166: contig of 1166 bp in length
* 1167 1266: gap of 100 bp
* 1267 2363: contig of 1097 bp in length
* 2364 2463: gap of 100 bp
* 2464 3608: contig of 1145 bp in length
* 3609 3708: gap of 100 bp
* 3709 5397: contig of 1689 bp in length
* 5398 5497: gap of 100 bp
* 5498 6933: contig of 1436 bp in length
* 6934 7033: gap of 100 bp
* 7034 10416: contig of 3383 bp in length
* 10417 10516: gap of 100 bp
* 10517 14071: contig of 3555 bp in length
* 14072 14171: gap of 100 bp
* 14172 16892: contig of 2721 bp in length
* 16893 16992: gap of 100 bp
* 16993 20502: contig of 3510 bp in length
* 20503 20602: gap of 100 bp
* 20603 24431: contig of 3829 bp in length
* 24432 24531: gap of 100 bp
* 24532 28247: contig of 3716 bp in length
* 28248 28347: gap of 100 bp
* 28348 32868: contig of 4521 bp in length
* 32869 32968: gap of 100 bp
* 32969 36983: contig of 4015 bp in length
* 36984 37083: gap of 100 bp
* 37084 39231: contig of 2148 bp in length
* 39232 39331: gap of 100 bp
* 39332 44516: contig of 5185 bp in length
* 44517 44616: gap of 100 bp
* 44617 48819: contig of 4203 bp in length
* 48820 48919: gap of 100 bp
* 48920 53656: contig of 4737 bp in length
* 53657 53756: gap of 100 bp
* 53757 59428: contig of 5672 bp in length
* 59429 59528: gap of 100 bp
* 59529 65695: contig of 6167 bp in length
* 65696 65795: gap of 100 bp
* 65796 71900: contig of 6105 bp in length
* 71901 72000: gap of 100 bp
* 72001 79394: contig of 7394 bp in length
* 79395 79494: gap of 100 bp
* 79495 90956: contig of 11462 bp in length
* 90957 91056: gap of 100 bp
* 91057 100913: contig of 9857 bp in length
```

```
* 100914 101013: gap of 100 bp
* 101014 111682: contig of 10669 bp in length
* 111683 111783: gap of 100 bp
* 111783 126305: contig of 14523 bp in length
* 126306 126405: gap of 100 bp
* 126406 142170: contig of 15765 bp in length
* 142171 142270: gap of 100 bp
* 142271 157726: contig of 15456 bp in length
* 157727 157826: gap of 100 bp
* 157827 173645: contig of 15819 bp in length.
FEATURES
      source
      1. 173645
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="RP11-127P14"
        /clone_lib="RPC1-11 Human Male BAC"
      1. 1166
        /note="assembly_fragment"
        1267..2363
        /note="assembly_fragment"
        2464..3608
        /note="assembly_fragment"
        3709..5397
        /note="assembly_fragment"
        5498..6933
        /note="assembly_fragment"
        7034..10416
        /note="assembly_fragment"
        10517..14071
        /note="assembly_fragment"
        clone_end:T7
        vector_side:left"
        14172..16892
        /note="assembly_fragment"
        16993..20502
        /note="assembly_fragment"
        20603..24431
        /note="assembly_fragment"
        24532..28247
        /note="assembly_fragment"
        28348..32868
        /note="assembly_fragment"
        32969..36983
        /note="assembly_fragment"
        37084..39231
        /note="assembly_fragment"
        clone_end:SP6
        vector_side:right"
        39332..44516
        /note="assembly_fragment"
        44617..48819
        /note="assembly_fragment"
        48920..53656
        /note="assembly_fragment"
        53757..59428
        /note="assembly_fragment"
        59529..65695
        /note="assembly_fragment"
        65796..71900
        /note="assembly_fragment"
        72001..79394
        /note="assembly_fragment"
        79495..90956
        /note="assembly_fragment"
        91057..100913
        /note="assembly_fragment"
        101014..111682
        /note="assembly_fragment"
        111783..126305
        /note="assembly_fragment"
        126406..142170
        /note="assembly_fragment"
        142271..157726
        /note="assembly_fragment"
```

```

misc_feature      /note="assembly_fragment"
157827..173645
/note="assembly_fragment"
BASE COUNT      52113 a 33977 c 34392 g 50438 t 2725 others
ORIGIN

Query Match      88.0%; Score 22; DB 2; Length 173645;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAAG 22
|||||
Db 27538 GGTTCAGTGCAGCCGAGATAAG 27559

RESULT 13
AC068460
LOCUS
DEFINITION      Homo sapiens chromosome 4 clone RP11-70N2 map 4, WORKING DRAFT
ACCESSION      AC068460
VERSION      AC068460.2 GI:8247907
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 180315)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 4, clone RP11-70N2
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 180315)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choquel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeAtelliano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Glend,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lenoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marguis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Melidrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,D., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severly,P., Spencer,B.,
Strange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 4, 2000 this sequence version replaced gi:7677942.
All repeats were identified using RepeatMasker:
Snit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WtBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L9488
Center clone name: 70_N_2
-----
Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 174907 bases at least Q40

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Consensus quality: 177492 bases at least Q30
Consensus quality: 178736 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 179615; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1047: contig of 1047 bp in length
* 1048 1147: gap of 100 bp
* 1148 5605: contig of 4458 bp in length
* 5606 5705: gap of 100 bp
* 5706 14016: contig of 8311 bp in length
* 14017 14116: gap of 100 bp
* 14117 21099: contig of 6983 bp in length
* 21100 21199: gap of 100 bp
* 21200 35211: contig of 14012 bp in length
* 35212 35311: gap of 100 bp
* 35312 61645: contig of 26334 bp in length
* 61646 61745: gap of 100 bp
* 61746 108461: contig of 46716 bp in length
* 108462 108561: gap of 100 bp
* 108562 180315: contig of 71754 bp in length.
FEATURES
Location/Qualifiers
Source
1..180315
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-70N2"
/clone_lib="RPC11-11 Human Male BAC"
1..1047
/note="assembly_fragment"
1148..5605
/note="assembly_fragment"
5706..14016
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
14117..21099
/note="assembly_fragment"
clone_end:17
vector_side:right"
21200..35211
/note="assembly_fragment"
35312..61645
/note="assembly_fragment"
61746..108461
/note="assembly_fragment"
108562..180315
/note="assembly_fragment"
BASE COUNT 57120 a 31493 c 31767 g 59234 t
ORIGIN

```

```

Query Match      88.0%; Score 22; DB 2; Length 180315;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAAG 22
|||||
Db 45092 GGTTCAGTGCAGCCGAGATAAG 45113

RESULT 14
AC012100
LOCUS      AC012100      195068 bp      DNA      linear      PRI 21-NOV-2001

```

```

DEFINITION Homo sapiens chromosome 15 clone RP11-507J18 map 15q21.1, complete
sequence.
ACCESSION AC012100
VERSION AC012100.7 GI:17027246
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 195068)
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195068)
AUTHORS Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
TITLE Sequencing of human chromosome 15 D15S146-D15S117 region
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 195068)
AUTHORS Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B.,
Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Madan,A.,
Owen,M.P., Ratcliffe,A., Shaffer,T. and Hood,L.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1999) Multimegabase Sequencing Center, University
of Washington, PO BOX 357730, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 195068)
AUTHORS Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S.,
Burke,J., Dors,M., Fleetwood,P., Kaur,A., Madan,A., Nesbitt,R.,
Pate,D. and Hood,L.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-2001) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
COMMENT On Nov 21, 2001 this sequence version replaced gi:13654329.
----- Genome Center
Center: Multimegabase Sequencing Center
Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowensystemsbiology.org
----- Summary Statistics
Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399

Note: Data from overlapping BACs AC084756 (drafting center:
WIBR), AC010770 (drafting center: WIBR), AC036168 (drafting center:
WIBR), and AC021752 (drafting center: UWMSC) were added for
finishing
-----
FEATURES             source
misc_feature         1..195068
                     /location/Qualifiers
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="15"
                     /map="15q21.1"
                     /clone="RP11-507J18"
                     /clone_lib="RP11-507J18"
                     /note="Data from overlapping BACs RP11-120K9, RP11-127P14,
                     RP11-623I18, and CTD-2378E12 was added and the consensus
                     sequence was determined from RP11-507J18 to the extent
                     possible"
                     1..118031
                     /note="overlap with Rpl1-127P14 AC010770"
                     1..33375
                     /note="overlap with RP11-120K9 AC084756"
                     42771..42789
                     /note="low quality data"
                     47633..47635
                     /note="low quality data"
                     102471..102472
                     /note="low quality data"
                     118026..1195068
                     /note="overlap with RP11-623I18 AC036168"
                     152001..152888
                     /note="covered by subcloned PCR product only"

```

```

misc_feature         165872..195068
                     /note="overlap with CTD-2378E12 AC021752"
                     193866..193871
                     /note="low quality data"
BASE COUNT          58212 a 41008 c 40204 g 55644 t
ORIGIN
Query Match          88.0%; Score 22; DB 9; Length 195068;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGGAGCCGAGATTAAG 22
|||||
Db 106127 GGTTCAGTGGAGCCGAGATTAAG 106148

RESULT 15
AL355499/c
LOCUS              198141 bp DNA linear PRI 30-NOV-2000
DEFINITION Human DNA sequence from clone Rpl1-328K6 on chromosome 6, complete
sequence.
ACCESSION AL355499
VERSION AL355499.15 GI:10086115
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198141)
Beasley,O.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Sep 11, 2000 this sequence version replaced gi:10039827.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements, where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; SW., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
RP11-328K6 is from the library RP11-11.2 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pBACE3.6
This sequence is the entire insert of clone Rpl1-328K6 The true
left end of clone Rpl1-203H2 is at 153730 in this sequence.
FEATURES             source
misc_feature         1..198141
                     /location/Qualifiers
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP11-328K6"
                     /clone_lib="RP11-11.2"
                     53..404
                     /note="MT1A1 repeat: matches 1..365 of consensus"
                     repeat_region
                     547..644
                     /note="TTGGER2 repeat: matches 2398..2500 of consensus"
                     repeat_region
                     1036..11337

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repeat_region /note="AluSg repeat: matches 1. .303 of consensus"
repeat_region 1971. .2264
repeat_region /note="AluSx repeat: matches 1. .293 of consensus"
repeat_region 2482. .2708
repeat_region /note="AluSx repeat: matches 2. .225 of consensus"
repeat_region 2847. .3275
repeat_region /note="Trigger2a repeat: matches 1. .433 of consensus"
repeat_region 3385. .3695
repeat_region /note="AluSx repeat: matches 1. .309 of consensus"
repeat_region 4027. .4135
repeat_region /note="L2 repeat: matches 2563. .2685 of consensus"
repeat_region 5269. .5327
repeat_region /note="L2 repeat: matches 2364. .2419 of consensus"
repeat_region 6287. .6583
repeat_region /note="AluSg repeat: matches 1. .297 of consensus"
repeat_region 6836. .6940
repeat_region /note="LIME3A repeat: matches 5996. .6103 of consensus"
repeat_region 7103. .7244
repeat_region /note="MIR repeat: matches 20. .192 of consensus"
repeat_region 7359. .7629
repeat_region /note="MER7A repeat: matches 5. .268 of consensus"
repeat_region 7631. .7918
repeat_region /note="AluSp repeat: matches 1. .288 of consensus"
repeat_region 7919. .7958
repeat_region /note="20 copies 2 mer ca 100% conserved"
repeat_region 8561. .9002
repeat_region /note="MER83 repeat: matches 1. .448 of consensus"
repeat_region 9110. .9410
repeat_region /note="AluSx repeat: matches 1. .301 of consensus"
repeat_region 9411. .9448
repeat_region /note="19 copies 2 mer ta 100% conserved"
repeat_region 9604. .9689
repeat_region /note="MIR repeat: matches 41. .126 of consensus"
repeat_region 9988. .10197
repeat_region /note="L2 repeat: matches 2472. .2671 of consensus"
misc_feature 10438. .10865
repeat_region /note="Cpg island"
repeat_region /evidence=not_experimental
repeat_region 12263. .13439
repeat_region /note="L1MC5 repeat: matches 6437. .7589 of consensus"
repeat_region 13548. .13696
repeat_region /note="MER5B repeat: matches 2. .159 of consensus"
repeat_region 14380. .14549
repeat_region /note="L2 repeat: matches 2534. .2690 of consensus"
repeat_region 14550. .14840
repeat_region /note="AluSg1 repeat: matches 1. .288 of consensus"
repeat_region 14841. .15039
repeat_region /note="L2 repeat: matches 2305. .2534 of consensus"
repeat_region 15098. .15448
repeat_region /note="MT2CB repeat: matches 3. .411 of consensus"
repeat_region 15449. .15807
repeat_region /note="THE1B repeat: matches 1. .364 of consensus"
repeat_region 15808. .15914
repeat_region /note="MT2CB repeat: matches 362. .466 of consensus"
repeat_region 15927. .16206
repeat_region /note="AluSg repeat: matches 1. .278 of consensus"
repeat_region 16208. .16494
repeat_region /note="L2 repeat: matches 2129. .2419 of consensus"
repeat_region 16587. .16715
repeat_region /note="L2 repeat: matches 2575. .2709 of consensus"
repeat_region 17070. .17215
repeat_region /note="MIR repeat: matches 100. .252 of consensus"
repeat_region 17925. .17969
repeat_region /note="L2 repeat: matches 2705. .2750 of consensus"
repeat_region 18038. .18356
repeat_region /note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 18394. .18566
repeat_region /note="FRAM repeat: matches -1. .171 of consensus"
repeat_region 18570. .18625
repeat_region /note="28 copies 2 mer aa 75% conserved"
repeat_region 19223. .19310
repeat_region /note="MT1J repeat: matches 103. .193 of consensus"
repeat_region 19877. .20039
/note="LTR33 repeat: matches 350. .519 of consensus"
20403. .20721
/note="AluSx repeat: matches 1. .308 of consensus"
21963. .22029
/note="L1M4 repeat: matches 5721. .5794 of consensus"
22047. .22340
/note="AluY repeat: matches 1. .294 of consensus"
22864. .23282
/note="L2 repeat: matches 2027. .2491 of consensus"
23285. .23570
/note="MLT1J repeat: matches 211. .514 of consensus"
23748. .24062
/note="MLT1J repeat: matches 36. .389 of consensus"
24289. .24401
/note="MER30 repeat: matches 11. .130 of consensus"
24402. .24712
/note="AluY repeat: matches 1. .307 of consensus"
24713. .24814
/note="MER30 repeat: matches 130. .229 of consensus"
25096. .25391
/note="AluSx repeat: matches 1. .294 of consensus"
25554. .25849
/note="AluYb repeat: matches 1. .295 of consensus"
26135. .26440
/note="AluSg repeat: matches 1. .312 of consensus"
27172. .27466
/note="AluSx repeat: matches 1. .296 of consensus"
27883. .27997
/note="L1M9 repeat: matches 6171. .6302 of consensus"
28577. .28610
/note="17 copies 2 mer tt 85% conserved"
28778. .28863
/note="MT1-INTERNAL repeat: matches 431. .525 of consensus"
28864. .29250
/note="MSTA repeat: matches 1. .426 of consensus"
29251. .29276
/note="MT1-INTERNAL repeat: matches 404. .431 of consensus"
29277. .29575
/note="AluYb repeat: matches 12. .308 of consensus"
29576. .29620
/note="MT1-INTERNAL repeat: matches 356. .404 of consensus"
29621. .29980
/note="MSTB repeat: matches 1. .357 of consensus"
29981. .30274
/note="AluSx repeat: matches 1. .291 of consensus"
30275. .30344
/note="MSTB repeat: matches 357. .426 of consensus"
30345. .30498
/note="MT1-INTERNAL repeat: matches 246. .356 of consensus"
30601. .30889
/note="AluSg repeat: matches 1. .293 of consensus"
32002. .32290
/note="AluSp repeat: matches 1. .290 of consensus"
32307. .32556
/note="L1ME3A repeat: matches 5894. .6163 of consensus"
32575. .32979
/note="L1ME2 repeat: matches 5754. .6315 of consensus"
32980. .33039
/note="L1ME3A repeat: matches 5849. .5908 of consensus"
33707. .34022
/note="AluJo repeat: matches 2. .312 of consensus"
34185. .34946
/note="L1PA16 repeat: matches 5368. .6145 of consensus"
35004. .35121
/note="FLAM_A repeat: matches 6. .123 of consensus"
35316. .35620
/note="AluYb repeat: matches 1. .306 of consensus"
36193. .36494
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Query Match      88.0%; Score 22; DB 9; Length 198141;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAAG 22
|||||
Db 112303 GGTTCAGTGCAGCCGAGATAAG 112282

RESULT 16
AL512373/c
LOCUS      AL512373      209790 bp      DNA      linear      HTG 12-SEP-2001
DEFINITION Homo sapiens chromosome 6 clone RP11-564014, *** SEQUENCING IN
ACCESSION  AL512373
VERSION     AL512373
KEYWORDS   HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 209790)
REFERENCE  Smith,M.
AUTHORS   Direct Submission
TITLE     Submitted (11-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL   CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT   requests: clonerequest@sanger.ac.uk
            On Sep 13, 2001 this sequence version replaced gi:13273887.
            ----- Genome Center
            Center: Sanger Centre
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
            ----- Project Information
            Center project name: BA564014
            ----- Summary Statistics
            Sequencing program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 209055 bases at least Q40
            Consensus quality: 209344 bases at least Q30
            Consensus quality: 209466 bases at least Q20
            Insert size: 209790; sum-of-contigs
            Insert size: 194715; 2.8% error; agarose-fp
            Quality coverage: 8.31x in Q20 bases; sum-of-contigs Quality
            coverage: 8.96x in Q20 bases; agarose-fp
            -----
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
     source           1..209790
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="RP11-564014"
                     /clone_lib="RP11-564014"
     misc_feature     1..209790
                     /note="assembly_fragment:04568"
BASE COUNT  58386 a 41949 c 43662 g 65793 t
ORIGIN
            1 GGTTCAGTGCAGCCGAGATAAG 22
            |||||||
Db 77902 GGTTCAGTGCAGCCGAGATAAG 77881

Query Match      88.0%; Score 22; DB 2; Length 209790;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAAG 22
|||||
Db 77902 GGTTCAGTGCAGCCGAGATAAG 77881

RESULT 17

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AX070981/c
LOCUS      AX070981      355 bp      DNA      linear      PAT 25-JAN-2001
DEFINITION Sequence 1453 from Patent WO0102568.
ACCESSION  AX070981
VERSION     AX070981.1 GI:12581254
KEYWORDS
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 355)
REFERENCE  Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.,
AUTHORS   Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
            Lamson,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
            Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE     Human genes and gene expression products
JOURNAL   Patent: WO 0102568-A 1453 11-JAN-2001;
            CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
     source           1..355
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT  87 a 94 c 72 g 102 t
ORIGIN
            1 GGTTCAGTGCAGCCGAGATAA 21
            |||||||
Db 60 GGTTCAGTGCAGCCGAGATAA 40

Query Match      84.0%; Score 21; DB 6; Length 355;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
|||||
Db 60 GGTTCAGTGCAGCCGAGATAA 40

RESULT 18
HSPA27G11/c
LOCUS      HSPA27G11      520 bp      DNA      linear      PRI 23-AUG-1996
DEFINITION H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA27G11.
ACCESSION  Z79279
VERSION     Z79279.1 GI:1508557
KEYWORDS   Anonymous marker; single read.
SOURCE     Homo sapiens.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 520)
REFERENCE  Mungall,A.J., Huckle,E., Langford,C., Ross,M.T. and Rice,C.M.
AUTHORS   Direct Submission
TITLE     Submitted (22-AUG-1996) The Sanger Centre, Wellcome Trust Genome
JOURNAL   Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:
            humquery@sanger.ac.uk
COMMENT    Vector: pBSISK+.
FEATURES             Location/Qualifiers
     source           1..520
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /clone="SC6pA27G11"
                     /sex="female"
                     /tissue_type="EBV lymphoblastoid cell line"
                     /clone_lib="SC6pA"
                     /dev_stage="adult"
                     /note="The estimated purity of the flow-sorted chromosome
                     6 library is >97%"
BASE COUNT  101 a 137 c 85 g 197 t
ORIGIN
            1 GGTTCAGTGCAGCCGAGATAA 21
            |||||||

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Db 419 GGTTCAGTGCAGCGAGATAA 399

RESULT 19
AX390380/c
LOCUS
DEFINITION Sequence 5308 from Patent WO0214500.
ACCESSION AX390380
VERSION AX390380.1 GI:19583510
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Escobedo,J., Garcia,P.D., Sudduth-Klinger,J., Reinhard,C.,
Randazzo,F., Lamson,G., Scott,E.M., Zhang,G., Kassam,A., Pot,D. and
Labat,I.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0214500-A 5308 21-FEB-2002;
MEDLINE CHIRON CORPORATION (US) ; Hyseq Inc. (US)
PUBMED
FEATURES
source
Location/Qualifiers
1..608
BASE COUNT 153 a 126 c 114 g 215 t
ORIGIN
Query Match 84.0%; Score 21; DB 6; Length 608;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
|||||
Db 501 GGTTCAGTGCAGCGAGATAA 481

RESULT 20
AX195315/c
LOCUS
DEFINITION Sequence 19 from Patent WO0151631.
ACCESSION AX195315
VERSION AX195315.1 GI:15385864
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Reske-Kunz,A., Ross,X., Ross,R. and Bros,M.
TITLE Regulatory sequence for the specific expression in dendritic cells
and uses thereof
JOURNAL Patent: WO 0151631-A 19 19-JUL-2001;
MEDLINE Reske-Kunz, Angelika (DE) ; Ross, Xiaolan (DE) ; Ross, Ralf (DE) ;
PUBMED Bros, Matthias (DE)
FEATURES
source
Location/Qualifiers
1..1242
BASE COUNT 230 a 330 c 387 g 295 t
ORIGIN
Query Match 84.0%; Score 21; DB 6; Length 1242;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
|||||
Db 522 GGTTCAGTGCAGCGAGATAA 502

RESULT 21
HUMER2B/c
LOCUS
DEFINITION Sequence 34 from Patent WO0151631.
ACCESSION AX195330
VERSION AX195330.1 GI:15385879
KEYWORDS
SOURCE human.

```

```

LOCUS HUMER2B 1838 bp DNA linear PRI 27-APR-1993
DEFINITION Human tyrosine kinase-type receptor (HER2) gene, partial cds.
ACCESSION M12036
VERSION M12036.1 GI:183988
KEYWORDS tyrosine kinase.
SOURCE Human fetal DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Coussens,L., Yang-Feng,T.L., Liao,Y.-C., Chen,E., Gray,A.,
McGrath,J., Seeburg,P.H., Libermann,T.A., Schlessinger,J.,
Francke,U., Levinson,A. and Ullrich,A.
TITLE Tyrosine Kinase receptor with extensive homology to EGF receptor
shares chromosomal location with neu oncogene
JOURNAL Science 230 (4730), 1132-1139 (1985)
MEDLINE 86070181
PUBMED
FEATURES
source
Location/Qualifiers
1..1838
/organism="Homo sapiens"
/db_xref="taxon:9606"
join(1..92,806..991,1129..1284,1405..1488)
/partial
/notes="HER2 receptor (AA at 3)"
/codon_start=3
/protein_id="AAA35978.1"
/db_xref="GI:183988"
/translation="IPDGENVKIPVAIKVLRNTSPKANKELDEAYVMAGVGPVYS
RLIGTCTSTVOLVTLMPYGCGLLDHVRNKGRLGSDLLNWCMIKAGMSYLEDVRL
VHRLAARNVLKSPNHVKITDFGLARLLDIDETREYHAGSGKVPKWMALRSILRRF
THQSDWNSYGV"
exon <1..92
exon 1..92
/partial
/notes="exon x"
intron 93..805
/notes="intron A"
exon <806..991
/notes="exon x+1"
exon 806..991
/notes="exon x+1"
intron 992..1128
/notes="intron B"
exon <1129..1284
/notes="exon x+2"
intron 1285..1404
/notes="intron C (no splice consensus); putative"
exon 1405..>1485
/notes="exon x+3"
intron 1486..>1838
/notes="intron D (no splice consensus); putative"
BASE COUNT 358 a 487 c 551 g 442 t
ORIGIN Chromosome 17q21-q22.
Query Match 84.0%; Score 21; DB 9; Length 1838;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGATAA 21
|||||
Db 282 GGTTCAGTGCAGCGAGATAA 262

RESULT 22
AX195330/c
LOCUS
DEFINITION Sequence 34 from Patent WO0151631.
ACCESSION AX195330
VERSION AX195330.1 GI:15385879
KEYWORDS
SOURCE human.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Reske-Kunz,A., Ross,X., Ross,R. and Bros.M.
TITLE Regulatory sequence for the specific expression in dendritic cells
and uses thereof
JOURNAL Patent: WO 0151631-A 34 19-JUL-2001;
Reske-Kunz, Angelika (DE) ; Ross, Xiaolan (DE) ; Ross, Ralf (DE) ;
Bros, Matthias (DE)
FEATURES
source Location/Qualifiers
1..2843
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 499 a 909 c 827 g 608 t
ORIGIN
Query Match 84.0%; Score 21; DB 6; Length 2843;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCCGAGATAA 21
|||||
Db 1607 GGTTCAGTGAGCCGAGATAA 1587
|||||

RESULT 23
HSAC000981/c HSAC000981 3761 bp DNA linear PRI 09-APR-1997
LOCUS Homo sapiens (subclone 2_c6 from p1 H31) DNA sequence, complete
sequence.
ACCESSION AC000981
VERSION AC000981.1 GI:1930997
KEYWORDS HTG.
SOURCE Homo sapiens (Subclones in pOT2 from p1 clone H31) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Martin,C.H., Arcaina,T.T., Bondoc,M.M., Chiang,A., Critz,P.A.,
Davis,C.A., Doyle,C.M., Ericsson,C.L., Farfan,D.E., Gunning,K.M.,
Houston,K.A., Jaklevic,M.A., Kadner,K.E., Kim,K., Kim,S.F.,
Ko,C.L., Lewis,K.D., Li,M., Lindquist,K.J., Lomotan,M.A.,
Lustre,V.M., Machrus,M.O., Mayeda,C.A., Miguel,T.M., Miller,C.A.,
Mok,M.S., Pacleb,J.M., Patel,S.G., Santos,R.F., Subramanian,S.,
Wan,K.H., Whitelaw,K.R., Yee,A., Yen,R.T., Yu,C. and Palazzolo,M.J.
Sequencing of human chromosome 5q
Unpublished (1996)
2 (bases 1 to 3761)
Martin,C.H., Arcaina,T.T., Bondoc,M.M., Chiang,A., Critz,P.A.,
Davis,C.A., Doyle,C.M., Ericsson,C.L., Farfan,D.E., Gunning,K.M.,
Houston,K.A., Jaklevic,M.A., Kadner,K.E., Kim,K., Kim,S.F.,
Ko,C.L., Lewis,K.D., Li,M., Lindquist,K.J., Lomotan,M.A.,
Lustre,V.M., Machrus,M.O., Mayeda,C.A., Miguel,T.M., Miller,C.A.,
Mok,M.S., Pacleb,J.M., Patel,S.G., Santos,R.F., Subramanian,S.,
Wan,K.H., Whitelaw,K.R., Yee,A., Yen,R.T., Yu,C. and Palazzolo,M.J.
Direct Submission
Submitted (09-APR-1997)
Sequence submitted by:
Human Genome Center
Lawrence Berkeley National Laboratory, MS 74-157
Berkeley, CA 94720
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Website (http://www.hgc.lbl.gov/sequence-archive.html) or
send email to humangenome.lbl.gov.
FEATURES
source Location/Qualifiers
1..3761
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="p1 H31 (5219)"
/sub_clone="2_c6"

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BASE COUNT 1040 a 824 c 639 g 1258 t
ORIGIN
Query Match 84.0%; Score 21; DB 9; Length 3761;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCCGAGATAA 21
|||||
Db 978 GGTTCAGTGAGCCGAGATAA 958
|||||

RESULT 24
AX195368/c AX195368 16951 bp DNA linear PAT 28-AUG-2001
LOCUS Sequence 72 from Patent WO0151631.
ACCESSION AX195368
VERSION AX195368.1 GI:15385917
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Reske-Kunz,A., Ross,X., Ross,R. and Bros.M.
TITLE Regulatory sequence for the specific expression in dendritic cells
and uses thereof
JOURNAL Patent: WO 0151631-A 72 19-JUL-2001;
Reske-Kunz, Angelika (DE) ; Ross, Xiaolan (DE) ; Ross, Ralf (DE) ;
Bros, Matthias (DE)
FEATURES
source Location/Qualifiers
1..16951
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 3224 a 4928 c 5200 g 3599 t
ORIGIN
Query Match 84.0%; Score 21; DB 6; Length 16951;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCCGAGATAA 21
|||||
Db 14694 GGTTCAGTGAGCCGAGATAA 14674
|||||

RESULT 25
AY044229/c AY044229 16952 bp DNA linear PRI 15-SEP-2001
LOCUS Homo sapiens fascin gene, complete cds.
ACCESSION AY044229
VERSION AY044229.1 GI:15625240
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Bros,M., Ross,X.L., Reske-Kunz,A.B. and Ross,R.
TITLE Human Fascin Gene Sequence
JOURNAL Unpublished
2 (bases 1 to 16952)
Bros,M., Ross,X.L., Reske-Kunz,A.B. and Ross,R.
Direct Submission
Submitted (08-JUL-2001) Clinical Research Unit, Department of
Dermatology, Johannes Gutenberg University, Obere Zahlbacher Str.
63, Mainz 55131, Germany
FEATURES
source Location/Qualifiers
1..16952
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
/map="7p22"

```



```

TATA_signal      /clone="RPCIF704C24766Q3/4"
mRNA             2924..2930
                join(2958..3910,13399..13555,13638..13759,14005..14172,
                15415..16791)
                /product="fascin"
CDS              join(3079..3910,13399..13555,13638..13759,14005..14172,
                15415..15617)
                /note="actin bundling protein"
                /codon_start=1
                /product="fascin"
                /protein_id="AA01526.1"
                /db_xref="GI:15625241"
                /translation="MTANGTAEAVIQFGLINGNKYLTAERGPKVNASASSLKKKO
                IWLQEPDDEAGSAACLRSLHGLYLAADKGNVTCREVPDPCDFLIIVADDGRWS
                LQSAHRRYEGGEDRLSCFAQTVSPAERKSVHIAHPQVNTYVTRKYAHLGARA
                DEIADVDPMGVDLSILPAQDYSYVQTADEHRLHDLGRLVAREPAATGYTLFFRS
                GKAFRCDEGRVLASGSGELKAGKATVKGDELFALQSCAVVLOAANERNVSR
                OGMLSANODEETDQTEFLEIDRDTKCAAFTHGKYWTLTATGSGVQSTASSKNASC
                YFLEMDRRLITLRASNGKFVTKKNGQLAASVETAGDSLFMLKILNRPILIVFRGH
                GFICRKVTGLDNRSSYDVFQLEFNDGAYNKDSGKYWTWGSASVTSSTGTPVD
                FFEFCDYNKVAKVGGRYLKGHAGLVKASNEVDFASLWEY"
BASE COUNT      3224 a 4928 c 5201 g 3599 t
ORIGIN
Query Match      84.0%; Score 21; DB 9; Length 16952;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCGGAGATAA 21
|||||
Db 14694 GGTTCAGTGAGCGGAGATAA 14674

RESULT 26
AC092149/c
LOCUS             AC092149             24144 bp    DNA    linear    HTG 22-JUN-2001
DEFINITION       Homo sapiens chromosome RPCI-11 clone RP11-96J6, WORKING DRAFT
ACCESSION        AC092149
VERSION          AC092149.1 GI:14523004
KEYWORDS          HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE            Homo sapiens.
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 24144)
Waterston,R.H.
Direct Submission
Submitted (22-JUN-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0096J06
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Consensus program: Phrap; version 0.990319
Consensus quality: 19352 bases at least Q40
Consensus quality: 20525 bases at least Q30
Consensus quality: 21376 bases at least Q20
Insert size: 194000; agarose-fp

```

Insert size: 22444; sum-of-contigs
Quality coverage: 0.17 in Q20 bases; agarose-fp
Quality coverage: 1.55 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 1181: contig of 1181 bp in length

* 1182: gap of unknown length

* 1282: contig of 1140 bp in length

* 2422: gap of unknown length

* 2522: contig of 1250 bp in length

* 3772: gap of unknown length

* 3872: contig of 1196 bp in length

* 5068: gap of unknown length

* 5168: contig of 1174 bp in length

* 6342: gap of unknown length

* 6442: contig of 1125 bp in length

* 7566: gap of unknown length

* 7667: contig of 1047 bp in length

* 8714: gap of unknown length

* 8814: contig of 1116 bp in length

* 9929: gap of unknown length

* 10029: contig of 1307 bp in length

* 11337: gap of unknown length

* 11437: gap of unknown length

* 12572: gap of unknown length

* 12672: contig of 1043 bp in length

* 13715: gap of unknown length

* 13815: contig of 1075 bp in length

* 14890: gap of unknown length

* 14990: contig of 1081 bp in length

* 16071: gap of unknown length

* 16171: contig of 1548 bp in length

* 17119: gap of unknown length

* 17819: contig of 1561 bp in length

* 19380: gap of unknown length

* 19480: contig of 1089 bp in length

* 20569: gap of unknown length

* 20669: contig of 1457 bp in length

* 22126: gap of unknown length

* 22226: contig of 1919 bp in length.

Location/Qualifiers

1..24144

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="RPCI-11"

/clone="RP11-96J6"

1..1181

/note="assembly_name:Contig19"

1282..2421

/note="assembly_name:Contig22"

2522..3771

/note="assembly_name:Contig24"

3872..5067

/note="assembly_name:Contig33"

5168..6341

/note="assembly_name:Contig35"

6442..7566

/note="assembly_name:Contig36"

7667..8713

/note="assembly_name:Contig38"

8814..9929

/note="assembly_name:Contig40"

10030..11336

/note="assembly_name:Contig41"

11437..12571

/note="assembly_name:Contig42"

FEATURES

source

1..24144

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="RPCI-11"

/clone="RP11-96J6"

1..1181

/note="assembly_name:Contig19"

1282..2421

/note="assembly_name:Contig22"

2522..3771

/note="assembly_name:Contig24"

3872..5067

/note="assembly_name:Contig33"

5168..6341

/note="assembly_name:Contig35"

6442..7566

/note="assembly_name:Contig36"

7667..8713

/note="assembly_name:Contig38"

8814..9929

/note="assembly_name:Contig40"

10030..11336

/note="assembly_name:Contig41"

11437..12571

/note="assembly_name:Contig42"

COMMENT

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misc_feature      12672..13714
/note="assembly_name:Contig43"
misc_feature      13815..14889
/note="assembly_name:Contig44"
misc_feature      14990..16070
/note="assembly_name:Contig46"
misc_feature      16171..17718
/note="assembly_name:Contig47"
misc_feature      17819..19379
/note="assembly_name:Contig48"
misc_feature      19480..20568
/note="assembly_name:Contig51"
misc_feature      20669..22125
/note="assembly_name:Contig52"
misc_feature      22226..24144
/note="assembly_name:Contig53"
BASE COUNT      6285 a 4871 c 4766 g 6518 t 1704 others
ORIGIN
Query Match      84.0%; Score 21; DB 2; Length 24144;
Best Local Similarity 100.0%; Pred. No. 0.0042;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
|||||
Db 14451 GGTTCAGTGAGCCGAGATAA 14431

RESULT 27
HSL112A12      25889 bp DNA linear PRI 23-NOV-1999
LOCUS
DEFINITION      Human DNA sequence from cosmid L112A12, Huntington's Disease.
ACCESSION      Z68225
VERSION      4p16.3; CpG island.
KEYWORDS
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
I (bases 1 to 25889)
Direct Submission
Submitted (12-DEC-1995) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RO, England. E-mail enquiries: humquery@sanger.ac.uk
IMPORTANT:
This sequence is the entire insert of clone L112A12. L112A12 is
from cosmid library LA04NC01 constructed at the Human Genome
Center, Los Alamos National Laboratory, NM 87545 under the auspices
of the U.S. Department of Energy. The library was constructed using
flow-sorted human chromosome 4 from a Hamster-Human hybrid cell
line (UV20HL21-27) containing human chromosomes 4, 8 and 21.
VECTOR: scos1
L112A12 is contained in a clone contig spanning
2Mb which is described in Baxendale et al, Nature Genetics 4 ( 1993
) 181- 186. See also Myers et al, Cytogenet Cell Genet. 66 ( 1994
) 218-230.
FEATURES
source
1..25889
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4p16.3"
/clone="LA04NC01-112A12"
/cell_line="UV20HL21-27"
/clone_lib="LA04NC01"
133..200
/note="2 copies of 34 mer 90 % conserved"
repeat_region
167..210
/note="11 copies of 4 mer 86 % conserved"
repeat_region
1102..1169
/note="2 copies of 34 mer 97 % conserved; 34 copies of 2
mer 97 % conserved"

```

```

repeat_region      1104..1167
/note="16 copies of 4 mer 98 % conserved"
repeat_region      1829..1872
/note="11 copies of 4 mer 100 % conserved"
repeat_region      3065..3170
/note="2 copies of 53 mer 93 % conserved"
repeat_region      4921..5272
/note="MLTIC element fragment"
5142..5258
/note="MLTIB element fragment"
5775..5818
/note="11 copies of 4 mer 89 % conserved"
repeat_region      7952..7997
/note="MLTID element fragment"
8593..8698
/note="2 copies of 53 mer 95 % conserved"
repeat_region      9263..9553
/note="Alu repeat: matches 1..308 of consensus"
12998..13096
/note="MIR element fragment"
15090..15264
/note="MER42C element fragment"
15272..15563
/note="Alu repeat: matches 1..308 of consensus"
15588..15879
/note="Alu repeat: matches 1..308 of consensus"
15898..16003
/note="MER42C element fragment"
16381..16530
/note="LI element fragment"
16755..16829
/note="MLTIC element fragment"
17329..17437
/note="MLTIC element fragment"
17331..17504
/note="MLTIB element fragment"
17513..17599
/note="MLTIC element fragment"
19285..19573
/note="Alu repeat: matches 1..308 of consensus"
19863..20421
/note="match: 5' EST T57716 clone 79379; Paired with EST
T57677 matching this cosmid"
/note="match: 3' EST T57677 clone 79379; Paired with EST
T57716 matching this cosmid"
21469..21672
/note="6 copies of 34 mer 94 % conserved"
repeat_region      22060..22125
/note="MIR element fragment"
24247..25887
/note="putative CpG island"
BASE COUNT      5888 a 7239 c 7460 g 5302 t
ORIGIN
Query Match      84.0%; Score 21; DB 9; Length 25889;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
|||||
Db 15804 GGTTCAGTGAGCCGAGATAA 15824

RESULT 28
AC108170
LOCUS
DEFINITION      Homo sapiens BAC clone RP11-1401P21 from 4, complete sequence.
ACCESSION      AC108170
VERSION      AC108170.4 GI:19807987
KEYWORDS      HTG.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

1 (bases 1 to 26913)
Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074
2 (bases 1 to 26913)
Scott,K., Haakenson,W., Dignan,G. and Bielicki,L.
The sequence of Homo sapiens BAC clone RP11-1401P21
Unpublished (2001)
3 (bases 1 to 26913)
Waterston,R.H.
Direct Submission
Submitted (25-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 26913)
Waterston,R.H.
Direct Submission
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 26913)
Waterston,R.H.
Direct Submission
Submitted (29-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 26913)
Waterston,R.
Direct Submission
Submitted (16-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 29, 2002 this sequence version replaced gi:19424678.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_NHI401P21

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanesi,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.chori.org>
VECTOR: pBACE3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC004045, 2000 bp overlap; the
clone sequenced to the right is RP11-286E11, 2000 bp overlap.
Actual start of this clone is at base position 140669 of
RP11-109F18; actual end is at base position 93148 of RP11-286E11.

FEATURES

Location/Qualifiers	Source
1..26913	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/chromosome="4"	
/map="4"	
/clone="RP11-1401P21"	
/clone_lib="RPCI-11"	
1..887	
/rpt_family="L1"	repeat_region
890..1082	repeat_region
/rpt_family="L1"	
1083..1403	repeat_region
/rpt_family="MER2_type"	
1404..1460	repeat_region
/rpt_family="L1"	
1520..1597	repeat_region
/rpt_family="MIR"	
2190..2627	repeat_region
/rpt_family="L1"	
2628..2753	repeat_region
/rpt_family="L1"	
3254..3275	repeat_region
/rpt_family="AT-rich"	
3320..3614	repeat_region
/rpt_family="Alu"	
4240..4831	repeat_region
/rpt_family="L1"	
4919..5249	repeat_region
/rpt_family="L1"	
5552..5758	repeat_region
/rpt_family="L1"	
5896..6077	repeat_region
/rpt_family="L1"	
6636..6820	repeat_region
/rpt_family="MER1_type"	
6946..7012	repeat_region
/rpt_family="MIR"	
7013..7322	repeat_region
/rpt_family="Alu"	
7323..7504	repeat_region
/rpt_family="MIR"	
8270..8495	repeat_region
/rpt_family="L1"	
8493..10585	repeat_region
/rpt_family="L1"	
10735..11094	repeat_region
/rpt_family="MaLR"	
11790..12230	repeat_region
/rpt_family="ERV1"	
13122..13148	repeat_region
/rpt_family="(CA)n"	
13465..13771	repeat_region
/rpt_family="Alu"	
13910..14213	repeat_region
/rpt_family="L1"	
14206..14287	repeat_region
/rpt_family="L1"	
14288..14578	repeat_region
/rpt_family="Alu"	
14579..15228	repeat_region
/rpt_family="L1"	
15230..15382	repeat_region
/rpt_family="L1"	
15383..15677	repeat_region
/rpt_family="Alu"	
15678..16179	repeat_region


```
repeat_region /note="MIR repeat: matches 12. .92 of consensus"
9503. .9745
repeat_region /note="MIR repeat: matches 8. .262 of consensus"
9844. .10070
repeat_region /note="AlusC repeat: matches 64. .290 of consensus"
10210. .10307
repeat_region /note="MIR repeat: matches 47. .147 of consensus"
10471. .10679
repeat_region /note="MER20 repeat: matches 1. .218 of consensus"
11021. .11373
repeat_region /note="L1MB4 repeat: matches 5816. .6181 of consensus"
11374. .11441
repeat_region /note="MER53 repeat: matches 105. .179 of consensus"
11379. .11458
repeat_region /note="MER53 repeat: matches 35. .113 of consensus"
11457. .11594
repeat_region /note="MER53 repeat: matches 1. .122 of consensus"
11952. .11997
repeat_region /note="23 copies 2 mer aa 84% conserved"
12155. .12335
repeat_region /note="MER58A repeat: matches 41. .224 of consensus"
12392. .12542
repeat_region /note="MIR repeat: matches 20. .182 of consensus"
12633. .12933
repeat_region /note="AlusX repeat: matches 1. .311 of consensus"
12944. .13496
repeat_region /note="Charliel repeat: matches 2217. .2760 of consensus"
14391. .14699
repeat_region /note="AluJo repeat: matches 1. .302 of consensus"
15229. .15423
repeat_region /note="AluJo repeat: matches 98. .287 of consensus"
complement(15661. .16169)
repeat_region /note="match: STS: Em:HS014H2S"
16135. .16443
repeat_region /note="Alusg repeat: matches 2. .308 of consensus"
16834. .16935
repeat_region /note="MIR repeat: matches 39. .146 of consensus"
17464. .17782
repeat_region /note="match: GSS: Em:AL172133"
complement(17467. .17750)
repeat_region /note="match: STS: Em:G05108"
17515. .17704
repeat_region /note="match: GSS: Em:AQ530947"
complement(17551. .17766)
repeat_region /note="match: GSS: Em:AL229216"
17555. .17704
repeat_region /note="match: GSS: Em:AQ530949"
17568. .17791
repeat_region /note="match: STS: Em:AQ029014"
complement(17578. .17778)
repeat_region /note="match: GSS: Em:AL003817"
17580. .17778
repeat_region /note="match: GSS: Em:AL306181 Em:AL348631"
complement(17625. .17823)
repeat_region /note="match: STS: Em:HS1024H7T"
17634. .17777
repeat_region /note="match: GSS: Em:AZ078596"
17650. .17808
repeat_region /note="match: GSS: Em:AQ740298"
17793. .18142
repeat_region /note="L2 repeat: matches 2366. .2705 of consensus"
18822. .18986
repeat_region /note="MIR repeat: matches 80. .257 of consensus"
19012. .19028
repeat_region /note="MIR repeat: matches 4. .19 of consensus"
19029. .19156
repeat_region /note="MER85 repeat: matches 1. .139 of consensus"
19157. .19368
repeat_region /note="MIR repeat: matches 19. .235 of consensus"
19722. .19944
repeat_region /note="MIR repeat: matches 25. .250 of consensus"
20583. .20864
repeat_region /note="AlusC repeat: matches 1. .297 of consensus"
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repeat_region 20927. .21114
/note="LTR33 repeat: matches 3. .184 of consensus"
22207. .22331
repeat_region /note="L2 repeat: matches 2572. .2702 of consensus"
22450. .22930
repeat_region /note="LTR32 repeat: matches 17. .471 of consensus"
23085. .23281
repeat_region /note="MLTJ repeat: matches 312. .516 of consensus"
24302. .24589
repeat_region /note="AluJb repeat: matches 1. .301 of consensus"
25088. .25185
repeat_region /note="49 copies 2 mer ct 68% conserved"
25726. .25766
repeat_region /note="MER5B repeat: matches 137. .178 of consensus"
25822. .25876
repeat_region /note="L1MBC repeat: matches 2239. .2291 of consensus"
25877. .26192
repeat_region /note="AlusX repeat: matches 1. .310 of consensus"
26193. .26687
repeat_region /note="L1MBC repeat: matches 1713. .2239 of consensus"
26705. .26758
repeat_region /note="MER5B repeat: matches 122. .174 of consensus"
27852. .27945
repeat_region /note="MIR repeat: matches 101. .197 of consensus"
27946. .28060
repeat_region /note="MER85 repeat: matches 1. .137 of consensus"
28061. .28093
repeat_region /note="MIR repeat: matches 70. .102 of consensus"
28268. .28716
repeat_region /note="match: GSS: Em:AQ320817"
28278. .28716
repeat_region /note="match: GSS: Em:AQ320816"
28302. .28479
repeat_region /note="L1PA5 repeat: matches 5966. .6141 of consensus"
28704. .29014
repeat_region /note="AlusQ repeat: matches 1. .310 of consensus"
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Query Match 84.0%; Score 21; DB 9; Length 31163;
Best Local Similarity 100.0%; Pred.No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTTCAGTGAGCGGAGATAA 21
|||||

Db 5405 GGTTCAGTGAGCGGAGATAA 5385

RESULT 30

AC005331

LOCUS

DEFINITION

AC005331

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC005331 Homo sapiens chromosome 19, cosmid R31341, complete sequence.
35581 bp DNA linear PRI 28-JUL-1998

AC005331 HTG.
GI:3342728

Homo sapiens.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Burkhardt-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regalia, W., Terry, A., Barnes, J.,
Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
Liu, S., Attix, C., Andreise, T., Frankheim, M., Amico-Keller, G.,
Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,
Kronmiller, B., Arellano, A., Olsen, A.S. and Carrano, A.V.

Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
serine protease gene cluster

Unpublished
2 (bases 1 to 35581)

Lamerdin, J.E.
Direct Submission

Submitted (28-JUL-1998) Joint Genome Institute, Lawrence Livermore


```

repeat_region complement(14942..15092)
repeat_region /rpt_family="LIMB7"
repeat_region 15107..15403
repeat_region /rpt_family="AluJo"
repeat_region 15416..15585
repeat_region /rpt_family="AluSg/x"
repeat_region 15604..15904
repeat_region /rpt_family="AluSx"
repeat_region 15936..16098
repeat_region /rpt_family="AluSg/x"
repeat_region complement(16215..16446)
repeat_region /rpt_family="LINE2"
repeat_region complement(16463..16631)
repeat_region /rpt_family="AluJb"
repeat_region complement(16632..16934)
repeat_region /rpt_family="AluSp"
repeat_region complement(16937..17068)
repeat_region /rpt_family="AluJb"
repeat_region complement(17373..17679)
repeat_region /rpt_family="AluSg"
repeat_region complement(17908..17985)
repeat_region /rpt_family="GC-rich"
repeat_region 18004..18063
repeat_region /rpt_family="(CGGG)n"
repeat_region complement(18056..18134)
repeat_region /rpt_family="(CGG)n"
repeat_region complement(18182..18237)
repeat_region /rpt_family="GC-rich"
misc_feature complement(18240..18367)

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Query Match      84.0% Score 21; DB 9; Length 35581;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAGTGGAGCGGAGATAA 21
|||||
Db 15820 GGTGAGTGGAGCGGAGATAA 15840

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RESULT 31
AC006138 LOCUS AC006138 37448 bp DNA linear PRI 05-DEC-1998
DEFINITION Homo sapiens clone UWGC:y54c194 from 6p21, complete sequence.
ACCESSION AC006138
VERSION AC006138.1 GI:3970958
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37448)
JANER,M., Guillaudoux,T., Vu,Q., Kutayavin,T., Harter,H. and Geraghty,D.E.
Large scale sequence analysis of the human MHC class I region
Unpublished (1998)
JOURNAL Fred Hutchinson Cancer Research Center
REMARK The Clinical Research Division
1100 Fairview Ave. N., P.O. Box 19024
Seattle, WA 98109-1024
Contact: Daniel E. Geraghty (geraghty@fhrc.org)
2 (bases 1 to 37448)
Geraghty,D.E. and Olson,M.V.
Direct Submission
JOURNAL Submitted (05-DEC-1998) Human Genome Center, University of
AUTHORS Washington, Box 352145, Seattle, WA 98195, USA
JOURNAL University of Washington Human Genome Center
REMARK Box 352145 Seattle, WA 98195
Contact: Daniel E. Geraghty (geraghty@fhrc.org)
COMMENT Overlapping Sequences:
5': UWGC:y54c222 (Genbank Accession: AC006049)
3': UWGC:y55c174
-----
Sequence Quality Assessment:

```

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

Double stranded (DS) coverage: 63.0%
DS or two chemistry coverage: 99.8%
Single stranded regions: 2

Sequence Validation:

This sequence has been validated by Multiple Complete Digest Mapping. Comparison of the experimentally derived map digest fragments with sequence-predicted fragments is given below. Small fragments below a variable cutoff (approximately 400-600bp) are not mapped and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragment groups are separated by dashed lines.

BgIII		HindIII		NsiI	
Map	Seq	Map	Seq	Map	Seq
10275.50	9934.00	4611.50	4460.00	2433.00	2383.00
7579.50	7368.00	6983.50	6709.00	1325.00	1321.00
2393.50	2344.00	2265.33	2230.00	2932.50	2884.00
1196.38	1179.00	16560.50	16097.00	2782.00	2732.00
7774.00	7466.00	3077.84	2987.00	5692.00	5546.00
3880.47	3758.00			6110.11	5903.00

FEATURES

Location/Qualifiers		source
1..37448	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	/chromosome="6"	
	/map="6p21"	
	/clone="CGM1:D100E8"	
	/sub_clone="UMGC:y54c194"	
	/cell_line="CGM1"	
	/clone_lib="Wash U YAC Library"	
1677..2279	/rpt_family="Alu"	repeat_region
	complement(4391..4681)	repeat_region
	/rpt_family="Alu"	repeat_region
	complement(9888..10175)	repeat_region
	/rpt_family="Alu"	repeat_region
10603..10887	/rpt_family="Alu"	repeat_region
10912..11167	/rpt_family="Alu"	repeat_region
11217..11803	/rpt_family="Alu"	repeat_region
11958..12256	/rpt_family="Alu"	repeat_region
12303..12582	/rpt_family="Alu"	repeat_region
	/rpt_family="Alu"	repeat_region
	complement(12597..12687)	repeat_region
	/rpt_family="MER5"	repeat_region
13133..13711	/rpt_family="Alu"	repeat_region
13765..14052	/rpt_family="Alu"	repeat_region
	/rpt_family="Alu"	repeat_region
	complement(14068..14349)	repeat_region
	/rpt_family="Alu"	repeat_region
	complement(14767..15042)	repeat_region
	/rpt_family="Alu"	repeat_region

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repeat_region 15558..15808
/rpt_family="Alu"
repeat_region 16088..16169
/rpt_family="Alu"
repeat_region 16408..16723
/rpt_family="Alu"
repeat_region complement(16826..16898)
/rpt_family="MIR"
repeat_region complement(16962..17246)
/rpt_family="Alu"
repeat_region 18131..18416
/rpt_family="Alu"
repeat_region 18430..18718
/rpt_family="Alu"
repeat_region complement(20650..20883)
/rpt_family="Alu"
repeat_region 20973..21256
/rpt_family="Alu"
repeat_region 21612..21899
/rpt_family="Alu"
repeat_region 22077..22371
/rpt_family="Alu"
repeat_region complement(22407..22621)
/rpt_family="Alu"
repeat_region complement(22623..23251)
/rpt_family="Alu"
repeat_region complement(25158..25487)
/rpt_family="Alu"
repeat_region 27289..27574
/rpt_family="Alu"
repeat_region 27918..28216
/rpt_family="Alu"
repeat_region 28576..28865
/rpt_family="Alu"
repeat_region 29305..29563
/rpt_family="Alu"
repeat_region complement(29902..30200)
/rpt_family="Alu"
repeat_region 30514..30810
/rpt_family="Alu"
repeat_region complement(31248..31533)
/rpt_family="Alu"
repeat_region 33681..33981
/rpt_family="Alu"
repeat_region complement(34178..34470)
/rpt_family="Alu"
repeat_region 34922..35197
/rpt_family="Alu"
repeat_region 35845..36119
/rpt_family="Alu"
BASE COUNT 9686 a 9222 c 8828 g 9712 t
ORIGIN
Query Match 84.0%; Score 21; DB 9; Length 37448;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGCGAGTGAGCCGAGATAA 21
|||||
Db 13639 GGTGCGAGTGAGCCGAGATAA 13659
|||||

RESULT 32
AC000035/c
LOCUS AC000035 38429 bp DNA linear PRI 01-JUN-2000
DEFINITION Homo sapiens Chromosome 22q12 Cosmid Clone 1147g11, complete
sequence.
ACCESSION AC000035
VERSION AC000035.2 GI:4560484
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 38429)
Pan, H., Hartman, K., Peyrard, M., Fransson, I., Dumanski, J. P. and
Roe, B. A.
Homo sapiens Chromosome 22q12 Cosmid Clone 1147g11 In NEFH, MDR
Region
Unpublished
REFERENCE 2 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REMARK 1147g11
AUTHORS 3 (bases 1 to 38429)
TITLE Direct Submission
JOURNAL Submitted (18-FEB-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 4 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 5 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 6 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 7 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 8 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 9 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (20-AUG-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 10 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 11 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 12 (bases 1 to 38429)
AUTHORS Roe, B. A.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

```


OK 73019, USA
 13 (bases 1 to 38429)
 Roë B.A.
 Direct Submission
 Submitted (13-NOV-1998) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 14 (bases 1 to 38429)
 Roë B.A.
 Direct Submission
 Submitted (22-NOV-1998) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 15 (bases 1 to 38429)
 Roë B.A.
 Direct Submission
 Submitted (04-DEC-1998) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 16 (bases 1 to 38429)
 Roë B.A.
 Direct Submission
 Submitted (09-APR-1999) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 17 (bases 1 to 38429)
 Pan,H., Hartman,K., Peyrard,M., Fransson,I., Dumanski,J.P. and
 Roë B.A.
 Direct Submission
 Submitted (01-JUN-2000) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 On Apr 9, 1999 this sequence version replaced gi:3962508.
 Because these overlapping clones came from different libraries
 there are numerous instances of insertions, deletions, and single
 nucleotide polymorphisms in the overlapping regions below
 AC000025(566c1) 27423 65851 (69554) overlaps AC000035(1147g11) 1
 38429 (0) AC000035(1147g11) 10813 38429 (0) overlaps
 AC005529(bk256d12) 1 27604 (290884) AC000035(1147g11) 11037 38429
 (0) overlaps AC005527(489d1) 1 27380 (121928).

FEATURES
 Location/Qualifiers
 I. .38429
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="22q12"
 /clone="1147g11"
 BASE COUNT 10052 a 9780 c 9922 g 8675 t
 ORIGIN

Query Match 84.0%; Score 21; DB 9; Length 38429;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTCAGCCGAGATAA 21
 |||||
 Db 25328 GGTTCAGTCAGCCGAGATAA 25308

RESULT 33
 HSU46H11
 LOCUS
 DEFINITION Human DNA sequence from clone LLOXNC01-46H11 on chromosome X
 Contains a gene for a novel protein, complete sequence.
 ACCESSION 282254
 VERSION 282254.1 GI:1817669
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 38540)
 AUTHORS Dodsworth,S.
 TITLE Direct Submission

JOURNAL

Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk

COMMENT

On Feb 6, 1997 this sequence version replaced gi:1781019.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em, EMBL; Sw,
 SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP
 database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep this sequence
 was generated from part of bacterial clone contigs of human
 chromosome X, constructed by the Sanger Centre Chromosome X Mapping
 Group. Further information can be found at
 http://www.sanger.ac.uk/HGP/ChrX

LLOXNC01-46H11 is from the Lawrence Livermore National Laboratory
 flow-sorted

X chromosome cosmid library LLOXNC01

VECTOR: lavrist16

This sequence is the entire insert of clone LLOXNC01-46H11.

FEATURES

source

Location/Qualifiers

I. .38540

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="X"

/clone="LLOXNC01-46H11"

/clone_lib="LLOXNC01"

I. .4

/note="orientation unknown"

repeat_region

27. .378

/note="L1P1A13 repeat: matches 203. .604 of consensus"

repeat_region

444. .837

/note="L1P1A13 repeat: matches -314. .84 of consensus"

repeat_region

836. .2696

/note="L1P1A12 repeat: matches -1416. .573 of consensus"

misc_feature

complement(2717. .3191)

/note="match: GSS: Em:AQ807555"

repeat_region

3326. .3415

/note="L2 repeat: matches 52. .142 of consensus"

repeat_region

3428. .3544

/note="FLAM_A repeat: matches 1. .124 of consensus"

repeat_region

3556. .4338

/note="L2 repeat: matches 157. .886 of consensus"

repeat_region

4339. .4665

/note="MLP1B repeat: matches 3. .388 of consensus"

repeat_region

4666. .4997

/note="L2 repeat: matches 886. .1229 of consensus"

repeat_region

5112. .5311

/note="L2 repeat: matches 2244. .2446 of consensus"

repeat_region

5306. .6783

/note="L2 repeat: matches 1218. .2746 of consensus"

repeat_region

6798. .7353

/note="L1ME repeat: matches 5397. .5937 of consensus"

repeat_region

7354. .7667

/note="L1P1A7 repeat: matches 5827. .6141 of consensus"

repeat_region

7668. .7860

/note="L1ME repeat: matches 5186. .5398 of consensus"

repeat_region

8020. .8605

/note="L1ME3A repeat: matches 5555. .6158 of consensus"

repeat_region

9188. .9554

/note="LTR40b repeat: matches 86. .462 of consensus"

misc_feature

complement(9221. .9731)

misc_feature /note="match: GSS: Em:AQ462192"
complement(9327..9723)
misc_feature /note="match: GSS: Em:AQ181119"
9734..10214
repeat_region /note="match: GSS: Em:AQ468867"
9888..10332
repeat_region /note="MSTRC repeat: matches 1..426 of consensus"
10467..10769
repeat_region /note="AluX repeat: matches 1..312 of consensus"
11111..11210
repeat_region /note="MIR repeat: matches 2..100 of consensus"
11485..11771
repeat_region /note="AluX repeat: matches 1..288 of consensus"
11772..11807
repeat_region /note="18 copies 2 mer ta 83% conserved"
12197..12286
repeat_region /note="L2 repeat: matches 2207..2296 of consensus"
12496..12599
repeat_region /note="L2 repeat: matches 2645..2750 of consensus"
12648..12767
repeat_region /note="L2 repeat: matches 1713..1843 of consensus"
13197..13501
repeat_region /note="AluSg repeat: matches 1..305 of consensus"
13592..14613
repeat_region /note="L1MB3 repeat: matches 4672..5721 of consensus"
14614..15487
repeat_region /note="L1MB4 repeat: matches 5424..6293 of consensus"
15488..15867
repeat_region /note="L1MB3 repeat: matches 5721..5895 of consensus"
15860..15923
repeat_region /note="L1MB3 repeat: matches 6044..6108 of consensus"
15926..16083
repeat_region /note="L2 repeat: matches 716..875 of consensus"
16885..17646
misc_feature /note="MER21B repeat: matches 1..790 of consensus"
17374..17791
repeat_region /note="match: GSS: Em:AQ773679"
17787..17983
misc_feature /note="L1MC4 repeat: matches 7797..7977 of consensus"
17948..18574
repeat_region /note="match: GSS: Em:AQ270655"
18538..18585
repeat_region /note="16 copies 3 mer att 79% conserved"
18792..18927
repeat_region /note="L2 repeat: matches 2528..2660 of consensus"
18928..19231
repeat_region /note="AluSp repeat: matches 1..301 of consensus"
19232..19450
misc_feature /note="L2 repeat: matches 2311..2528 of consensus"
complement(19468..20114)
misc_feature /note="match: GSS: Em:AQ381550"
complement(19830..19905)
misc_feature /note="match: STR: Em:L77851"
20128..20685
misc_feature /note="match: GSS: Em:AQ802353"
complement(20418..20763)
misc_feature /note="match: GSS: Em:AQ585332"
21561..22019
repeat_region /note="match: GSS: Em:AQ267614"
22028..22249
repeat_region /note="MER20 repeat: matches 1..218 of consensus"
22858..22957
repeat_region /note="5 copies 20 mer 85% conserved"
22967..23026
repeat_region /note="3 copies 20 mer 83% conserved"
22997..23152
repeat_region /note="4 copies 39 mer 86% conserved"
23100..23175
repeat_region /note="2 copies 38 mer 90% conserved"
24241..24404
repeat_region /note="MIR repeat: matches 17..187 of consensus"
25362..25482
/note="MIR repeat: matches 21..142 of consensus"

repeat_region 25715..25937
/note="MIR repeat: matches 25..262 of consensus"
25946..26418
misc_feature /note="match: GSS: Em:B44804"
27225..27406
repeat_region /note="MER5A repeat: matches 11..188 of consensus"
27405..27497
repeat_region /note="MIR repeat: matches 15..120 of consensus"
27566..27625
repeat_region /note="30 copies 2 mer aa 80% conserved"
27852..27939
repeat_region /note="MIR repeat: matches 67..150 of consensus"
28131..31922
gene /gene="cu46H11.1"
mRNA join(28131..28265,28627..28883,29277..29328,29516..29740)
/gene="cu46H11.1"
/product="cu46H11.1 (novel protein)"
/note="isoform 3"
match: CDNAS: Em:AK026512"
/evidence=not_experimental
mRNA join(28213..28265,28813..28954)
/gene="cu46H11.1"
/product="cu46H11.1 (novel protein)"
/note="isoform 4"
match: ESTs: Em:AA334897"
/evidence=not_experimental
misc_feature 28423..28956
/gene="cu46H11.1"
/note="CpG island"
/evidence=not_experimental
mRNA join(28628..28765,29235..29339,29523..29684,30095..31922)
/gene="cu46H11.1"
/product="cu46H11.1 (novel protein)"
/note="isoform 1"
match: CDNAS: Em:AK005317
match: ESTs: Em:BG700477 Em:BG702186 Em:BG713924
Em:BG706249 Em:BG716383 Em:BG708033 Em:BG706537
Em:BG715540"
/evidence=not_experimental
repeat_region 29083..29168
/note="43 copies 2 mer gg 62% conserved"
Query Match 84.0%; Score 21; DB 9; Length 38540;
Best Local Similarity 100.0%; Pred.No.0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCGAGATAA 21
|||||
Db 11701 GGTTCAGTGAGCGAGATAA 11721
RESULT 34
AC093236
LOCUS AC093236 38634 bp DNA linear PRI 29-NOV-2001
DEFINITION Homo sapiens chromosome 19 clone LLNLR-275D8, complete sequence.
ACCESSION AC093236
VERSION AC093236.2 GI:17149385
KEYWORDS HTG
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 38634)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 38634)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 38634)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission
JOURNAL Submitted (29-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 29, 2001 this sequence version replaced gi:15193370.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES
source
Location/Qualifiers
1..38634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="LLNLF-275D8"
BASE COUNT 9175 a 10661 c 9950 g 8848 t
ORIGIN

Query Match 84.0%; Score 21; DB 9; Length 38634;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGAGTGCAGCCGAGATAA 21
|||||
DB 17592 GGTGCGAGTGCAGCCGAGATAA 17612

RESULT 35
AC011516
LOCUS AC011516 40014 bp DNA linear PRI 26-JUN-2001
DEFINITION Homo sapiens chromosome 19 clone LLNLF-163G11, complete sequence.
ACCESSION AC011516
VERSION AC011516.3 GI:14550303
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 40014)
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.

REFERENCE
AUTHORS Direct Submission
TITLE 2 (bases 1 to 40014)
JOURNAL DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
JOURNAL DOE Joint Genome Institute and Stanford Human Genome Center.

COMMENT
Submitted (26-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES
source
Location/Qualifiers
1..40014
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="LLNLF-163G11"
BASE COUNT 13275 a 8501 c 8120 g 10118 t
ORIGIN

Query Match 84.0%; Score 21; DB 9; Length 40014;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGAGTGCAGCCGAGATAA 21
|||||
DB 17874 GGTGCGAGTGCAGCCGAGATAA 17894

RESULT 36
HSB42B1
LOCUS HSB42B1 40943 bp DNA linear PRI 12-DEC-1999
DEFINITION Human DNA sequence from clone SC22CB-42B1 on chromosome 22 Contains STSs and GSSs, complete sequence.

ACCESSION Z75890
VERSION Z75890
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 40943)
JOURNAL Hunt, S.
COMMENT Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
SC22CB-42B1 is from the human chromosome 22-specific cosmid library (SC22CB) constructed at the Sanger Centre by Mark Ross and Cordelia Langford.
VECTOR: lawrist16

This sequence is the entire insert of clone SC22CB-42B1.
FEATURES
source
Location/Qualifiers
1..40943
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="22"
/clone="SC22CB-42B1"
/clone_lib="SC22CB"
repeat_region 1269..1565
/note="AluSg repeat: matches 1..296 of consensus"
repeat_region 1269..1562
/note="Alu repeat: matches 1..308 of consensus"
repeat_region 2199..2359
/note="AluSx repeat: matches 135..296 of consensus"
repeat_region complement(2204..2366)
/note="Alu repeat: matches 138..308 of consensus"
repeat_region 2360..2655
/note="Alu repeat: matches 1..298 of consensus"
repeat_region complement(2367..2655)
/note="Alu repeat: matches 1..308 of consensus"
repeat_region 2656..2782
/note="AluSx repeat: matches 9..135 of consensus"
repeat_region complement(2657..2792)
/note="Alu repeat: matches 1..150 of consensus"
repeat_region 2823..3122

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repeat_region /note="AluSx repeat: matches 1. .299 of consensus"
complement(2830. .3122)
repeat_region /note="Alu repeat: matches 1. .308 of consensus"
3510. .3639
repeat_region /note="MIR repeat: matches 20. .144 of consensus"
3987. .4282
misc_feature /note="L1 repeat: matches 4735. .5039 of consensus"
5043. .5528
repeat_region /note="match: GSS: Em:AQ560214"
5469. .5565
repeat_region /note="L1MEC repeat: matches 2340. .2085 of consensus"
5584. .5653
repeat_region /note="35 copies 2 mer ct 70 conserved"
5874. .6994
misc_feature /note="L1MEC repeat: matches 1127. .2299 of consensus"
6653. .7277
repeat_region /note="match: GSS: Em:AQ371546"
7258. .7629
repeat_region /note="L1MEC repeat: matches 271. .669 of consensus"
7665. .7776
repeat_region /note="MER3 repeat: matches 1. .113 of consensus"
7831. .8164
repeat_region /note="L1MCb repeat: matches 137. .458 of consensus"
8263. .8376
repeat_region /note="HERVL repeat: matches 791. .900 of consensus"
8377. .8497
repeat_region /note="MER20 repeat: matches 98. .218 of consensus"
8506. .8858
repeat_region /note="L1MC4 repeat: matches 6243. .6607 of consensus"
8909. .8994
repeat_region /note="43 copies 2 mer at 74 conserved"
8910. .8993
repeat_region /note="14 copies 6 mer tatata 75 conserved"
8937. .10192
repeat_region /note="L1MC4 repeat: matches 6605. .7977 of consensus"
11506. .11825
repeat_region /note="AluSg repeat: matches 1. .310 of consensus"
11506. .11805
repeat_region /note="Alu repeat: matches 1. .308 of consensus"
11835. .11902
repeat_region /note="34 copies 2 mer tt 72 conserved"
12297. .12712
misc_feature /note="L2 repeat: matches 2370. .2749 of consensus"
complement(12728. .13109)
repeat_region /note="match: GSS: Em:AQ421066"
13814. .13959
repeat_region /note="MIR repeat: matches 50. .203 of consensus"
14346. .14472
repeat_region /note="L2 repeat: matches 2370. .2749 of consensus"
14691. .14812
repeat_region /note="MIR repeat: matches 127. .252 of consensus"
14763. .14820
repeat_region /note="L2 repeat: matches 2646. .2702 of consensus"
15030. .15228
repeat_region /note="MIR repeat: matches 6. .210 of consensus"
15849. .16240
repeat_region /note="L2 repeat: matches 2325. .2700 of consensus"
16325. .16374
repeat_region /note="L2 repeat: matches 2144. .2194 of consensus"
17563. .17790
repeat_region /note="MIR repeat: matches 1. .251 of consensus"
18915. .19244
misc_feature /note="MER2 repeat: matches 13. .344 of consensus"
19333. .19777
repeat_region /note="match: GSS: Em:AQ353457"
19734. .19917
repeat_region /note="MER58A repeat: matches 28. .222 of consensus"
20077. .20112
repeat_region /note="MIR repeat: matches 84. .119 of consensus"
21875. .22039
repeat_region /note="L2 repeat: matches 2579. .2745 of consensus"
22033. .22261
repeat_region /note="L2 repeat: matches 1838. .2050 of consensus"

```

```

repeat_region 22262. .22589
/note="AluSx repeat: matches 1. .309 of consensus"
repeat_region 22262. .22552
/note="Alu repeat: matches 1. .308 of consensus"
repeat_region 22570. .23052
/note="L2 repeat: matches 1288. .1838 of consensus"
23840. .24130
repeat_region /note="Alu repeat: matches 1. .308 of consensus"
23842. .24136
repeat_region /note="AluSg repeat: matches 3. .299 of consensus"
24154. .24365
misc_feature /note="MIRL1 repeat: matches 198. .408 of consensus"
24337. .24562
/note="match: GSS: Em:T91723"
24434. .24553
repeat_region /note="L2 repeat: matches 1157. .1276 of consensus"
24580. .24871
repeat_region /note="Alu repeat: matches 1. .308 of consensus"
24584. .24879
repeat_region /note="AluSg repeat: matches 5. .301 of consensus"
24950. .25190
repeat_region /note="L1 repeat: matches 4576. .4812 of consensus"
25198. .25489
repeat_region /note="Alu repeat: matches 1. .308 of consensus"
25200. .25502
repeat_region /note="AluSg repeat: matches 3. .305 of consensus"
25509. .26154
repeat_region /note="L1M4A repeat: matches 5461. .6139 of consensus"
26178. .26217
repeat_region /note="20 copies 2 mer at 97 conserved"
26180. .26215
misc_feature /note="6 copies 6 mer atatat 100 conserved"
complement(26608. .27122)
repeat_region /note="match: GSS: Em:AQ594970"
27081. .27325
repeat_region /note="L1MC/D repeat: matches 5330. .5587 of consensus"
27339. .27368
repeat_region /note="15 copies 2 mer gt 100 conserved"
27605. .27745
repeat_region /note="L2 repeat: matches 2560. .2709 of consensus"
29581. .29746
repeat_region /note="L2 repeat: matches 2587. .2750 of consensus"
29839. .30025
repeat_region /note="L2 repeat: matches 2121. .2301 of consensus"
complement(30157. .30263)
repeat_region /note="Alu repeat: matches 28. .153 of consensus"
30162. .30262
repeat_region /note="FLAM_A repeat: matches 28. .128 of consensus"
30497. .30538
repeat_region /note="7 copies 6 mer ctctct 85 conserved"
30506. .30537
repeat_region /note="16 copies 2 mer tc 90 conserved"
31615. .31765
repeat_region /note="MIR repeat: matches 98. .262 of consensus"
32163. .32488
repeat_region /note="L2 repeat: matches 2059. .2491 of consensus"
32499. .32862
misc_feature /note="THEIB repeat: matches 1. .364 of consensus"
complement(32876. .33457)
/note="match: GSS: Em:AQ582892"
complement(32969. .33457)

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Query Match 84.0%; Score 21; DB 9; Length 40943;
 Best Local Similarity 100.0%; Pred. NO. 0.0039;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGAGCCGAGATAA 21
 |||||

Db 22478 GGTTCAGTGAGCCGAGATAA 22498

RESULT 37
 AL355881/c

LOCUS AL355881 42304 bp DNA linear PRI 01-MAR-2001
 DEFINITION Human DNA sequence from clone RP11-332B14 on chromosome 6, complete sequence.
 ACCESSION AL355881
 VERSION AL355881.15 GI:13234900
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 42304)
 AUTHORS Hall, R.
 JOURNAL Direct Submission
 Submitted (01-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 COMMENT requests: clonerequest@sanger.ac.uk
 On Mar 5, 2001 this sequence version replaced gi:12750841.
 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: ENBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 was generated from part of bacterial clone contigs This sequence Chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-332B14 is from the library RPC1-11.2 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6
 IMPORTANT: This sequence is not the entire insert of clone RP11-332B14. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
 The true left end of clone RP3-528L19 is at 42205 in this sequence.
 The true right end of clone RP1-188K17 is at 100 in this sequence.
 FEATURES
 Source
 1..42304
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone="RP11-332B14"
 /clone_lib="RPC1-11.2"
 612..977
 /note="L1MC1 repeat: matches 5902..6332 of consensus"
 1652..1724
 /note="FLAM_A repeat: matches 52..129 of consensus"
 1725..1908
 /note="FLAM_C repeat: matches 33..125 of consensus"
 1976..2003
 /note="ALUSg/x repeat: matches 81..280 of consensus"
 2004..2096
 /note="BC200 repeat: matches 1..26 of consensus"
 2167..2306
 /note="MIR repeat: matches 110..259 of consensus"
 2465..2741
 /note="ALUJo repeat: matches 1..284 of consensus"
 2985..3116
 /note="ALUSg/x repeat: matches 1..125 of consensus"
 3154..3309
 /note="MIR repeat: matches 26..187 of consensus"

repeat_region 3320..3630
 /note="AluY repeat: matches 1..310 of consensus"
 3856..4159
 /note="AluJo repeat: matches 1..299 of consensus"
 4390..4703
 /note="AluSg repeat: matches 1..313 of consensus"
 4766..4817
 /note="26 copies 2 mer ta 88% conserved"
 4821..4856
 /note="18 copies 2 mer ta 94% conserved"
 5041..5154
 /note="AluY repeat: matches 1..108 of consensus"
 5186..5496
 /note="AluSx repeat: matches 1..310 of consensus"
 5539..5840
 /note="AluSx repeat: matches 1..295 of consensus"
 6385..6462
 /note="39 copies 2 mer tt 78% conserved"
 6517..6804
 /note="AluJo repeat: matches 1..290 of consensus"
 7656..7954
 /note="AluY repeat: matches 1..301 of consensus"
 8630..8896
 /note="AluSx repeat: matches 42..309 of consensus"
 9126..9439
 /note="AluSg repeat: matches 1..308 of consensus"
 10248..10538
 /note="AluSx repeat: matches 2..297 of consensus"
 10832..11041
 /note="L1PA14 repeat: matches 5941..6148 of consensus"
 11049..11353
 /note="AluSx repeat: matches 1..305 of consensus"
 11354..11665
 /note="AluSx repeat: matches 1..299 of consensus"
 12034..12123
 /note="L2 repeat: matches 1326..1414 of consensus"
 12264..12412
 /note="MIR repeat: matches 105..261 of consensus"
 12470..12554
 /note="L2 repeat: matches 2448..2518 of consensus"
 12555..12834
 /note="AluY5 repeat: matches 35..311 of consensus"
 12835..12921
 /note="L2 repeat: matches 2357..2448 of consensus"
 13051..13169
 /note="FLAM_C repeat: matches 2..120 of consensus"
 13213..13515
 /note="AluSx repeat: matches 1..303 of consensus"
 13714..13950
 /note="MER46A repeat: matches 1..236 of consensus"
 14007..14320
 /note="AluSx repeat: matches 1..311 of consensus"
 14438..14558
 /note="AluY repeat: matches 1..121 of consensus"
 15342..15413
 /note="L2 repeat: matches 2632..2703 of consensus"
 15982..16284
 /note="AluY repeat: matches 1..311 of consensus"
 16309..16544
 /note="Alu repeat: matches 6..293 of consensus"
 18245..18349
 /note="AluY8 repeat: matches 100..210 of consensus"
 18362..18670
 /note="AluSx repeat: matches 1..310 of consensus"
 19118..19431
 /note="AluJo repeat: matches 1..303 of consensus"
 19656..19789
 /note="FLAM_C repeat: matches 1..132 of consensus"
 19997..20298
 /note="AluSx repeat: matches 1..302 of consensus"
 20725..21017
 /note="AluJo repeat: matches 1..305 of consensus"
 21387..21452

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repeat_region /note="Alu repeat: matches 237. .302 of consensus"
21551. .21586
repeat_region /note="MLP2E repeat: matches 110. .143 of consensus"
21587. .21885
repeat_region /note="Alusx repeat: matches 5. .303 of consensus"
21886. .22127
repeat_region /note="MLR2E repeat: matches 143. .397 of consensus"
22305. .22403
repeat_region /note="HY3 repeat: matches 2. .100 of consensus"
22421. .22716
repeat_region /note="Alusx repeat: matches 1. .296 of consensus"
22778. .23115
repeat_region /note="AluJb repeat: matches 1. .312 of consensus"
23297. .23606
repeat_region /note="Alusx repeat: matches 1. .308 of consensus"
23607. .23687
repeat_region /note="LIPB2 repeat: matches 5890. .5973 of consensus"
23688. .23995
repeat_region /note="Alusx repeat: matches 1. .310 of consensus"
23996. .24388
repeat_region /note="LIPB2 repeat: matches 5541. .5890 of consensus"
24389. .24708
repeat_region /note="Alusx repeat: matches 1. .301 of consensus"
24709. .24958
repeat_region /note="LIPB2 repeat: matches 5281. .5541 of consensus"
25450. .25683
repeat_region /note="AluJb repeat: matches 1. .291 of consensus"
25691. .25978
repeat_region /note="Aluy repeat: matches 1. .302 of consensus"
26205. .26483
repeat_region /note="Alusx repeat: matches 1. .301 of consensus"
26556. .26671
repeat_region /note="58 copies 2 mer tt 59% conserved"
28625. .28939
repeat_region /note="MER33 repeat: matches 8. .323 of consensus"
28978. .29078
repeat_region /note="AluJo repeat: matches 43. .146 of consensus"
29079. .29386
repeat_region /note="Alusq repeat: matches 1. .307 of consensus"
29387. .29565
repeat_region /note="AluJo repeat: matches 146. .312 of consensus"
29575. .29635
repeat_region /note="MERS1B repeat: matches 466. .527 of consensus"
29875. .30078
repeat_region /note="L2 repeat: matches 2192. .2408 of consensus"
30074. .30168
repeat_region /note="L2 repeat: matches 2654. .2750 of consensus"
30491. .30609
repeat_region /note="MERS7-internal repeat: matches 7148. .7267 of consensus"
30991. .31288
repeat_region /note="Alusx repeat: matches 1. .296 of consensus"
31415. .31453
repeat_region /note="MIR repeat: matches 106. .144 of consensus"
84.0%; Score 21; DB 9; Length 42304;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATTA 21
|||||
Db 33829 GGTTCAGTGCAGCCGAGATTA 33809

RESULT 38
HSU63963
DEFINITION Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds.
ACCESSION U63963.X14720
VERSION U63963.1 GI:1915975
KEYWORDS
SOURCE Homo sapiens.

Query Match 84.0%; Score 21; DB 9; Length 42304;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATTA 21
|||||
Db 33829 GGTTCAGTGCAGCCGAGATTA 33809

RESULT 38
HSU63963
DEFINITION Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds.
ACCESSION U63963.X14720
VERSION U63963.1 GI:1915975
KEYWORDS
SOURCE Homo sapiens.

```

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 35100)
AUTHORS Hampe,A., Shamoon,B.M., Gobet,M., Sherr,C.J. and Galibert,F.
TITLE Nucleotide sequence and structural organization of the human FMS
proto-oncogene
JOURNAL Oncogene Res. 4 (1), 9-17 (1989)
MEDLINE 89239490
PUBMED 2524025
REFERENCE 2 (bases 1 to 42874)
AUTHORS Gastier,J.M., Brody,T., Pullido,J.C., Businga,T., Sundén,S., Hu,X.,
Maitra,S., Buetow,K.H., Murray,J.C., Sheffield,V.C., Boguski,M.,
Duyk,G.M. and Hudson,T.J.
TITLE Development of a screening set for new (CAG/CTG)n dynamic mutations
JOURNAL Genomics 32 (1), 75-85 (1996)
MEDLINE 96230328
PUBMED 8786123
REFERENCE 3 (bases 1 to 42874)
AUTHORS Andre,C., Hampe,A., Lachaux,P., Martin,E., Wang,X.P., Manus,V.,
Hu,W.X. and Galibert,F.
TITLE Sequence analysis of two genomic regions containing the KIT and the
FMS receptor tyrosine kinase genes
JOURNAL Genomics 39 (2), 216-226 (1997)
MEDLINE 97179223
PUBMED 9027509
REFERENCE 4 (bases 1 to 42874)
AUTHORS Hampe,A.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-1996) UPR41, CNRS, Avenue Leon Bernard, Rennes
35000, France
COMMENT On Apr 12, 1997 this sequence version replaced gi:30238.
FEATURES
source
1..42874
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5q33.3-q34"
/tissue_type="placenta"
1..35016
/gene="FMS"
<1..1735
/number=1
/number=1
308..591
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/rpt_type-dispersed
complement(719..902)
/rpt_family="MER32"
1264..1347
/rpt_family="Alu J"
/rpt_type-dispersed
join(11736..1964,7314..7571,8002..8286,10090..10226,
10903..11062,14843..15035,17766..17881,18035..18155,
18274..18464,20007..20122,26478..26604,26732..26836,
27354..27464,28464..28626,30734..30822,30942..31039,
31985..32107,32189..32300,32991..33090,33897..34005,
34103..34258)
/gene="FMS"
/product="CSF-1 receptor"
1736..1964
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/number=2
join(1916..1964,7314..7571,8002..8286,10090..10226,
10903..11062,14843..15035,17766..17881,18035..18155,
18274..18464,20007..20122,26478..26604,26732..26836,
27354..27464,28464..28626,30734..30822,30942..31039,
31985..32107,32189..32300,32991..33090,33897..34005,
34103..34258)
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/function="growth factor receptor"
/function="tyrosine kinase receptor"
/note="c-fms proto-oncogene; transmembrane glycoprotein"

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/protein_id="AAB51696.1"
/db_xref="GI:1915976"
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NGSVEWDGPPSPHWTLYSDGSSSLTNNATFNTGTYRTEPGDPLGSAAILHYVK
DPAPRNVLAEQVYFEDDALLPCLLTDPLEAGVSLVRGRPLMRHTNYSFSPWH
GFTIIRAKFIQSODYQCSALMGGRKVMISIRLKVKVIGPPALTLVPAELVIRGE
AAQIVASASVDVNFDFLOHNTKLAIPQSDQNNHNYOKVLTNLQDQDFPAGNY
SCVASNYQGHSTSMFFRVESAYLNLSEQNLQEVTVGEGNLKVMWYAPGLQGF
NWTYLGPFSDHOPEPKLANATTKDVTYHTFTLSLPRLKPSBGRKYSFLARPPGWRAL
TFELTLRYPEYSVLWTFINGSGILLCAAGSPQPNVTWLOCSGHTDRDCAQLQVW
DDPYEVLQSPFPHKVTQSLTIVTELEHNTYICRAHNSVSGSWAFIPISAGATHH
PPDFLETPVYVACMSIMALLLGLLLLYTKQKPYQVRWKIIESYEGSYTFIDP
TQLYNEKWEFFRNNOFGKTLGAGAFGVVEATFGLGEDAVLKAVKMLKSTAH
DEKALMSKELMHLGHEINVLGACTHGGPVLVITYCCYGLDLNELLRAEAM
LGPSLPGDPEGVDYKNIHLKKYVRDGSFGQVDIYVEMRPVSTSNDSFSQ
DLKEDGRPLELRLDLHFSQVAGMAFLASKNLIHRDVAARNVLLTNGHAKIGDFG
LARDIMDSNYIVKGNARLPVKWMAPEFDCVITYVSDVMSYGLLWEIFSLGLNPY
PGILVNSKFKLVKDGQMAQPAFAPKNIIYSIMQACWALEPHRPTFQIQCSFLQEA
QEURRERYTNLPSSRSRGGSSSELESSESHLTCCQGDIAQLPLQPNNYQFC
"
1965..7313
/gene="FMS"
/number=2
complement(3069..3346)
/rpt_family="Alu Sx"
/rpt_type-dispersed
3592..3872
/rpt_family="Alu Sx"
/rpt_type-dispersed
3872..3995
/note="(CCTT)19(CTTT)12 repeat"
/rpt_type-tandem
/rpt_unit-CCTT
complement(4009..4284)
/rpt_family="Alu Sx"
/rpt_type-dispersed
4938..4989
/note="(GT)26 repeat"
/rpt_type-tandem
/rpt_unit-GT
7314..7571
/gene="FMS"
/number=3
7572..8001
/gene="FMS"
/number=3
8002..8286
/gene="FMS"
/number=4
8287..10089
/gene="FMS"
/number=4
10090..10226
/gene="FMS"
/number=5
10227..10902
/gene="FMS"
/number=5
10903..11062
/gene="FMS"
/number=6
11063..14842
/gene="FMS"
/number=6
12099..12173
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/rpt_type-dispersed
13861..14008
/rpt_family="Alu Sc"
/rpt_type-dispersed

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exon 14843..15035
/gene="FMS"
/number=7
15036..17765
/gene="FMS"
/number=7
repeat_region complement(15848..16124)
/rpt_family="Alu Sx"
/rpt_type-dispersed
17766..17881
/gene="FMS"
/number=8
17882..18034
/gene="FMS"
/number=8
18035..18155
/gene="FMS"
/number=9
18156..18273
/gene="FMS"
/number=9
18274..18464
/gene="FMS"
/number=10
18465..20006
/gene="FMS"
/number=10
repeat_region 19098..19143
/note="repeat sequence I"
repeat_region 19915..19967
/note="repeat sequence I"
exon 20007..20122
/gene="FMS"
/number=11
20123..26477
/gene="FMS"
/number=11
repeat_region 20366..20480
/rpt_family="Alu J"
/rpt_type-dispersed
repeat_region complement(22534..22568)
/rpt_family="IVR"
repeat_region 22759..22799
/note="repeat sequence II"
repeat_region complement(24034..24217)
/rpt_family="MER13"
repeat_region 24460..24499

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Query Match 84.0%; Score 21; DB 9; Length 42874;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
 |||||
 DB 37789 GGTTCAGTGCAGCCGAGATAA 37809

RESULT 39
 AL357952/c

LOCUS

DEFINITION

AL357952

Human DNA sequence from clone RP11-479K1 on chromosome 1 Contains

STSS and GSSs, complete sequence.

ACCESSION

AL357952

VERSION

AL357952.7

GI:9863832

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

43456 bp DNA linear PRI 03-JAN-2001

Human DNA sequence from clone RP11-479K1 on chromosome 1 Contains

STSS and GSSs, complete sequence.

AL357952

AL357952

AL357952.7

GI:9863832

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 43456)

Walls, J.

Direct Submission

Submitted (03-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,

CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT

On Aug 21, 2000 this sequence version replaced gi:9801404. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.: EMBL; Sw.: SWISSPROT; Tr.: TREMBL; Wp.: WORMPEP; Information

on the WORMPEP database can be found at

<http://www.sanger.ac.uk/projects/C.elegans/wormpep> This sequence

was generated from part of bacterial clone contigs of human

chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping

Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

IMPORTANT: This sequence is not the entire insert of clone

RP11-479K1. It may be shorter because we sequence overlapping

sections only once, except for a 100 base overlap.

The true right end of clone RP11-479K1 is at 43456 in this

sequence. This sequence has been finished according to sequence map

criteria as follows. An attempt is made to resolve all sequencing

problems, such as compressions and repeats, but not necessarily

within known annotated repeat sequence elements. Where the

sequence is ambiguous there is an annotation using the 'unsure'

feature key. RP11-479K1 is from the library RPCI-11.2 constructed

by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6.

FEATURES

```

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    1. 43456
       /organism="Homo sapiens"
       /db_xref="taxon:9606"
       /chromosome="1"
       /clone="RP11-479K1"
       /clone_lib="RPCI-11.2"
       complement(1.. 99)
       /note="match: STS: Em:G57779
match: GSS: Em:AQ342139"
       /note="match: GSS: Em:AQ392651 Em:AQ774490"
       135..665
       /note="match: GSS: Em:AQ421310"
       2454..2513
       /note="30 copies 2 mer tt 71% conserved"
       2680..3215
       /note="match: GSS: Em:AQ150243"
       2703..3134
       /note="match: GSS: Em:AQ150226"
       4243..4368
       /note="3 copies 42 mer 95% conserved"
       4799..4872
       /note="MADE1 repeat: matches 1..78 of consensus"
       complement(7723..8138)
       /note="match: GSS: Em:AQ220413"
       complement(7774..8138)
       /note="match: GSS: Em:AQ038343"
       8688..8751
       /note="16 copies 4 mer gtgt 87% conserved"
       8689..8750
       /note="31 copies 2 mer tg 88% conserved"
       11442..11485
       /note="22 copies 2 mer at 86% conserved"
       11443..11482
       /note="10 copies 4 mer tata 87% conserved"
       17383..17430
       /note="12 copies 4 mer attc 85% conserved"
       19048..19092
       /note="15 copies 3 mer gat 82% conserved"
       21210..21249

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```

misc_feature
    complement(26376..26897)
       /note="match: GSS: Em:AQ676452"
       complement(28822..29342)
       /note="match: GSS: Em:AQ741080"
       30351..30791
       /note="match: GSS: Em:AQ442484"
       30772..31126
       /note="THEIA repeat: matches 1..354 of consensus"
       31127..32702
       /note="THEIA-internal repeat: matches 1..1580 of
consensus"
       32703..33069
       /note="THEIA repeat: matches 1..354 of consensus"
       3436..34366
       /note="Single clone region region. Assembly confirmed by
restriction digest data."
       35077..35597
       /note="L1LMA4A repeat: matches 5785..6300 of consensus"
       35598..35653
       /note="28 copies 2 mer ta 80% conserved"
       35663..35690
       /note="14 copies 2 mer ca 96% conserved"
       35666..35689
       /note="6 copies 4 mer acac 100% conserved"
       35692..35787
       /note="L1LMA4A repeat: matches 5688..5782 of consensus"
       35789..35974
       /note="L1 repeat: matches 3191..3373 of consensus"
       35977..42134
       /note="L1PA3 repeat: matches 1..6146 of consensus"
       42136..43189
       /note="L1 repeat: matches 2124..3209 of consensus"
BASE COUNT 12269 a 8310 c 8428 g 14449 t
ORIGIN

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Query Match 84.0% Score 21; DB 9; Length 43456;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGTTCAGTGTGCGCAGATAA 21
      |||||
DB 4483 GGTTCAGTGTGCGCAGATAA 4463

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```

RESULT 40
AC068187
LOCUS
DEFINITION Homo sapiens chromosome 4 clone RP11-360F5 map 4, LOW-PASS SEQUENCE
SAMPLING.
AC068187
ACCESSION AC068187.1 GI:7670230
VERSION AC068187.1
KEYWORDS HTG; HGS_PHASE0.
SOURCE Homo sapiens.
ORGANISM

```

```

REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
TITLE Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 44986)
REFERENCE Homo sapiens chromosome 4, clone RP11-360F5
AUTHORS

```

```

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bada,E.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campiano,A., Castle,A., Choepe,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galaqu,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Liu,G., Locke,K., Macdonald,P., Marquis,N.,

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McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
Meldrim, J., Meneus, L., Minova, T., Miranda, C., Mlenga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Notman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL

COMMENT

Submitted (29-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L9598
Center clone name: 360_F_5

* NOTE: This record contains 51 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
801 900: contig of 800 bp in length
901 1676: contig of 776 bp in length
1677 1776: gap of 100 bp
1777 2556: contig of 780 bp in length
2557 2656: gap of 100 bp
2657 3449: contig of 793 bp in length
3450 3549: gap of 100 bp
3550 4345: contig of 796 bp in length
4346 4445: gap of 100 bp
4446 5207: contig of 762 bp in length
5208 5307: gap of 100 bp
5308 6082: contig of 775 bp in length
6083 6182: gap of 100 bp
6183 6980: contig of 798 bp in length
6981 7080: gap of 100 bp
7081 7873: contig of 793 bp in length
7874 7973: gap of 100 bp
7974 8762: contig of 789 bp in length
8763 8862: gap of 100 bp
8863 9641: contig of 779 bp in length
9642 9741: gap of 100 bp
9742 10526: contig of 785 bp in length
10527 10626: gap of 100 bp
10627 11391: contig of 765 bp in length
11392 11491: gap of 100 bp
11492 12275: contig of 784 bp in length
12276 13375: gap of 100 bp
13376 13169: contig of 794 bp in length
13170 13269: gap of 100 bp
13270 14043: contig of 774 bp in length
14044 14143: gap of 100 bp
14144 14932: contig of 789 bp in length
14933 15032: gap of 100 bp
15033 15817: contig of 785 bp in length
15818 15917: gap of 100 bp
15918 16690: contig of 773 bp in length

FEATURES
source

1. .44986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/map="4"
/clone="RP11-360F5"
/clone.lib="RP11-360F5"
/clone.lib="RP11-360F5"
9880 a 9802 c 8943 g 11118 t 5243 others
BASE COUNT
Location/Qualifiers

16591 16790: gap of 100 bp
16791 17583: contig of 793 bp in length
17584 17683: gap of 100 bp
17684 18469: contig of 786 bp in length
18470 18569: gap of 100 bp
18570 19361: contig of 792 bp in length
19362 19461: gap of 100 bp
19462 20254: contig of 793 bp in length
20255 20354: gap of 100 bp
20355 21145: contig of 791 bp in length
21146 21245: gap of 100 bp
21246 22048: contig of 803 bp in length
22049 22148: gap of 100 bp
22149 22940: contig of 792 bp in length
22941 23040: gap of 100 bp
23041 23828: contig of 788 bp in length
23829 23928: gap of 100 bp
23929 24722: contig of 794 bp in length
24723 24822: gap of 100 bp
24823 25608: contig of 786 bp in length
25609 25708: gap of 100 bp
25709 26475: contig of 767 bp in length
26476 26575: gap of 100 bp
26576 27372: contig of 797 bp in length
27373 27472: gap of 100 bp
27473 28235: contig of 763 bp in length
28236 28335: gap of 100 bp
28336 29118: contig of 783 bp in length
29119 29218: gap of 100 bp
29219 30000: contig of 782 bp in length
30001 30100: gap of 100 bp
30101 30879: contig of 779 bp in length
30880 30979: gap of 100 bp
30980 31780: contig of 801 bp in length
31781 31880: gap of 100 bp
31881 32652: contig of 772 bp in length
32653 32752: gap of 100 bp
32753 33539: contig of 787 bp in length
33540 33639: gap of 100 bp
33640 34424: contig of 785 bp in length
34425 34524: gap of 100 bp
34525 35282: contig of 758 bp in length
35283 35382: gap of 100 bp
35383 36137: contig of 755 bp in length
36138 36237: gap of 100 bp
36238 37026: contig of 789 bp in length
37027 37126: gap of 100 bp
37127 37898: contig of 772 bp in length
37899 37998: gap of 100 bp
37999 38783: contig of 785 bp in length
38784 38883: gap of 100 bp
38884 39673: contig of 790 bp in length
39674 39773: gap of 100 bp
39774 40535: contig of 762 bp in length
40536 40635: gap of 100 bp
40636 41424: contig of 789 bp in length
41425 41524: gap of 100 bp
41525 42294: contig of 770 bp in length
42295 42394: gap of 100 bp
42395 43204: contig of 810 bp in length
43205 43304: gap of 100 bp
43305 44105: contig of 801 bp in length
44106 44205: gap of 100 bp
44206 44986: contig of 781 bp in length.

ORIGIN

Query Match 84.0%; Score 21; DB 2; Length 44986;
 Best Local Similarity 100.0%; Pred. No. 0.0039;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGATAA 21
 |||||
 DB 35085 GGTTCAGTGGCCGAGATAA 35105

RESULT 41
 AC005387
 LOCUS
 DEFINITION Homo sapiens chromosome 19, cosmid R29473, complete sequence.
 ACCESSION AC005387
 VERSION AC005387.1 GI:3395417
 KEYWORDS HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 46213)
 Lamerdin,J.E., McCready,P.M., Skowronski,E., Adamson,A.W.,
 Burkhardt-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stilwagen,S.,
 Phan,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J.,
 Danganan,L., Poundstone,P., Christensen,M., Georgescu,A., Avila,J.,
 Liu,S., Attix,C., Andreise,F., Frankheim,M., Amico-Keller,G.,
 Coefield,J., Duarte,S., Lucas,S., Bruce,R., Thomas,P., Quan,G.,
 Krommiller,B., Arellano,A., Montgomery,M., Ow,D., Nolan,M.,
 Truong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V.
 Sequence analysis of an ~1 Mb region containing the MEF2B gene in
 19p12

TITLE
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 46213)
 AUTHORS Lamerdin,J.E.
 TITLE Direct Submission
 JOURNAL Submitted (05-AUG-1998) Joint Genome Institute, Lawrence Livermore
 National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
 Map and sequence oriented from p telomere to centromere. Cosmid
 R29473 is the telomeric end of the current sequencing tiling path.
 R29473 overlaps cosmid R26645 (AC005253) to the right from bases
 37,603 to 46,213. Additional chr 19 map and sequence information
 are available at: <http://www-bio.llnl.gov/genome/genome.html>.

FEATURES
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 1..46213
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="19"
 /map="19p12 between UBA52 and D19S451"
 /clone="R29473"
 /cell_line="5HL2-B"
 /clone_lib="LL19NC03 R chromosome 19 cosmid library"
 /note="LL19NC03 cosmid library constructed at LLNL from
 flow-sorted chromosomes from hybrid 5HL2-B, which carries
 chromosome 19 as its only human chromosome."
 19..179
 /rpt_family="FRAM"
 repeat_region
 514..720
 /rpt_family="MER58A"
 repeat_region
 1405..1522
 /rpt_family="(CA)n"
 repeat_region
 1951..2252
 /rpt_family="AluSx"
 repeat_region
 2534..2703
 /rpt_family="LINE"
 repeat_region
 2704..2849
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 repeat_region
 2850..3144
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 repeat_region
 3145..3274
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 3276..3459
 /rpt_family="AluSx"

/rpt_family="LINE"
 3601..3735
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 3739..4038
 /rpt_family="AluSg"
 4039..4209
 /rpt_family="AluJo"
 4220..4451
 /rpt_family="AluJb"
 5514..5814
 /rpt_family="AluY"
 6096..6397
 /rpt_family="AluY"
 8358..8479
 /rpt_family="LINE2"
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 9454..9770
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 9804..10070
 /rpt_family="AluSx"
 10083..10370
 /rpt_family="AluJo"
 10374..10676
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 10917..11115
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 11391..11692
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 /rpt_family="GC-rich"
 complement(<13787..13933)
 /product="Human ELL mRNA"
 complement(<13787..13921)
 /gene="ELL"
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 complement(<13787..13921)
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 /note="ELL PROTEIN"
 /codon_start=1
 /product="ELL_HUMAN"
 /protein_id="BAC28752.1"
 /db_xref="GI:3393418"
 /translation="MAALKEKDRSYGLSCGRVSGSKYSVFHVKLTDSALRAFTSYRAR
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 complement(15173..15479)
 /rpt_family="AluSg"
 complement(15531..15572)
 /rpt_family="LINE6"
 complement(15580..15877)
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 16345..16626
 /rpt_family="AluSg"
 complement(16733..17040)
 /rpt_family="AluSx"
 complement(17043..17355)
 /rpt_family="AluJb"
 complement(17367..17655)
 /rpt_family="AluSg"
 17693..17995
 /rpt_family="AluY"
 18090..18234
 /rpt_family="MIR"

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repeat_region 19113..19406
repeat_region /rpt_family="AluSx"
repeat_region 19482..19656
repeat_region /rpt_family="FRAM"
repeat_region 19716..20010
repeat_region /rpt_family="AluSg"
repeat_region complement(20084..20356)
repeat_region /rpt_family="AluSg"
repeat_region 20362..20459
repeat_region /rpt_family="AluSg/x"
repeat_region 20478..20675
repeat_region /rpt_family="AluSg/x"
repeat_region 20676..20976
repeat_region /rpt_family="AluSg"
repeat_region 21095..21320
repeat_region /rpt_family="AluSg/x"
repeat_region 21321..21397
repeat_region /rpt_family="AluSg/x"
repeat_region complement(22118..22380)
repeat_region /rpt_family="AluSg1"
repeat_region complement(22386..22495)
repeat_region /rpt_family="FLAM_C"
repeat_region 22521..22821
repeat_region /rpt_family="MIR"
repeat_region 22824..23121
repeat_region /rpt_family="AluSc"
repeat_region complement(23165..23249)
repeat_region /rpt_family="AluJo/FRAM"
repeat_region 23451..23490
repeat_region /rpt_family="MIR"
misc_feature 23623..24055
/notes="DSS similarity to overlapping ESTs:
neuroepithelium (#937231) Homo sapiens cDNA clone 530677
3'; Score: 627 Identity: 395/449 (87%).-(23623..23966)
W48683 zc45h08.s1 Soares senescent fibroblasts NBHSF Homo
sapiens cDNA clone 325311 3';
Score: 609 Identity: 326/345 (94%).-Additional EST
matches:
H16570, H45028, R37825, Z40550, F02707, M79056"
/feature="FKBP38"
/notes="Human FK506-binding protein homologue encoding
gene"
complement(join(24035..24121,24530..24661,25136..25213,
29467..29639,30082..30299,31237..31325,31417..31586,
33545..33665))
/feature="FKBP38"
/codon_start=1
/product="FK-506 binding protein homologue"
/protein_id="AAC28753.1"
/db_xref="GI:3395419"
/translation="MGQPEAEAEQPGALAREFLAAMEPEPAPAPAPAEWLDLNGSL
LRKTLVPGPSRPVKGQVTVHLQTSLENGTVQEEELFTLGDCDVIQALDLS
VPLMDVGETAMVTADSKYCPQGRSPYIPPAALCLEVTLKTVADPGDLEMLQGER
VALANRREGNAHQVADFIANSTDLAIKAITSSAKVDMTFEEEAQLLQVKCL
NLAASQLKDIHRAALRSCSLVLEHOPDNIKALFRKGVLAQOGEYSAPILRAL
KLEPNTIHAELSKLVKKHAAQRTETALYRKMLGNPSRLPAKCPGKANSIPKKWL
FGATVALGQVALSVVIAARN"
complement(25137..25214)
/feature="FKBP38"
/notes="DSS similarity to HSU53083 Human clone 5/24 mRNA
sequence; (85..7); 97% identity."
/rpt_family="AluSg/x"

Query Match 84.0%; Score 21; DB 9; Length 46213;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21

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Db 9988 GGTTCAGTGAGCCGAGATAA 10008
|||||
RESULT 42
AB065918 49228 bp DNA linear PRI 23-JUL-2002
LOCUS cds, isolate:CBRC7TM_481.
DEFINITION Homo sapiens gene for seven transmembrane helix receptor, complete
AB065918
ACCESSION AB065918
VERSION AB065918
KEYWORDS AB065918.1 GI:21929096
SOURCE Homo sapiens (isolate:CBRC7TM_481) DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Suwa,M., Sato,T., Okouchi,I., Arita,M., Futami,K., Matsumoto,S.,
Tsutsumi,S., Aburatani,H., Asai,K. and Akiyama,Y.
TITLE Genome-wide discovery and analysis of human seven transmembrane
helix receptor genes
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 49228)
Suwa,M.
JOURNAL Direct Submission
SUBMITTED (11-JUL-2001) Makiko Suwa, Computational Biology Research
Center (CBRC), National Institute of Advanced Industrial Science
and Technology (AIST); 2-41-6 Aomi Koto-ku, Tokyo 135-0064, Japan
(E-mail:m-suwa@aist.go.jp, URL:http://www.cbrc.jp/,
Tel:81-3-3599-8080, Fax:81-3-3599-8081)
COMMENT This sequence is a seven transmembrane helix receptor candidate
predicted from the whole human genome sequences using our automated
system that contains programs of gene
finding(GeneDecoder), sequence search, motif-domain assignment and
transmembrane helix prediction.
And the sequence is submitted by the collaborative project between
[Computational Biology Research Center (CBRC), National Institute
of Advanced Industrial Science and Technology (AIST)] and [Genome
Science Division, Research Center for Advanced Science and
Technology (RCAT), University of Tokyo].
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PMLVVISASVQPGVMNRNCLMTGFIHNSFLGPGVCTVINTLITLTLILQ
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    Best Local Similarity 100.0%; Pred. No. 0.0038;
    Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATAA 21
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DB 42476 GGTTCAGTGCAGCCGAGATAA 42496
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RESULT 43
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DEFINITION Sequence 19 from Patent WO9950284.
ACCESSION  AX015916
VERSION     AX015916.1 GI:10041659
KEYWORDS   human.
SOURCE     Homo sapiens
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1 (bases 1 to 49999)
AUTHORS   Aigner,T., Hess,J., Rosenthal,A., Rump,A. and Wirth,T.
TITLE     Nucleic acid molecules which code proteins influencing bone
            development
JOURNAL   Patent: WO 9950284-A 19 07-OCT-1999;
            AIGNER THOMAS (DE); HESS JOCHEN (DE); ROSENTHAL ANDRE (DE); RUMP
            ANDREAS (DE); WIRTH THOMAS (DE)
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Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS      AC068390
DEFINITION Homo sapiens clone RP11-303B11, LOW-PASS SEQUENCE SAMPLING.
ACCESSION  AC068390
VERSION     AC068390.1 GI:7677761
KEYWORDS   HTG; HTGS-PHASE0.
SOURCE     Homo sapiens.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1 (bases 1 to 52687)
AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE     Homo sapiens, clone RP11-303B11
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 52687)
AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
            Boguslavskiy,L., Boukagalter,B., Brown,A., Burkett,G.,
            Campolano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
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            Grand-Pierre,N., Grant,G., Hagos,B., Hearford,A., Horton,L.,
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            Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,

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Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
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Meidrum,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
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O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
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Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-rhomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WISR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LI0258
Center clone name: 303_B_11
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* NOTE: This record contains 68 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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1 691: contig of 691 bp in length
692 791: gap of 100 bp
792 1466: contig of 675 bp in length
1467 1566: gap of 100 bp
1567 2246: contig of 680 bp in length
2247 2346: gap of 100 bp
2347 3025: contig of 679 bp in length
3026 3125: gap of 100 bp
3126 3810: contig of 685 bp in length
3811 3910: gap of 100 bp
3911 4604: contig of 694 bp in length
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4705 5311: contig of 607 bp in length
5312 5411: gap of 100 bp
5412 6070: contig of 659 bp in length
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6171 6850: contig of 680 bp in length
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6951 7637: contig of 687 bp in length
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12282 12381: gap of 100 bp
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TITLE
JOURNAL

COMMENT

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Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26192 GGTGTCAGTGCAGCCGAGATAA 26212

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RESULT 45

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ACCESSION            AC091585
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                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE            Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
                     Barina, N., Bastien, V., Boguslavskiy, J., Bouckgalter, B., Brown, A.,
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                     Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
                     1 (bases 1 to 59305)
                     2 (bases 1 to 59305)

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Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:13959202.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L13172
Center clone name: 466_I_9

* NOTE: This record contains 72 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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4984 5666: contig of 683 bp in length
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5767 6499: contig of 733 bp in length
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6600 7301: contig of 702 bp in length
7302 7401: gap of 100 bp
7402 8118: contig of 717 bp in length
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8219 8946: contig of 728 bp in length
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9047 9793: contig of 747 bp in length
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9894 10624: contig of 731 bp in length
10625 10724: gap of 100 bp
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37980 38701: contig of 722 bp in length
38702 38801: gap of 100 bp
38802 39526: contig of 725 bp in length
39527 39626: gap of 100 bp
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40337 40436: gap of 100 bp
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41170 41269: gap of 100 bp
41270 41999: contig of 730 bp in length
42000 42099: gap of 100 bp
42100 42837: contig of 738 bp in length
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45303 45402: gap of 100 bp
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* 47020 47753: contig of 734 bp in length
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Query Match      84.0%; Score 21; DB 2; Length 59305;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATAA 21
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DB 55482 GGTTCAGTGAGCCGAGATAA 55462

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Search completed: November 24, 2002, 14:17:41
Job time : 2087.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 13:27:24 ; Search time 1549.5 Seconds
(without alignments)
261.302 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTGCCAGACACGAAATTTACAG 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
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13: gb_est4:*
14: gb_est5:*
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25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	18	72.0	838	12	BG414651
c 2	18	72.0	977	17	CNS046T0
c 3	17	68.0	287	9	AV296392
4	17	68.0	522	9	AA865753
5	17	68.0	642	14	BQ269298
6	17	68.0	821	12	BE877455

c 7	17	68.0	857	13	BM401231
c 8	17	68.0	961	14	BQ711606
c 9	16	64.0	229	14	BQ280096
c 10	16	64.0	246	10	AV357770
c 11	16	64.0	311	10	B8534005
c 12	16	64.0	320	9	AV219319
c 13	16	64.0	394	12	BG158653
c 14	16	64.0	395	14	AV219319
c 15	16	64.0	396	17	AZ282651
c 16	16	64.0	397	14	T77962
c 17	16	64.0	408	17	BH878510
c 18	16	64.0	447	17	BH876286
c 19	16	64.0	449	9	AA126284
c 20	16	64.0	464	9	AI325084
c 21	16	64.0	468	9	AI747269
c 22	16	64.0	471	17	BH879621
c 23	16	64.0	489	17	B98791
c 24	16	64.0	505	12	BF610439
c 25	16	64.0	533	14	BM725916
c 26	16	64.0	543	14	BQ701598
c 27	16	64.0	551	17	BH876388
c 28	16	64.0	557	12	BG039852
c 29	16	64.0	574	10	AW644504
c 30	16	64.0	581	17	BH876387
c 31	16	64.0	586	17	BH876535
c 32	16	64.0	601	10	AW043028
c 33	16	64.0	601	10	AW043050
c 34	16	64.0	601	10	AW043091
c 35	16	64.0	608	17	AE009748
c 36	16	64.0	613	10	BE000467
c 37	16	64.0	628	12	BG033085
c 38	16	64.0	636	12	BF511713
c 39	16	64.0	663	14	BM678024
c 40	16	64.0	667	17	AG133215
c 41	16	64.0	686	17	BH882704
c 42	16	64.0	698	10	AW340752
c 43	16	64.0	752	17	AQ745078
c 44	16	64.0	806	12	BG681831
c 45	16	64.0	825	12	BF978854

ALIGNMENTS

RESULT 1
BG414651/c

LOCUS

DEFINITION

BG414651 838 bp mRNA linear EST 23-OCT-2001
HVSMEK0003D14f Hordeum vulgare testa/pericarp EST library
HYCDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEK0003D14f, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Mar 13, 2001 this sequence version replaced gi:13320202.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

BG414651 838 bp mRNA linear EST 23-OCT-2001
HVSMEK0003D14f Hordeum vulgare testa/pericarp EST library
HYCDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEK0003D14f, mRNA
sequence.
BG414651 GI:16328533
Hordeum vulgare.
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
Wing, R., Close, T.J., Klein, A., Choi, D.W., Fenton, R.D., Kianian
Wetstein, D., Akhunov, E., Zhang, D., Begum, D., Frisch, D., Yu, Y.,
P., Otto, C., Simons, K., Rambo, T., Simmons, J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex testa/pericarp cDNA library
Unpublished (2001)
On Mar 13, 2001 this sequence version replaced gi:13320202.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemsun.edu
Total hg bases = 117
Seq primer: AATTACCTCCTCAATGAAGG
High quality sequence stop: 502.
Location/Qualifiers
1. .838
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_lib="HVSX0003D14f"
HvCDNA0013 (normal)
/tissue.type="testa/pericarp"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were raised from seeds in a Controlled Environments
growth chamber maintained in continuous light at 180C, and
testa and pericarp were dissected from developing kernels
at Washington State University, Pullman, WA (Rannangara,
von Wettstein). Total RNA was prepared, poly(A) RNA was
purified, one cDNA library was made, and 1 million pfu
were in vivo excised to give pBluescript SK(-) cDNA
phagemids in the TJ Close lab at the University of
California, Riverside (Akhunov, Chin, Choi, Close, Fenton,
Kilian, Otto, Simons, Zhang). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT 208 a 196 c 178 g 236 t
ORIGIN

Query Match 72.0%; Score 18; DB 12; Length 838;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCCAGAAATTT 21
|||||
Db 620 GCCAGGACCCAGAAATTT 603

RESULT 2
CNS046T0/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence pUC-ori end of clone
086a22 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL277101
VERSION AL277101.1 GI:8011304
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 977)

REFERENCE
AUTHORS Roest-Crollius H., Jaillon O., Dasilva C., Bouneau L., Fisher C.,
Bernot A., Fizames C., Wincker P., Brottier P., Quetier F.,
Saurin W. and Weissenbach J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished

2 (bases 1 to 977)
REFERENCE Roest-Crollius H., Jaillon O., Dasilva C., Fizames C., Fisher C.,
AUTHORS Bouneau L., Billault A., Quetier F., Saurin W., Bernot A. and
Weissenbach J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 977)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/tetraodon>.

FEATURES
source
1. .977
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="086A22"
/clone_lib="G"
/note="Genoscope sequence ID : COBG0869A11SPI-end :
PUC-ori"

BASE COUNT 305 a 185 c 161 g 306 t 20 others
ORIGIN

Query Match 72.0%; Score 18; DB 17; Length 977;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCCAGAAATTTACA 24
|||||
Db 177 AGGAACCCAGAAATTTACA 160

RESULT 3
AV296392/c
LOCUS
DEFINITION
AV296392 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730441H16 3' similar to X15013 Rat mRNA for ribosomal
protein L7a, mRNA sequence.
AV296392 287 bp mRNA linear EST 10-NOV-1999
AV296392 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730441H16 3' similar to X15013 Rat mRNA for ribosomal
protein L7a, mRNA sequence.
AV296392
VERSION AV296392.1 GI:6328409
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 287)

REFERENCE
AUTHORS Konno H., Aizawa K., Akahira S., Akiyama J., Carninci P., Endo T.,
Fukuda S., Fukunishi Y., Hara A., Hayatsu N., Hirozane T., Hori F.,
Ishii Y., Ishikawa T., Itoh M., Izawa M., Kadota K., Kagawa I., Kai
C., Kawai J., Kikuchi N., Kojima Y., Koya S., Kusakabe M.,
Matsuyama T., Miki R., Mizuno Y., Nakamura M., Oda H., Okazaki Y.,
Owa C., Ozawa Y., Saito H., Sano M., Sato K., Shibata K., Shibata
Y., Shigenoto Y., Shiraki T., Sogabe Y., Sugahara Y., Suzuki H.,
Suzuki H., Takahashi F., Tateo M., Tomioka N., Tsunoda Y.,
Watahiki A., Watanabe S., Yamamura T., Yasunishi A., Yokota T.,
Yoshiki A., Yoshino M., Yamamatsu M. and Hayashizaki Y.
RIKEN Mouse ESTs (Konno H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Sasaki N., Izawa M., Watahiki M., Ozawa K., Tanaka T., Yoneda Y.,
Matsura S., Carninci P., Muramatsu M., Okazaki Y. and Hayashizaki
Y.

(hinoue@im.wustl.edu)
 Seq primer: -4ORP from Gibco
 High quality sequence stop: 481.
 Location/Qualifiers
 1. .642

FEATURES

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5782074"
 /clone_lib="HR85 islet"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size: selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Allan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

BASE COUNT

166 a 179 c 190 g 107 t

Query Match

Best Local Similarity 68.0%; Score 17; DB 14; Length 642;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCCAGGACGACGAAT 19

|||||

Db 409 TCCAGGACGACGAAT 425

RESULT 6

BE877455

LOCUS

DEFINITION 601485493F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888094 5',
 mRNA sequence.

ACCESSION BE877455

VERSION BE877455.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 821)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/OTF/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9667 row: i column: 23

High quality sequence stop: 715.

Location/Qualifiers

1. .821

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3888094"

/clone_lib="NIH_MGC_69"

/tissue_type="large cell carcinoma, undifferentiated"

/lab_host="DH10B (phage-resistant)"

/note="Organ: lung; Vector: pCMV-Sport6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 1.1 kb. Library constructed by Life

Technologies."

BASE COUNT 228 a 270 c 115 g 208 t

ORIGIN

Query Match 68.0%; Score 17; DB 12; Length 821;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACGACGAATTTAC 23

|||||

Db 713 AGGAACGACGAATTTAC 729

RESULT 7

BM401231/c

LOCUS

DEFINITION 5009-0-84-E04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM401231

VERSION BM401231

KEYWORDS EST.

SOURCE EST.

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 857)

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel

J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

JOURNAL

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. .857

/organism="Tetrahymena thermophila"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 196 a 165 c 213 g 282 t

ORIGIN 1 others

Query Match 68.0%; Score 17; DB 13; Length 857;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAA 17

|||||

Db 408 TGTGCCAGGACCAAGAA 392

RESULT 8

BQ711606

LOCUS

DEFINITION BQ711606

5', mRNA sequence.

ACCESSION BQ711606

VERSION BQ711606.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 961)

AUTHORS NIH-MGC

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing By: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM2521 row: e column: 08
 High quality sequence start: 8
 High quality sequence stop: 542.
 Location/Qualifiers
 1..961

FEATURES

source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6302959"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC Library."

BASE COUNT 237 a 260 c 227 g 236 t 1 others
 ORIGIN

Query Match 68.0%; Score 17; DB 14; Length 961;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCAGGACCGAATTT 21
 Db 829 CCAGGACCGAATTT 845
 RESULT 9
 BQ280096/c
 LOCUS
 DEFINITION
 1091034F06.x1 1091 - Immature ear with common ESTs screened by
 Schmidt lab Zea mays cDNA, mRNA sequence.
 BQ280096
 ACCESSION
 BQ280096
 VERSION
 BQ280096
 KEYWORDS
 EST.
 SOURCE
 Zea mays.
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 229)
 Walbot,V.
 University
 Maize ESTs from various cDNA libraries sequenced at Stanford
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1091034 row: F column: 06.
 Location/Qualifiers
 1..229
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="1091 - Immature ear with common ESTs screened
 by Schmidt lab"
 /tissue_type="Inflorescence meristem - floral organ
 primordia"

FEATURES

source

Location/Qualifiers
 1..229
 /organism="Zea mays"
 /cultivar="OH43"
 /db_xref="taxon:4577"
 /clone_lib="1091 - Immature ear with common ESTs screened
 by Schmidt lab"
 /tissue_type="Inflorescence meristem - floral organ
 primordia"

/dev_stage="0.5 cm to 2 cm"
 /lab_host="Stratagene XL0LR"
 EcoRI="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
 EcoRI; Site_2: XhoI; RNA from library 606 was filtered for
 common ESTs found in 606."
 BASE COUNT 80 a 32 c 38 g 79 t
 ORIGIN

Query Match 64.0%; Score 16; DB 14; Length 229;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGAACCAGA 16
 Db 43 TGTGCCAGGAACCAGA 28
 RESULT 10
 AV357770/c
 LOCUS
 DEFINITION
 AV357770 RIKEN full-length enriched, in vitro fertilized eggs Mus
 musculus cDNA clone 7420408P18 3', mRNA sequence.
 AV357770
 ACCESSION
 AV357770.1 GI:6404772
 VERSION
 EST.
 KEYWORDS
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 246)
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
 Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
 Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai
 ,C., Kawai,J., Kikuchi,N., Koijima,Y., Koya,S., Kusakabe,M., Kai
 Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
 Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K., Shibata
 ,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H.,
 Suzuki,H., Takahashi,F., Tateo,M., Tominaga,N., Tsunoda,Y.,
 Wathiki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T.,
 Yoshihiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Konno,H., et al. 1999)
 Unpublished (1999)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Sasaki,N., Izawa,M., Wathiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
 Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
 ,Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh,M., Kitsumai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
 ,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (<http://genome.ritc.riken.go.jp>) for
 further details.

FEATURES

source

Location/Qualifiers
 1..246
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="7420408P18"
 /clone_lib="RIKEN full-length enriched, in vitro

```

fertilized eggs"
/sex="female"
/tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI"
BASE COUNT      69 a   33 c   42 g   101 t   1 others
ORIGIN
Query Match      64.0%; Score 16; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAATTA 22
|||||
Db 234 AGGAACCAAGAAATTA 219

RESULT 11
BB534005
LOCUS
DEFINITION
BB534005 RIKEN full-length enriched, 0 day neonate lung Mus
musculus cDNA clone E030032P21 3' similar to L28801 Rat
transcription factor IIIC alpha-subunit mRNA, mRNA sequence.
ACCESSION
BB534005.1 GI:9585934
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 311)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiaki,A., Yoshino
,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and thermoactivation of thermolabile enzymes by

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trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
1..311
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="E030032P21"
/clone_lib="RIKEN full-length enriched, 0 day neonate
lung"
/tissue_type="lung"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCACTCGAGTTTCTTTTCTTTTCTTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT      103 a   89 c   68 g   51 t
ORIGIN
Query Match      64.0%; Score 16; DB 10; Length 311;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

FEATURES

source

FEATURES
source

Location/Qualifiers
1. 395
/organism="Homo sapiens"
/db_xref="GDB:475349"
/db_xref="taxon:9606"
/clone="IMAGE:122804"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' ACTGGAGAAATATTAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."

BASE COUNT 110 a 89 c 92 g 99 t 5 others
ORIGIN

Query Match 64.0%; Score 16; DB 14; Length 395;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCCAGGAGAACAGAAA 18
|||||
Db 50 TCCAGGAGAACAGAAA 65

RESULT 15
AZ282651/c

LOCUS AZ282651 396 bp DNA linear GSS 27-JUL-2000
DEFINITION RPCI-23-152D24-TV RPCI-23 Mus musculus genomic clone RPCI-23-152D24
ACCESSION AZ282651
VERSION AZ282651.1 GI:9524437
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 396)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., McGann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M.

TITLE
JOURNAL
COMMENT

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@ed.jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics (inforesgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 152 row: D column: 24
Seq primer: SP6
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1. 396
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-152D24"
/sex="Female"

FEATURES
source

Location/Qualifiers
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site.1: EcoRI; Site.2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

BASE COUNT 70 a 126 c 61 g 139 t
ORIGIN

Query Match 64.0%; Score 16; DB 17; Length 396;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCCAGGAGAACAGAAA 18
|||||
Db 169 TCCAGGAGAACAGAAA 154

RESULT 16

T77962
LOCUS T77962 397 bp mRNA linear EST 07-MAR-1995
DEFINITION YC97D11.r1 Soares infant brain 1N1B Homo sapiens cDNA clone
IMAGE:24089 5', mRNA sequence.

ACCESSION T77962
VERSION T77962.1 GI:696471
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Bultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,B., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilton RK

TITLE
JOURNAL
COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1685
High quality sequence stops: 310 Source: IMAGE Consortium, LML
This clone is available royalty-free through LML; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 1685 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 310.

FEATURES
source

Location/Qualifiers
1. 397
/organism="Homo sapiens"
/db_xref="GDB:396436"
/db_xref="taxon:9606"
/clone="IMAGE:24089"
/clone_lib="Soares infant brain 1N1B"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lfamid BA; Site.1: Not I; Site.2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGAGAGATTCGGCCGACGAGATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lfamid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Patima Bonaldo."

BASE COUNT 85 a 115 c 92 g 102 t 3 others
ORIGIN

```

Query Match          64.0%; Score 16; DB 14; Length 397;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 GTGCCAGGACCGAA 17
Db  193 GTGCCAGGACCGAA 208

|||||
|||||

RESULT 17
BH878510
LOCUS
DEFINITION
hs82e08.bl WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION
BH878510
VERSION
BH878510.1 GI:22114407
KEYWORDS
GSS.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 408)
Rabinowicz,P.D., O'Shaughnessy,A.L., Baliya,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hs82 row: e column: 08
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 408.
Location/Qualifiers
1..408
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="hs82e08"
/clone_host="JM107 or DH5a"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

BASE COUNT  161 a  71 c  57 g  119 t
ORIGIN
Query Match          64.0%; Score 16; DB 17; Length 408;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TGTGCCAGGACCGA 16
Db  384 TGTGCCAGGACCGA 399

|||||
|||||

RESULT 18
BH876286
LOCUS
DEFINITION
hr30b07.bl WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hr30b07 5', DNA sequence.

```

```

ACCESSION
BH876286
VERSION
BH876286.1 GI:22112183
KEYWORDS
GSS.
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 447)
Rabinowicz,P.D., O'Shaughnessy,A.L., Baliya,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr30 row: b column: 07
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 447.
Location/Qualifiers
1..447
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="hr30b07"
/clone_host="JM107 or DH5a"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."

BASE COUNT  155 a  86 c  65 g  137 t
ORIGIN
Query Match          64.0%; Score 16; DB 17; Length 447;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 TGTGCCAGGACCGA 16
Db  350 TGTGCCAGGACCGA 365

|||||
|||||

RESULT 19
AA126284
LOCUS
DEFINITION
zm79e02.sl Stratagene neuroepithelium (#937231) Homo sapiens cDNA
clone IMAGE:531866 3', mRNA sequence.
ACCESSION
AA126284
VERSION
AA126284.1 GI:1685940
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 449)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags

```


JOURNAL
MEDLINE
COMMENT

Genome Res. 6 (9), 807-828 (1996)

97044478

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1893 Std Error: 0.00

Seq primer: -40M13 fwd. from Amersham

High quality sequence stop: 353.

FEATURES
source

```
1. .449
/organism="Homo sapiens"
/db_xref="GDB:3921378"
/db_xref="taxon:9606"
/clone="IMAGE:531866"
/dev_stage="Ntera-2/RA neuroepithelial cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2
cells (Ntera-2/ci.D1) induced with Retinoic Acid for 24
hours. Average insert size: 1.5 Kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT      128 a      90 c      120 g      110 t      1 others
ORIGIN
```

```
Query Match      64.0%; Score 16; DB 9; Length 449;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 AGGACACGAAATTTA 22
|||||
Db      418 AGGACACGAAATTTA 433
```

RESULT 20
AI325084/c

```
LOCUS      AI325084      464 bp      mRNA      linear      EST 23-DEC-1998
DEFINITION      mq95f12.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:586511 3' similar to TR:P70441 P70441 PROTEIN CO-FACTOR. ;'
mRNA sequence.
```

```
ACCESSION      AI325084      GI:4059513
```

```
VERSION      EST.
```

```
KEYWORDS      house mouse.
```

```
SOURCE      Mus musculus
```

```
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
REFERENCE      1 (bases 1 to 464)
```

```
AUTHORS      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
```

```
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
```

```
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
```

```
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
```

```
Waterston,R.
```

```
TITLE      The WashU-HHMI Mouse EST Project
```

```
JOURNAL      Unpublished (1996)
```

```
COMMENT      Contact: Marra M/Mouse EST Project
```

```
Washington University School of Medicine
```

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
```

```
Tel: 314 286 1800
```

```
Fax: 314 286 1810
```

```
Email: mouseest@watson.wustl.edu
```

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:361159

This clone was previously sequenced on the 5' end only, this new

data is from the 3' end

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 454.

FEATURES
source

```
Location/Qualifiers
1. .464
/organism="Mus musculus"
/strain="NIH Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:586511"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
/tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 Kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT      104 a      141 c      114 g      105 t
ORIGIN
```

```
Query Match      64.0%; Score 16; DB 9; Length 464;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 TGTGCGGAGAACCCAGA 16
|||||
Db      110 TGTGCGGAGAACCCAGA 95
```

RESULT 21
AI747269/c

```
LOCUS      AI747269      468 bp      mRNA      linear      EST 22-JUN-1999
DEFINITION      IMAGE:2076772 3' mRNA sequence.
```

```
ACCESSION      AI747269      GI:5125533
```

```
VERSION      EST.
```

```
KEYWORDS      house mouse.
```

```
SOURCE      Mus musculus
```

```
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
REFERENCE      1 (bases 1 to 468)
```

```
AUTHORS      Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
```

```
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
```

```
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
```

```
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
```

```
Waterston,R. and Wilson,R.
```

```
TITLE      The WashU-NCI Mouse EST Project 1999
```

```
JOURNAL      Unpublished (1999)
```

```
COMMENT      Contact: Marra M/WashU-NCI Mouse EST Project 1999
```

```
Washington University School of Medicine
```

```
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
```

```
Tel: 314 286 1800
```

```
Fax: 314 286 1810
```

```
Email: mouseest@watson.wustl.edu
```

```
This clone is available royalty-free through LLNL; contact the
```

```
IMAGE Consortium (info@image.llnl.gov) for further information.
```

```
MGI:995208
```

```
Seq primer: custom primer used
```

```
High quality sequence stop: 437.
```

```
Location/Qualifiers
```

```
1. .468
```

```
/organism="Mus musculus"
```

```
/strain="C57BL"
```

```
/db_xref="taxon:10090"
```

```
/clone="IMAGE:2076772"
```

```

/clone_lib="Sugano mouse embryo mewa"
/dev_stage="embryo, 14 dpc"
/lab_host="DH10B"
/notes="Vector: pME18S-FL3; site.1: DraIII (CACTGTG);
site.2: DraIII (CAACATG); 1st strand cDNA was primed
with an oligo(dT) primer [AGTGGCCITTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[TTTGGCTACTGG], digested and cloned into distinct DraIII
sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site
CAACATG). XhoI should be used to isolate the cDNA
insert. Size selection was performed to exclude fragments
<1.5kb. Library constructed by Dr. Sumio Sugano
(University of Tokyo Institute of Medical Science).
Custom primers for sequencing: 5' end primer
CTTCTGCTAAAGCTGCG and 3' end primer
CGACCTGCAGCTCGACACA."
BASE COUNT      151 a      82 c      70 g      164 t      1 others
ORIGIN

Query Match      64.0%; Score 16; DB 9; Length 468;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AGGACACCAAAATTTA 22
|||||
Db 249 AGGACACCAAAATTTA 234

RESULT 22
BH879621/c
LOCUS      BH879621
DEFINITION ht47f08.g1 WGS-ZmaysF (JM107 adapted methyl filtered) GSS 05-AUG-2002
ACCESSION  BH879621
VERSION     BH879621.1 GI:22115518
KEYWORDS    GSS.
SOURCE      Zea mays.
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 471)
AUTHORS    Rabinowicz,P.D., O'Shaughnessy,A.L., Balijs,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimeto,L.,
Zucaver,T., McCombie,W.R. and Martienssen,R.A.
TITLE      Genomic shotgun sequences from Zea mays (methyl-filtered)
JOURNAL    Unpublished (2002)
COMMENT    Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: ht47 row: f column: 08
Seq primer: -2LM13UnivFwd
Class: Shotgun
High quality sequence stop: 471.
FEATURES
source
1..471
Location/Qualifiers
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ht47f08"
/lab_host="JM107 or DH5a"
/notes="Organ: immature ears; Site.1: Xba I; Site.2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
BASE COUNT      173 a      72 c      68 g      156 t
ORIGIN

Query Match      64.0%; Score 16; DB 17; Length 471;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACACAGA 16
|||||
Db 288 TGTGCCAGGAACACAGA 273

RESULT 23
B98791/c
LOCUS      B98791
DEFINITION CIT-HSP-2280N3.TR CIT-HSP Homo sapiens genomic clone 2280N3, DNA
sequence.
ACCESSION  B98791
VERSION     B98791.1 GI:3026015
KEYWORDS    GSS.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 489)
AUTHORS    Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE      Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL    Unpublished (1998)
COMMENT    Other_GSSs: CIT-HSP-2280N3.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1..489
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="GDB:714695"
/db_xref="taxon:9606"
/clone="2280N3"
/clone_lib="CIT-HSP"
/cell_type="Sperm"
/sex="Male"
/notes="Vector: pBelobAC11; Site.1: HindIII; Site.2:
HindIII"
BASE COUNT      130 a      97 c      106 g      156 t
ORIGIN

Query Match      64.0%; Score 16; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACACAGA 16
|||||
Db 462 TGTGCCAGGAACACAGA 447

RESULT 24
BF610439/c
LOCUS      BF610439
DEFINITION NXSI_058_E06_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda CDNA
clone NXSI_058_E06_5', mRNA sequence.
505 bp mRNA linear EST 14-DEC-2000

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ACCESSION      BF610439
VERSION        BF610439.1 GI:11779094
KEYWORDS       EST
SOURCE         Loblolly pine.
ORGANISM       Pinus taeda

REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
AUTHORS        1 (bases 1 to 505)
TITLE          Sederoff, R.
JOURNAL        Molecular Basis of Wood Formation in the Pine Megagenome
COMMENT        Unpublished (2000)
               Contact: Johnson, Arthur
               North Carolina State University
               Tel: 919 515 7800
               Fax: 919 515 7801
               Email: ajohnson@unity.ncsu.edu
               Seq primer: T3.

FEATURES       source
               1..505
               /organism="Pinus taeda"
               /strain="Coastal plain loblolly pine from North Carolina"
               /db_xref="taxon:3352"
               /clone_lib="NXSI_058_E06"
               /tissue_type="Xylem"
               /cell_type="Side"
               /dev_stage="Juvenile"
               /lab_host="XLI-Blue"
               /note="Vector: BlueScript SK; Site.1: Eco RI; Site.2: XhoI
               : The library is from early (spring) wood, taken from
               : three six-year old trees (three different genotypes), in
               : the juvenile phase. These trees were induced to form side
               : wood by bending to a 45 degree angle and tying them to the
               : ground. Differentiating xylem was harvested from the sides
               : of the inclined stems, and a mixture of all three
               : genotypes was used for the library. oligo-dt primed cDNA
               : was directionally cloned into the EcoRI-XhoI Bluescript SK
               : vector arms. NOTE: The sequences contain a 'cDNA adapter'
               : between the EcoRI site and the start of the EST. The
               : adapter sequence is 'AATCGGACGAG'."
BASE COUNT     134 a 114 c 111 g 130 t 16 others
ORIGIN
Query Match    64.0%; Score 16; DB 12; Length 505;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACAGAAAT 19
Db 181 GCCAGGACAGAAAT 166
|||||
|||||

RESULT 25
BM725916
LOCUS          BM725916
DEFINITION     UI-E-EJ0-aig-i-22-0-UI.r1 UI-E-EJ0 Homo sapiens cDNA clone
               533 bp mRNA linear EST 01-MAR-2002
               UI-E-EJ0-aig-i-22-0-UI 5', mRNA sequence.
ACCESSION      BM725916
VERSION        BM725916
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 533)
AUTHORS        Bernaldo, M.F., Lennon, G. and Soares, M.B.
TITLE          Normalization and subtraction: two approaches to facilitate gene
               discovery
JOURNAL        Genome Res. 6 (9), 791-806 (1996)
MEDLINE        97044477
COMMENT        Contact: Soares, MB
               Program for Rat Gene Discovery and Mapping
               University of Iowa

```

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451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: mssoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.

FEATURES       Location/Qualifiers
               1..533
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="UI-E-EJ0-aig-i-22-0-UI"
               /clone_lib="UI-E-EJ0"
               /tissue_type="fetal eyes, lens, eye anterior segment,
               optic nerve, retina, Retina Foveal and Macular, RPE and
               Choroid"
               /dev_stage="fetal and adult"
               /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
               /note="Organ: eye. Vector: pT7T3-Pac (Pharmacia) with a
               modified polylinker; Site.1: EcoR I; Site.2: Not I;
               UI-E-EJ0 is a subcloned cDNA library constructed
               according to Bernaldo, Lennon and Soares, Genome Research,
               6:791-806, 1996. First strand cDNA synthesis was primed,
               with an oligo-dT primer containing a Not I site. Double
               stranded cDNA was ligated to an EcoR I adaptor, digested
               with Not I, and cloned directionally into pT7T3-Pac
               vector. The oligonucleotide used to prime the synthesis of
               first-strand cDNA contains a library tag sequence that is
               located between the Not I site and the (dT)18 tail. The
               sequence tags for this library are: fetal eyes, AGAATCAGAA
               ; lens, CGATACGCA; eye anterior segment, AATGCCGAT;
               optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and
               Macular, GTCC; RPE and Choroid, ACCTA. This library was
               created for the program, Gene Discovery in the Visual
               System, supported by National Eye Institute (NEI)."
BASE COUNT     96 a 175 c 121 g 141 t
ORIGIN
Query Match    64.0%; Score 16; DB 14; Length 533;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCCAGGACACGAA 17
Db 105 GTGCCAGGACACGAA 120
|||||
|||||

RESULT 26
BQ701598/c
LOCUS          BQ701598/c
DEFINITION     NXSI_111_E01_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
               clone NXSI_111_E01 5', mRNA sequence.
ACCESSION      BQ701598
VERSION        BQ701598
KEYWORDS       EST.
SOURCE         loblolly pine.
ORGANISM       Pinus taeda
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE      1 (bases 1 to 543)
AUTHORS        Sederoff, R.
TITLE          Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL        Unpublished (2000)
COMMENT        Contact: Johnson, Arthur
               North Carolina State University
               Tel: 919 515 7800
               Fax: 919 515 7801
               Email: ajohnson@unity.ncsu.edu
               Seq primer: T3.

```

FEATURES
source

Location/Qualifiers
1. 543
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone_lib="NXSI_111_E01"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dt primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGCACGAG'."
BASE COUNT 148 a 127 c 118 g 139 t 11 others
ORIGIN
Query Match 64.0%; Score 16; DB 14; Length 543;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCAGGACCAGAAAT 19
Db 241 GCCAGGACCAGAAAT 226
|||||

RESULT 27
BH876388

LOCUS
DEFINITION hr30406.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION BH876388
VERSION
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays

REFERENCE
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 551)
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)

TITLE
JOURNAL
COMMENT

Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr30 row: g column: 06
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 551.

FEATURES
source

Location/Qualifiers
1. 551
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"

/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
BASE COUNT 204 a 100 c 78 g 169 t
ORIGIN

Query Match 64.0%; Score 16; DB 17; Length 551;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCAGGAACACAGA 16
Db 388 TGTCCAGGAACACAGA 403
|||||

RESULT 28
BG039852/c

LOCUS
DEFINITION BG039852 557 bp mRNA linear EST 24-JAN-2001
clone NXSI_104_G04_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
ACCESSION BG039852
VERSION
KEYWORDS EST.
SOURCE BG039852.1 GI:12482533
ORGANISM loblolly pine.
Pinus taeda

REFERENCE
AUTHORS Sederoff, R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source

Location/Qualifiers
1. 557
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXSI_104_G04"
/clone_lib="NXSI (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"

/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dt primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGCACGAG'."
BASE COUNT 149 a 123 c 121 g 147 t 17 others
ORIGIN

Query Match

Best Local Similarity 64.0%; Score 16; DB 12; Length 557;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCAGAAAT 19

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|||||
Db 195 GCCAGGAACAGAAAT 180

RESULT 29
AW644504/c
LOCUS
DEFINITION
cm41h08.w1 Blackshear/Soares normalized Xenopus egg library xenopus
laevis cDNA clone PBX0140H08 5', mRNA sequence.
ACCESSION
AW644504
VERSION
AW644504.1 GI:7401893
KEYWORDS
EST.
SOURCE
African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 574)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.,
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman,
J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)
21211403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
phone 800-533-4363 ext.cdn, fax 256-536-9016 att:cdna, email
cdna@resgen.com
DNA sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAAACGACGGCCAGT
BACKWARD: CAGGAACAGCTATGACC
Plate: 0140 row: H column: 08
Seq primer: R7 primer.
FEATURES
Source
Location/Qualifiers
1..574
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone_lib="PBX0140H08"
/clone_lib="Blackshear/Soares normalized Xenopus egg
library"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT73-Pac; Site1: EcoRI; Site2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dt18 primer. Double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 x 10^5
recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT
165 a 109 c 116 g 184 t
ORIGIN

Query Match
Best Local Similarity 64.0%; Score 16; DB 10; Length 574;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30
BH876387/c
LOCUS
DEFINITION
hr30g06.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hr30g06 5', DNA sequence.
ACCESSION
BH876387
VERSION
BH876387.1 GI:22112284
KEYWORDS
GSS.
SOURCE
Zea mays.
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 581)
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N.,
Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L.,
Zutavern, T., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr30 row: g column: 06
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 581.
FEATURES
Source
Location/Qualifiers
1..581
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="hr30g06"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"
/note="Organ: immature ears; Site1: Xba I; Site2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mp19, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
BASE COUNT
178 a 83 c 97 g 223 t
ORIGIN

Query Match
Best Local Similarity 64.0%; Score 16; DB 17; Length 581;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
BH876535
LOCUS
DEFINITION
hr31g03.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hr31g03 5', DNA sequence.
ACCESSION
BH876535
VERSION
BH876535.1 GI:22112432
KEYWORDS
GSS.

```

SOURCE Zea mays.
ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 596)
Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N., King, L., Miller, B., Muller, S., Nascimben, L., Katzenburger, F., McCombie, W.R. and Martienssen, R.A.
Zutavern, I., McCombie, W.R. and Martienssen, R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr31 row: g column: 03
Seq primer: -21M13univFwd
Class: shotgun
High quality sequence stop: 596.

FEATURES
source
1. 596
Location/Qualifiers
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hr31g03"
/lab_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/lab_host="JM107 or DH5a"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (-x/y reads in M13mp19, b/y reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 165 a 109 c 105 g 217 t

Query Match 64.0%; Score 16; DB 17; Length 596;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCAGGACAGCA 16
Db 481 TGTGCAGGACAGCA 496

RESULT 32
AW043028/c
LOCUS
DEFINITION AW043028 Pine Triplex shoot tip library Pinus taeda cDNA clone
ACCESSION AW043028
VERSION
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda

REFERENCE 1 (bases 1 to 601)
AUTHORS Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
TITLE The Pine Gene Discovery Project
JOURNAL Unpublished (1999)
COMMENT Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801

Query Match 64.0%; Score 16; DB 17; Length 596;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCAGGACAGCA 16
Db 481 TGTGCAGGACAGCA 496

RESULT 32
AW043028/c
LOCUS
DEFINITION AW043028 Pine Triplex shoot tip library Pinus taeda cDNA clone
ACCESSION AW043028
VERSION
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda

REFERENCE 1 (bases 1 to 601)
AUTHORS Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
TITLE The Pine Gene Discovery Project
JOURNAL Unpublished (1999)
COMMENT Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801

Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda Triplex2 Sequencing Primer.
Location/Qualifiers
1. 601
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST28D06"
/lab_host="E. coli BM25.8"
/note="Organ: shoot tips; Vector: Lambda Triplex; Site_1: SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda Triplex vector. Plasmid subclones in pTriplex were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

BASE COUNT 166 a 133 c 118 g 170 t 14 others

ORIGIN

Query Match 64.0%; Score 16; DB 10; Length 601;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGAACAGAAAT 19
Db 512 GCCAGGAACAGAAAT 497

RESULT 33
AW043050/c
LOCUS
DEFINITION AW043050 601 bp mRNA linear EST 18-SEP-1999
ST28F07 Pine Triplex shoot tip library Pinus taeda cDNA clone
ACCESSION ST28F07, mRNA sequence.
VERSION AW043050.1 GI:5903579
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda

REFERENCE 1 (bases 1 to 601)
AUTHORS Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
TITLE The Pine Gene Discovery Project
JOURNAL Unpublished (1999)
COMMENT Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801

Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda Triplex2 Sequencing Primer.
Location/Qualifiers
1. 601
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST28F07"
/lab_host="E. coli BM25.8"
/note="Organ: shoot tips; Vector: Lambda Triplex; Site_1: SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda Triplex vector. Plasmid subclones in pTriplex were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

BASE COUNT 176 a 135 c 121 g 169 t

ORIGIN

Query Match 64.0%; Score 16; DB 10; Length 601;

```

Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCAAGAAT 19
|||||
Db 514 GCCAGGACCAAGAAT 499

RESULT 34
AW043091
LOCUS
DEFINITION ST29C02 Pine Triplex shoot tip library Pinus taeda cDNA clone
ACCESSION AW043091
VERSION AW043091.1 GI:5903620
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 601)
AUTHORS Whetten,R.W., Kinlaw,C.S., Retzel,B. and Sederoff,R.R.
TITLE The Pine Gene Discovery Project
JOURNAL Unpublished (1999)
COMMENT Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
, NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda Triplex2 Sequencing Primer.

FEATURES
source
1..601
/organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST29C02"
/clone_lib="Pine Triplex shoot tip library"
/note="Organ: shoot tips; Vector: Lambda Triplex; Site_1:
SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from
apex) were collected during the spring, frozen and used
for mRNA isolation. The SMART-PCR method (Clontech) was
used to prepare a library from 1 ug total RNA, using the
Lambda Triplex vector. Plasmid subclones in pTriplex were
recovered by cre-lox excision in E. coli strain BM25.8 and
sequenced from the 5' end."
BASE COUNT 187 a 134 c 135 g 141 t 4 others
ORIGIN

Query Match 64.0%; Score 16; DB 10; Length 601;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GAACCAAGAAATTACA 24
|||||
Db 34 GAACCAAGAAATTACA 49

RESULT 35
AQ009748/c
LOCUS
DEFINITION CIT-HSP-2280C6.TRB CIT-HSP Homo sapiens genomic clone 2280C6, DNA
sequence.
ACCESSION AQ009748
VERSION AQ009748.1 GI:3129133
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 608)

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AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Grainger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other GSSs: CIT-HSP-2280C6.TFB CIT-HSP-2280C6.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source
1..608
/organism="Homo sapiens"
/db_xref="GDB:7146704"
/db_xref="taxon:9606"
/clone="2280C6"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelOBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 191 a 107 c 132 g 176 t 2 others
ORIGIN

Query Match 64.0%; Score 16; DB 17; Length 608;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAGA 16
|||||
Db 313 TGTGCCAGGACCAGA 298

RESULT 36
BE600467
LOCUS
DEFINITION PIL_96.D12.q1.A002 Pathogen induced 1 (PIL) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BE600467
VERSION BE600467.1 GI:9855526
KEYWORDS EST.
SOURCE Sorghum.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 613)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: pathogen-induced plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 14
High quality sequence stop: 608

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POLYA=NO.
FEATURES
  source
    Location/Qualifiers
      1..613
        /organism="Sorghum bicolor"
        /db_xref="taxon:4558"
        /clone_lib="Pathogen induced 1 (PII)"
        /note="Organ: Anthracnose-infected leaves from
          two-week-old sorghum plants 48 hr after inoculation;
          Vector: pBluescript II from lambda Zap II; Site1: xhoI;
          Site2: EcoRI; Two-week-old sorghum plants (BX 623
          cultivar) were infected with pathogen (isolate PM42I of
          Colletotrichum graminicola, which is a sorghum isolate).
          RNA was prepared from infected leaves harvested from 45
          seedlings 48 hours after inoculation. Note: young
          seedlings (2 weeks old) exhibit juvenile resistant
          reaction, which is an incompatible interaction. As they
          grow older (4 weeks or older), plants resume susceptibility
          to anthracnose disease. The library was made from poly-A
          RNA in the cloning vector lambda Zap II. Clones to be
          sequenced were prepared by mass excision. WARNING: While
          most or all ESTs are expected to derive from the host
          plant, no effort was made to eliminate ESTs deriving from
          the pathogen."
      228 a 104 c 94 g 187 t
      BASE COUNT
      ORIGIN
        Query Match 64.0%; Score 16; DB 10; Length 613;
        Best Local Similarity 100.0%; Pred. No. 95;
        Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

      Qy 1 TGTGCCAGGACACAGA 16
          |||||
      Db 377 TGTGCCAGGACACAGA 392

      RESULT 37
      BG003085/c
      LOCUS
      DEFINITION
      ACCESSION
      VERSION
      KEYWORDS
      SOURCE
      ORGANISM
        Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      1 (bases 1 to 628)
      Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
      Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.,
      Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H.,
      Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare
      M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
      Simpson, A.J.
      Shotgun sequencing of the human transcriptome with ORF expressed
      sequence tags
      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
      20202663
      Contact: Simpson A.J.G.
      Laboratory of Cancer Genetics
      Ludwig Institute for Cancer Research
      Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
      Brazil
      Tel: +55-11-2704922
      Fax: +55-11-2707001
      Email: asimpson@ludwig.org.br
      This sequence was derived from the FAPESP/LICR Human Cancer Genome
      Project. This entry can be seen in the following URL
      (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3&t2=MR3-GN0187-
      171100-011-f05&t3=2000-11-17&t4=1)
      Seq primer: puc 18 forward
      High quality sequence stop: 617.
      Location/Qualifiers
        1..628
  
```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0187"
/dev_stage="Adult"
/note="Organ: Placenta_normal; Vector: puc18; Site1: SmaI
; Site2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
129 a 154 c 197 g 148 t
BASE COUNT
ORIGIN
  Query Match 64.0%; Score 16; DB 12; Length 628;
  Best Local Similarity 100.0%; Pred. No. 95;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Qy 1 TGTGCCAGGACACAGA 16
      |||||
  Db 507 TGTGCCAGGACACAGA 492

  RESULT 38
  BF511713/c
  LOCUS
  DEFINITION
  ACCESSION
  VERSION
  KEYWORDS
  SOURCE
  ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    1 (bases 1 to 636)
    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
    National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
    Unpublished (1997)
    Tumor Gene Index
    Contact: Robert Strausberg, Ph.D.
    Email: cgaps-r@mail.nih.gov
    The sequence contained an oligo-dT track that was present in the
    oligonucleotide that was used to prime the synthesis of first
    strand cDNA and therefore this may represent a bonafide poly A
    tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
    NCI-CGAP clone distribution information can be found through the
    I.M.A.G.E. Consortium/LLNL at:
    www.bio.llnl.gov/bbrp/image/image.html The following repetitive
    elements were found in this cDNA sequence: 228-285, >MIR
    Seq primer: M13 Forward
    POLYA=Yes.
    Location/Qualifiers
      1..636
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone_lib="NCI-CGAP_Sub8"
      /lab_host="DH10B (Life Technologies)"
      /note="Vector: pT73D-Pac (Pharmacia) with a modified
        polylinker; Site1: Not I; Site2: Eco RI; NCI-CGAP_Sub8
        is a subtracted library derived from NCI-CGAP_Sub5. The
        NCI-CGAP_Sub8 library had 2.5 million recombinants. A
        single-stranded DNA preparation of NCI-CGAP_Sub5 was used
        as a tracer in a subtractive hybridization with a driver
        comprising: a pool of clones from NCI-CGAP_Sub5 (IMAGE
        clone ids 2732833-2737415, 3068040-3069191; 25% of the
        driver population), a pool of clones from NCI-CGAP_Sub4
        (IMAGE clone ids 2723592-2729326; 25% of the driver
        population), NCI-CGAP_Sub6 (pool AIF-AJU, IMAGE ids
        2728969-2733190; 25% of the driver population), and
        NCI-CGAP_Sub7 (IMAGE ids 3069192-3072238, 3081864-3084550
        ; 25% of the driver population). Subtraction was
  
```


performed as previously described [Bonaldo, Lennon & Soares (1996)]: Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.

BASE COUNT 187 a 135 c 119 g 194 t 1 others
ORIGIN

Query Match 64.0%; Score 16; DB 12; Length 636;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGCAACAGAAAT 19
|||||
DB 163 GCCAGCAACAGAAAT 148

RESULT 39
BM678024/c
LOCUS BM678024 663 bp mRNA linear EST 27-FEB-2002
DEFINITION UI-E-EJ0-aig-1-22-0-UI.s1 UI-E-EJ0 Homo sapiens cDNA clone
UI-E-EJ0-aig-1-22-0-UI 3', mRNA sequence.

ACCESSION BM678024
VERSION BM678024.1 GI:18987920
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477

COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1..663
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJ0-aig-1-22-0-UI"
/clone_lib="UI-E-EJ0"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT7n3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7n3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA

; lens, CCATTAGCGA; eye anterior segment, AATGCCGAT;
optic nerve, CCATTAGTG; retina, CCGCG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJ0
TAG_ISSUE=human retina
TAG_SEQ=CCGCG"

BASE COUNT 162 a 159 c 196 g 145 t 1 others
ORIGIN

Query Match 64.0%; Score 16; DB 14; Length 663;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTCCAGCAACAGAA 17
|||||
DB 550 GTCCAGCAACAGAA 535

RESULT 40
AG133215
LOCUS AG133215 667 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-145N04.F, genomic survey sequence.
ACCESSION AG133215
VERSION AG133215.1 GI:16662893
KEYWORDS GSS.

SOURCE Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library clone:PTB-145N04.F.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

REFERENCE 1
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE BAC end sequences of Library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 667)
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
Tel:81-45-503-9111, Fax:81-45-503-9170)

COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..667
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-145N04.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 176 a 191 c 135 g 165 t
ORIGIN

Query Match 64.0%; Score 16; DB 17; Length 667;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCCAGCAACAGAA 16
|||||
DB 307 TGTCCAGCAACAGAA 322

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RESULT 41
BH882704
LOCUS          BH882704          686 bp      DNA          linear      GSS 05-AUG-2002
DEFINITION    hw39501.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
ACCESSION     BH882704
VERSION       BH882704.1 GI:22118601
KEYWORDS      GSS.
SOURCE        Zea mays.
ORGANISM      Zea mays
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
               clade; Panicoidae; Andropogoneae; Zea.
REFERENCE     1 (bases 1 to 686)
AUTHORS       Rabinowicz,P.D.; O'Shaughnessy,A.L.; Balija,V.; Dedhia,N.;
               Katzenburger,F.; King,L.; Miller,B.; Muller,S.; Nasclmento,L.;
               Zutavern,T.; McCombie,W.R. and Martienssen,R.A.
TITLE         Genomic shotgun sequences from Zea mays (methyl-filtered)
JOURNAL       Unpublished (2002)
COMMENT       Contact: W. Richard McCombie
               Lita Annenberg Hazen Genome Sequencing Center
               Cold Spring Harbor Laboratory
               PO Box 100, Cold Spring Harbor, NY 11724, USA
               Tel: 516 367 8884
               Fax: 516 367 8874
               Email: mcombie@cshl.org
               Seq primer: hw39 row: b column: 01
               Class: Shotgun
               High quality sequence stop: 686.
FEATURES      Location/Qualifiers
               1..686
               /organism="Zea mays"
               /cultivar="B73"
               /db_xref="taxon:4577"
               /clone="hw39b01"
               /clone_lib="WGS-ZmaysF (JM107 or DH5a)"
               /lab_host="JM107 or DH5a"
               /note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
               The vector was digested with XbaI and one nucleotide was
               added by fill in in the recessive 3' end. The genomic DNA
               was nebulized, end repaired, adaptor ligated and size
               fractionated using sephadex. The resulting fragments were
               between 0.8 and 3 kb and were cloned into the vector
               (X/Y reads in M13mpl9, B/g reads in pUC19). The same
               ligation was transformed in either JM107 or DH5a."
BASE COUNT    243 a 109 c 121 g 213 t
ORIGIN
Query Match      64.0%; Score 16; DB 17; Length 686;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAGA 16
Db 111 TGTGCCAGGACCCAGA 126

RESULT 42
AW340752/c
LOCUS          AW340752          698 bp      mRNA          linear      EST 31-JAN-2000
DEFINITION    hd01g09.x1 Soares_NFL.T.GBC.S1 Homo sapiens cDNA clone
IMAGE:2908288 3' similar to WP:707A9.5 CEL7214 ; mRNA sequence.
ACCESSION     AW340752
VERSION       AW340752.1 GI:6837378
KEYWORDS      EST.
SOURCE        Human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 698)

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AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cyapbs@mail.nih.gov
               This clone is available royalty-free through LNL; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Seq primer: -400P from Gibco
               High quality sequence stop: 462.
FEATURES      Location/Qualifiers
               1..698
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:2908288"
               /clone_lib="Soares_NFL.T.GBC.S1"
               /lab_host="DH10B"
               /note="Organ: pooled; Vector: pMT3D-Pac (Pharmacia) with
               a modified polylinker; Site_1: Not I; Site_2: Eco RI;
               Equal amounts of plasmid DNA from three normalized
               libraries (fetal lung NDHL19W, testis NHT, and B-cell
               NCI-CGAP-GC81) were mixed, and ss circles were made in
               vitro. Following HAP purification, this DNA was used as
               tracer in a subtractive hybridization reaction. The driver
               was PCR-amplified cDNAs from pools of 5,000 clones made
               from the same 3 libraries. The pools consisted of
               I.M.A.G.E. clones 297480-302087, 682632-687239,
               726408-728711, and 729096-731399. Subtraction by Bento
               Soares and M. Fatima Bonaldo. "
BASE COUNT    207 a 153 c 135 g 201 t
ORIGIN
Query Match      64.0%; Score 16; DB 10; Length 698;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCCAGAAAT 19
Db 145 GCCAGGACCCAGAAAT 130

RESULT 43
AQ745078
LOCUS          AQ745078          752 bp      DNA          linear      GSS 16-JUL-1999
DEFINITION    HS_5506.AL.E07 SP6 RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plates-1082 Col-13 Row=1, DNA sequence.
ACCESSION     AQ745078
VERSION       AQ745078.1 GI:5522523
KEYWORDS      GSS.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 752)
AUTHORS       Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
               Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
               Hood,L.
TITLE         Sequence-tagged connectors: A sequence approach to mapping and
               scanning the human genome
JOURNAL       Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE       99380589
COMMENT       Contact: Mahairas GG, Wallace JC, Hood L
               High Throughput Sequencing Center
               University of Washington
               401 Queen Anne Avenue North, Seattle, WA 98109, USA
               Tel: (206) 616-3618
               Fax: (206) 616-3887
               Email: jwallace@u.washington.edu
               Clones are derived from the human BAC library RPCI-11. For BAC
               library availability, please contact Pieter de Jong
               (pieterdejong.med.buffalo.edu). Clones may be purchased from
               BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
               or from Resear h Genetics (info@resgen.com). BAC end Web Server:

```

http://www.htsc.washington.edu
 Plate: 1082 row: I column: 13
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 752.
 Location/Qualifiers

FEATURES

1..752
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate:1082 Col=13 Row=I"
 /clone_lib="RPC1-11 Human Male BAC Library"
 /sex="male"
 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 Male blood DNA was isolated from one randomly chosen donor
 and partially digested with a combination of EcoRI and
 EcoRI Methylase. Size selected DNA was cloned into the
 pBACe3.6 vector at EcoRI sites"
 224 a 156 c 168 g 204 t

BASE COUNT

ORIGIN

Query Match 64.0%; Score 16; DB 17; Length 752;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCCAGGAGAACAGAA 18
 |||||
 Db 27 TCCAGGAGAACAGAA 42

RESULT 44

BG681831

LOCUS

DEFINITION 602629761F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4754414 5',
 mRNA sequence.

ACCESSION BG681831

VERSION BG681831.1 GI:13913228

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: LLAM10615 row: j column: 15
 High quality sequence stop: 745.

FEATURES

source

1..806
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4754414"
 /clone_lib="NCI_CGAP_Skn4"
 /lab_host="DH10B (T1 phage-resistant)"
 /tissue_type="squamous cell carcinoma"
 /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

ORIGIN

197 a 230 c 204 g 175 t

Query Match 64.0%; Score 16; DB 12; Length 806;
 Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GTCCAGGAGAACAGAA 17
 |||||
 Db 534 GTCCAGGAGAACAGAA 549

RESULT 45

BG978854/c

LOCUS

DEFINITION 602149311F2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4308099 5',
 mRNA sequence.

ACCESSION BG978854

VERSION BG978854.1 GI:12346069

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/BCID/DTF
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: L1CM1179 row: f column: 04
 High quality sequence stop: 659.

FEATURES

source

1..825
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4308099"
 /clone_lib="NIH_MGC_62"
 /tissue_type="melanotic melanoma, high MDR"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: skin; Vector: pBMR-LIB (Clontech); Site_1:
 SfiI (ggccgctcgcc); Site_2: SfiI (ggccattggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGCCGCGCGGACATG-dt(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

BASE COUNT

ORIGIN

164 a 171 c 209 g 281 t

Query Match 64.0%; Score 16; DB 12; Length 825;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCAGGAGAACAGAAAT 19

|||||

Db 784 GCCAGGAGAACAGAAAT 769

Search completed: November 24, 2002, 15:01:49
 Job time : 1554.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: November 24, 2002, 12:19:18 : Search time 211.5 Seconds
(without alignments)
266.194 Million cell updates/sec

Title: US-09-784-423-125
Perfect score: 25
Sequence: 1 TGTGCGAGAACAGAAATTTACAG 25
Scoring table: OLIGO.NUC
Gapop 60.0 , Gapext 60.0
Searched: 2185239 seqs, 1125999159 residues
Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :			
N_Geneseq_101002.*			
1:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*		
2:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*		
3:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*		
4:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*		
5:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*		
6:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*		
7:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*		
8:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*		
9:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*		
10:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*		
11:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*		
12:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*		
13:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*		
14:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*		
15:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*		
16:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*		
17:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*		
18:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*		
19:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*		
20:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*		
21:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*		
22:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*		
23:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*		
24:	/SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	AA227825	PCR primer for hum
c 2	25	100.0	1000	AA227732	Human DNA marker c
c 3	16	64.0	442	ABA58891	Human foetal liver
c 4	16	64.0	442	AAK07051	Human brain expres
c 5	16	64.0	442	AAK32792	Human bone marrow
c 6	16	64.0	442	AAI38606	Probe #7292 used t
c 7	16	64.0	442	ABS07591	Human genome-deriv
c 8	16	64.0	585	AA221494	Human sensory neur
c 9	16	64.0	2640	ABA09725	Human bone marrow

c 10	16	64.0	22080	20	AA06751	Salmonella enteric
c 11	16	64.0	134525	11	AA04525	Total base sequenc
c 12	16	64.0	2944528	24	ABA03041	Listeria monocytog
c 13	15	60.0	134	20	AA051637	Human secreted pro
c 14	15	60.0	244	21	AA026452	Human secreted pro
c 15	15	60.0	478	22	AAI92971	Human polynucleoti
c 16	15	60.0	535	21	AAZ56768	Human transmembran
c 17	15	60.0	569	24	ABK62291	Rat sequence diffe
c 18	15	60.0	591	23	ABL26995	Drosophila melanog
c 19	15	60.0	1302	23	AA056010	Salmonella typhi D
c 20	15	60.0	2433	23	AA090113	DNA encoding novel
c 21	15	60.0	2433	23	AA091291	Drosophila melanog
c 22	15	60.0	2649	23	ABL26994	Human musculoskele
c 23	15	60.0	11821	22	AAI36492	Human immune/haema
c 24	15	60.0	13395	22	AAK74325	Human musculoskele
c 25	15	60.0	15535	22	AAI36490	Human musculoskele
c 26	15	60.0	26241	22	ABA16222	Human nervous syst
c 27	15	60.0	28720	19	AAV49655	Human SC3 DNA. Ho
c 28	15	60.0	65632	21	AA081502	N. meningitidis pa
c 29	15	60.0	349980	21	AA021544	Neisseria meningit
c 30	14	56.0	123	21	AA031935	Human secreted pro
c 31	14	56.0	246	21	AA043073	Human 5' EST isola
c 32	14	56.0	318	24	ABN24228	Human ORFX polynuc
c 33	14	56.0	350	23	ABV01847	Human prostate exp
c 34	14	56.0	351	23	ABV11016	Human prostate exp
c 35	14	56.0	353	23	ABV02282	Human prostate exp
c 36	14	56.0	365	23	ABV21450	Human prostate exp
c 37	14	56.0	365	23	ABV27268	Human prostate exp
c 38	14	56.0	388	21	AAH30937	Human colon cancer
c 39	14	56.0	396	23	ABV32164	Human prostate exp
c 40	14	56.0	396	23	ABV41096	Human prostate exp
c 41	14	56.0	408	23	ABV32596	Human prostate exp
c 42	14	56.0	408	23	ABV41521	Human prostate exp
c 43	14	56.0	435	23	ABV11451	Human prostate exp
c 44	14	56.0	439	24	ABN75835	Human GPF/82 CDNA,
c 45	14	56.0	454	22	AAK60019	Human immune/haema

ALIGNMENTS

RESULT 1	
AA227825	
ID	AA227825 standard; DNA; 25 BP.
XX	
AC	AA227825;
XX	
DT	23-DEC-1999 (first entry)
XX	
DE	PCR primer for human DNA marker clone SI32.
XX	
KW	Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
KW	ITR sequence; pentanucleotide tandem repeat; stutter artifact;
KW	DNA typing; DNA profiling; linkage analysis; criminal justice;
KW	paternity testing; animal lineage analysis; microsatellite loci;
KW	polymorphism detection; PCR primer; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	W09940194-A1.
XX	
PD	12-AUG-1999.
XX	
PF	04-FEB-1999; 99WO-US02345.
XX	
PR	04-FEB-1998; 98US-0018584.
XX	
PA	(PROM-) PROMEGA CORP.
XX	
PI	Schumm JW, Bacher JW;
XX	
DR	WPI; 1999-590696/50.

XX Isolating DNA containing intermediate tandem repeat sequences, useful
PT in DNA profiling -
XX Claim 30; Page 21; 111pp; English.
XX This sequence is a PCR primer for a human DNA marker clone used in the
CC method of the invention. The method is for isolating a fragment of DNA
CC containing an intermediate tandem repeat (ITR) sequence using
CC hybridization selection, and comprises: (a) providing several DNA
CC fragments, at least one of which contains an ITR sequence, a region of
CC the DNA fragment which contains at least one repeat unit consisting of a
CC sequence of five, six or seven bases repeated in tandem at least two
CC times; (b) providing a stationary support having at least one
CC oligonucleotide associated with it, where the oligonucleotide includes a
CC sequence of nucleotides which is complementary to a portion of the ITR
CC conditions where the DNA fragments including the DNA fragment containing
CC the ITR sequence hybridize to the support. The method is particularly
CC used to isolate DNA containing pentanucleotide tandem repeat sequences as
CC well as to detect target ITR DNA sequences having a low incidence of
CC stutter artifacts (no more than 2.4%). The method is useful in DNA
CC profiling for linkage analysis, criminal justice, paternity testing and
CC the lineage of horses, dogs and other prize animals. The invention
CC overcomes problems related to the use of microsatellite loci in DNA
CC profiling. The method can detect polymorphisms with a low incidence of
CC stutter artifacts, which has previously been a problem in interpreting
CC allelic content of loci. The development of markers based on larger
CC repeat units, enables easier separation of the fragments on larger
CC electrophoretic gels. This allows the simultaneous analysis of more loci.
XX
SQ Sequence 25 BP; 9 A; 5 C; 6 G; 5 T; 0 other;
Query Match 100.0%; Score 25; DB 20; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTGCCAGCAACCAAGAAATTTACAG 25
|||||
Db 1 TGTGCCAGCAACCAAGAAATTTACAG 25
RESULT 2
AAZ27732/C
ID AAZ27732 standard; DNA; 1000 BP.
AC AAZ27732;
XX
DT 23-DEC-1999 (first entry)
XX
XX Human DNA marker clone s132.
XX
XX Tandem repeat sequence; DNA isolation; intermediate tandem repeat;
KW ITR sequence; pentanucleotide tandem repeat; stutter artifact;
KW DNA typing; DNA profiling; linkage analysis; criminal justice;
KW paternity testing; animal lineage analysis; microsatellite loci;
KW polymorphism detection; ds.
XX
XX Homo sapiens.
XX
XX WO9940194-A1.
XX
XX 12-AUG-1999.
XX
XX 04-FEB-1999; 99WO-US02345.
XX
XX 04-FEB-1998; 98US-0018584.
XX (PROM-) PROMEGA CORP.
XX
XX Schumm JW, Bacher JW;
XX

DR WPI; 1999-590696/50.
XX Isolating DNA containing intermediate tandem repeat sequences, useful
PT in DNA profiling -
XX Claim 22; Page 78; 111pp; English.
XX This sequence represents a human DNA marker clone used in the method of
CC the invention. The method is for isolating a fragment of DNA containing
CC an intermediate tandem repeat (ITR) sequence using hybridization
CC selection, and comprises: (a) providing several DNA fragments, at least
CC one of which contains an ITR sequence, a region of the DNA fragment which
CC contains at least one repeat unit consisting of a sequence of five, six
CC or seven bases repeated in tandem at least two times; (b) providing a
CC stationary support having at least one oligonucleotide associated with
CC it, where the oligonucleotide includes a sequence of nucleotides which is
CC complementary to a portion of the ITR sequence; and (c) combining the DNA
CC fragments with the support under conditions where the DNA fragments
CC including the DNA fragment containing the ITR sequence hybridize to the
CC support. The method is particularly used to isolate DNA containing
CC pentanucleotide tandem repeat sequences as well as to detect target ITR
CC DNA sequences having a low incidence of stutter artifacts (no more than
CC 2.4%). The method is useful in DNA profiling for linkage analysis,
CC criminal justice, paternity testing and other forensic and medical uses.
CC DNA typing is also useful for confirming the lineage of horses, dogs and
CC other prize animals. The invention overcomes problems related to the use
CC of microsatellite loci in DNA profiling. The method can detect
CC polymorphisms with a low incidence of stutter artifacts, which has
CC previously been a problem in interpreting allelic content of loci. The
CC development of markers based on larger repeat units, enables easier
CC separation of the fragments on electrophoretic gels. This allows the
CC simultaneous analysis of more loci.
XX
SQ Sequence 1000 BP; 302 A; 240 C; 231 G; 226 T; 1 other;
Query Match 100.0%; Score 25; DB 20; Length 1000;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TGTGCCAGCAACCAAGAAATTTACAG 25
|||||
Db 726 TGTGCCAGCAACCAAGAAATTTACAG 702
RESULT 3
ABA58891/C
ID ABA58891 standard; DNA; 442 BP.
XX
AC ABA58891;
XX
DT 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #7196.
XX
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX Homo sapiens.
XX
XX WO2000157277-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US00669.
XX
XX 04-FEB-2000; 2000US-0180312.
XX 26-MAY-2000; 2000US-0207456.
XX 30-JUN-2000; 2000US-0608408.
XX 03-AUG-2000; 2000US-0632366.
XX 21-SEP-2000; 2000US-0234687.
XX 27-SEP-2000; 2000US-0236359.
XX 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX
 PS Claim 1; SEQ ID NO 7196; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 442 BP; 123 A; 85 C; 98 G; 136 T; 0 other;
 Query Match 64.0%; Score 16; DB 22; Length 442;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGACCCAGA 16
 Db |||||||||||||||
 Db 226 TGTGCCAGGACCCAGA 211
 RESULT 4
 AAK07051/c
 ID AAK07051 standard; DNA; 442 BP.
 XX
 AC AAK07051;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe SEQ ID NO: 7042.
 XX
 KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PE 30-JAN-2001; 2001WO-US00667.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234667.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 PS Example 4; SEQ ID NO: 7042; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 XX
 SQ Sequence 442 BP; 123 A; 85 C; 98 G; 136 T; 0 other;

Query Match 64.0%; Score 16; DB 22; Length 442;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAGA 16
 Db |||||||||||||||
 Db 226 TGTGCCAGGACCCAGA 211

RESULT 5

AAK32792/c
 ID AAK32792 standard; DNA; 442 BP.

XX
 AC AAK32792;

XX
 DT 06-NOV-2001 (first entry)

XX
 DE Human bone marrow expressed single exon probe SEQ ID NO: 7349.

XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX
 OS Homo sapiens.

XX
 PN WO200157276-A2.

XX
 PD 09-AUG-2001.

XX
 PE 30-JAN-2001; 2001WO-US00668.

XX
 PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234667.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.

XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX
 DR WPI; 2001-488900/53.

XX
 PT Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -

XX
 PS Example 4; SEQ ID NO: 7349; 658pp + Sequence Listing; English.

XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
 CC the probes of the invention.

XX
 SQ Sequence 442 BP; 123 A; 85 C; 98 G; 136 T; 0 other;

Query Match 64.0%; Score 16; DB 22; Length 442;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAGA 16
 Db |||||||||||||||

CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 442 BP; 123 A; 85 C; 98 G; 136 T; 0 other;
 Query Match 64.0%; Score 16; DB 24; Length 442;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTCCAGGACACAGA 16
 |||||
 Db 226 TGTCCAGGACACAGA 211
 RESULT 8
 AAZ21494/C
 ID AAZ21494 standard; cDNA; 585 BP.
 XX
 AC AAZ21494;
 XX
 DT 03-DEC-1999 (first entry)
 XX
 DE Human sensory neurone specific 2a nucleotide sequence fragment #14.
 XX
 KW Sensory neurone specific 2a; SNS-2a; sodium channel protein; pain;
 KW voltage gated; hypersensitivity; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9947670-A1.
 XX
 PD 23-SEP-1999.
 XX
 PF 18-MAR-1999; 99WO-GE00838.
 XX
 PR 18-MAR-1998; 98GB-0005793.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Grose DT, Hick CA, Tate SN;
 XX
 DR WPI; 1999-562112/47.
 XX
 PT Mammalian sodium channel protein for treating pain and hypersensitivity
 XX
 PS Claim 6; Page 67-68; 73pp; English.
 XX
 CC AAZ21481 to AAZ21495 represent fragments of the human sensory neurone
 CC specific 2a (SNS-2a) nucleotide sequence. SNS-2a is a sodium channel
 CC protein. SNS-2a can be used in a method for the identification of a
 CC modulator of a sodium channel, and for assaying for compounds which
 CC modulate sodium flux. The sodium channel modulators can be used in a
 CC medicament for the treatment of pain or hypersensitivity.
 XX
 SQ Sequence 585 BP; 181 A; 117 C; 112 G; 175 T; 0 other;
 Query Match 64.0%; Score 16; DB 20; Length 585;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GGAACAGAAATTAC 23
 |||||
 Db 471 GGAACAGAAATTAC 456
 RESULT 9
 ABA09725
 ID ABA09725 standard; DNA; 2640 BP.
 XX
 AC ABA09725;
 XX
 DT 15-JAN-2002 (first entry)
 XX
 DE Human bone marrow expressed oligonucleotide SEQ ID NO: 234.
 XX
 KW Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnary;
 KW antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
 KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
 KW antitumor; fungicide; antidiabetic; antisthmatic; antiallergic;
 KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
 KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200174836-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10472.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 XX
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PR 23-AUG-2000; 2000US-0649267.
 XX
 PR 30-NOV-2000; 2000US-250583P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
 PI WPI; 2001-626375/72.
 XX
 DR
 XX
 PT New bone marrow-expressed nucleic acids and polypeptides, useful for
 PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
 PT and increasing hematopoiesis, stem cell survival and bone growth and
 PT remodeling
 XX
 PS Claim 1; Page 295-296; 380pp; English.
 XX
 CC The present invention relates to bone marrow expressed polynucleotides
 CC and proteins. These sequences can be used in the treatment of
 CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
 CC and peripheral nervous system diseases and neuropathies, such as
 CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
 CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
 CC cell disorders, platelet disorders, stem cell disorders, bone
 CC degenerative disorders, autoimmune disorders, for example multiple
 CC sclerosis, diabetes and arthritis, viral and bacterial infections,
 CC allergies and blood coagulation disorders. The present sequence is a DNA
 CC of the invention.
 XX
 SQ Sequence 2640 BP; 706 A; 631 C; 674 G; 629 T; 0 other;
 Query Match 64.0%; Score 16; DB 22; Length 2640;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GCCAGAACACAGAAAT 19
 |||||
 Db 2496 GCCAGAACACAGAAAT 2511
 RESULT 10
 AAX06751
 ID AAX06751 standard; DNA; 22080 BP.
 XX
 AC AAX06751;
 XX
 DT 26-APR-1999 (first entry)
 XX
 DE Salmonella enterica serovar B O antigen gene cluster.
 XX
 KW O antigen; diagnosis; wzx gene; wbaV gene; transferase; polymerase;
 KW flippase; diarrhoea; haemorrhagic colitis; ds.
 XX
 OS Salmonella enterica.
 XX
 FH Key Location/Qualifiers

FT CDS 4099..5184
 FT /tag= a
 FT /product= TDP-rhamnose_pathway_protein"
 FT /note= "rmlB gene; encodes AAW88335"
 FT CDS 5184..6083
 FT /tag= b
 FT /product= TDP-rhamnose_pathway_protein"
 FT /note= "rmlD gene; encodes AAW88336"
 FT CDS 6131..7009
 FT /tag= c
 FT /product= TDP-rhamnose_pathway_protein"
 FT /note= "rmlA gene; encodes AAW88337"
 FT CDS 7010..7561
 FT /tag= d
 FT /product= TDP-rhamnose_pathway_protein"
 FT /note= "rmlC gene; encodes AAW88338"
 FT CDS 7567..8559
 FT /tag= e
 FT /product= CDP-adequose_pathway_protein"
 FT /note= "ddhd gene; encodes AAW88339"
 FT CDS 8556..9329
 FT /tag= f
 FT /product= CDP-adequose_pathway_protein"
 FT /note= "ddhA gene; encodes AAW88340"
 FT CDS 9334..10413
 FT /tag= g
 FT /product= CDP-adequose_pathway_protein"
 FT /note= "ddhB gene; encodes AAW88341"
 FT CDS 10440..11753
 FT /tag= h
 FT /product= CDP-adequose_pathway_protein"
 FT /note= "ddhC gene; encodes AAW88342"
 FT CDS 11781..12680
 FT /tag= i
 FT /product= CDP-adequose_pathway_protein"
 FT /note= "abe gene; encodes AAW88343"
 FT CDS 12762..14034
 FT /tag= j
 FT /product= flippase
 FT /note= "wzx gene, this region is specifically
 FT claimed in Claim 9; encodes AAW88344"
 FT CDS 14059..15060
 FT /tag= k
 FT /product= abequosyl_transferase
 FT /note= "wbav gene, this region is specifically
 FT claimed in Claim 9; ; encodes AAW88345"
 FT CDS 15379..16440
 FT /tag= l
 FT /product= mannosyl_transferase
 FT /note= "wbaU gene; encodes AAW88346"
 FT CDS 16441..17385
 FT /tag= m
 FT /product= rhamnosyl_transferase
 FT /note= "wbaN gene; encodes AAW88347"
 FT CDS 17386..18825
 FT /tag= n
 FT /product= GDP_mannose_pathway_protein
 FT /note= "manC gene; encodes AAW88348"
 FT CDS 18812..20245
 FT /tag= o
 FT /product= GDP_mannose_pathway_protein
 FT /note= "mabB gene; encodes AAW88349"
 FT CDS 20317..21747
 FT /tag= h
 FT /product= galactosyl_transferase
 FT /note= "wbaP gene; encodes AAW88350"
 FT CDS 21748..21749
 FT /tag= h
 FT /product= galactosyl_transferase
 FT /note= "wbaP gene; encodes AAW88350"
 PN W09850531-A1.
 XX 12-NOV-1998.
 XX 01-MAY-1998:
 XX 98WO-AU00315.

PR 22-JUL-1997; 97AU-0008162.
 PR 01-MAY-1997; 97AU-0006545.
 XX (UNSY) UNIV SYDNEY.
 PA Reeves PR, Wang L;
 PI WPI; 1999-059669/05.
 DR P-PDB; AAW88335, AAW88336, AAW88337, AAW88338, AAW88339, AAW88340,
 DR AAW88341, AAW88342, AAW88343, AAW88344, AAW88345, AAW88346, AAW88347,
 DR AAW88348, AAW88349, AAW88350.
 XX
 PT Nucleic acid molecules specific for bacterial polysaccharide
 PT antigens - useful for detecting specific strains in, e.g. food,
 PT faeces or patient samples
 XX
 PS Claim 9; Fig 10; 165pp; English.
 XX
 CC This is the nucleotide sequence of a gene cluster involved in
 CC the biosynthesis of the Salmonella enterica serotype B (strain
 CC LT2) O antigen. 16 Open reading frames within the gene cluster
 CC were identified on the basis of homology to known sequences. The
 CC genes encode proteins (see AAW88335-50) involved in the synthesis of
 CC sugars present in the polysaccharide or oligosaccharide units. The use
 CC of processing of polysaccharide antigen, and in the transport
 CC of nucleic acid molecules derived from assembly and transport
 CC genes, particularly wbd (transferase), wzx (flippase) and wzy
 CC (polymerase) genes, within O antigen gene clusters improves the
 CC specificity of methods for the detection and identification of O
 CC antigens, e.g. in testing food- or faecal-derived samples, or
 CC samples from patients. The O antigen is a major virulence factor
 CC of S. enterica.
 XX
 SQ Sequence 22080 BP; 6284 A; 4028 C; 5152 G; 6616 T; 0 other;
 Query Match 64.0%; Score 16; DB 20; Length 22080;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AGGACACAGAAATTTA 22
 |||||
 Db 16641 AGGACACAGAAATTTA 16656
 RESULT 11
 AAW04525/C
 ID AAW04525 standard; DNA; 134525 BP.
 AC AAW04525;
 XX
 DT 01-OCT-1990 (first entry)
 DE Total base sequence of rice plant chloroplast DNA.
 XX Chloroplast; true grass; rice plant; ss.
 KW Oryza sativa.
 OS JP02100682-A.
 XX
 PD 12-APR-1990.
 XX
 PF 07-OCT-1988; 88JP-0251967.
 XX
 PR 07-OCT-1988; 88JP-0251967.
 XX
 PA (MITK) MITSUI TOATSU CHEM INC.
 XX
 DR WPI; 1990-159709/21.
 XX
 PT Chloroplast DNA of true grasses - used to produce various
 PT DNA base sequences by decomposition of rice plant DNA.
 XX

PS Claim 1; Fig 1; 20pp; Japanese.
XX The sequence is that of the whole of rice chloroplast DNA.
XX
SQ Sequence 134525 BP; 41249 A; 26129 C; 26331 G; 40816 T; 0 other;
Query Match 64.0%; Score 16; DB 11; Length 134525;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTCCGAGGACGAGA 16
|||||
Db 47499 TGTCCGAGGACGAGA 47484

RESULT 12
ABA03041
ID ABA03041 standard; DNA; 2944528 BP.
XX
AC ABA03041;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes EGD-e genome sequence.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease; ds.
XX
OS Listeria monocytogenes.
XX
PN W0200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR01118.
XX
PR 11-APR-2000; 2000FR-0004629.
XX
PA (INSP) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Deboux P;
PI Dussurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and
XX related polypeptides.
XX
PS Claim 1; SEQ ID No 1; 192pp; French.
XX
XX The present sequence is the genome sequence of Listeria monocytogenes
XX EGD-e. This sequence and fragments of this sequence are useful for
XX selecting probes and primers for detecting genes in L. monocytogenes and
XX related organisms, and to study genetic polymorphisms and other genomes.
XX Proteins (ABB47297-ABB50149) expressed from the present sequence are
XX useful for raising specific antibodies, identification of L.
XX monocytogenes and related organisms, and for biosynthesis and
XX biodegradation, especially biosynthesis of Vitamin B12. This sequence and
XX proteins encoded by it are also useful for selecting compounds that
XX regulate gene expression and cell replication and modulate L.
XX monocytogenes-related diseases. In addition, this sequence and proteins
XX encoded by it are useful in pharmaceutical and vaccines compositions for
XX the treatment or prevention of infections by L. monocytogenes and related
XX organisms.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;
Query Match 64.0%; Score 16; DB 24; Length 2944528;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 AACCCAGAAATTTACAG 25
|||||
Db 226486 AACCCAGAAATTTACAG 226501

RESULT 13
AA51637
ID AA51637 standard; cDNA; 134 BP.
XX
AC AA51637;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:216.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX
PN W09506549-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-IB01231.
XX
PR 01-AUG-1997; 97US-0905279.
XX
XX (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
XX WPI: 1999-153779/13.
DR
DR P-PSDB; AA12859.
XX
XX New nucleic acids encoding human secreted proteins - obtained from
XX cDNA libraries derived from testis, ovary, uterus and spleen tissue
XX
XX Claim 1; Page 308; 522pp; English.
XX
XX AA51459 to AA51691 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AA12681 to
XX AA12913, respectively. The proteins given represent the signal peptide
XX and an N-terminal fragment of a secreted protein. The nucleic acid
XX sequences can be used for producing secreted human gene products. They
XX can also be used to develop products for diagnosis and therapy. The
XX proteins obtained may have cytokine activity, cell
XX proliferation/differentiation activity, haematopoiesis regulating
XX activity, tissue growth regulating activity, chemotactic/chemokinetic activity, cell
XX regulating activity, chemotactic/chemokinetic activity, reproductive hormone
XX thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, tumour inhibition activity or other activities. The products
XX can be used in forensic, gene therapy and chromosome mapping procedures.
XX The sequences can also be used for obtaining corresponding promoter
XX sequences. The nucleic acids encoding the signal peptide can be used for
XX directing extracellular secretion of a polypeptide or the insertion of a
XX polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ Sequence 134 BP; 30 A; 25 C; 29 G; 48 T; 2 other;
XX
XX Query Match 60.0%; Score 15; DB 20; Length 134;

Best Local Similarity 100.0%; Pred. No. 54;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACACAGAAATTT 21
Db 28 AGGAACACAGAAATTT 42

RESULT 14
AAC26452
ID AAC26452 standard; cDNA; 244 BP.
XX
AC AAC26452;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein 5' EST, SEQ ID NO: 30527.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI: 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 30527; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 244 BP; 67 A; 53 C; 50 G; 73 T; 1 other;

Query Match 60.0%; Score 15; DB 21; Length 244;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACACCAG 15
Db 98 TGTGCCAGGACACCAG 112

RESULT 15
AAI92971/c
ID AAI92971 standard; cDNA; 478 BP.
XX

AC AAI92971;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 13031.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX WPI: 2001-514838/56.
DR P-PSDB; AA013040.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 1; SEQ ID NO 13031; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 478 BP; 130 A; 64 C; 166 G; 115 T; 3 other;

Query Match 60.0%; Score 15; DB 22; Length 478;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACACCAG 15
Db 398 TGTGCCAGGACACCAG 384

RESULT 16
AAZ56768
ID AAZ56768 standard; cDNA; 535 BP.
XX
AC AAZ56768;
XX
DT 23-MAR-2000 (first entry)
XX
DE Human transmembrane protein HTMPN-71 encoding cDNA.
XX
KW Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
KW antiproliferative; neuroprotective; immune disorder;

KW reproductive disorder; smooth muscle disorder; neurological disorder;
 KW gastrointestinal disorder; developmental disorder;
 KW cell proliferative disorder; ss.

OS Homo sapiens.
 XX WO9961471-A2.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US11904.
 XX PR 29-MAY-1998; 98US-0087260.
 XX PR 02-JUL-1998; 98US-0091674.
 XX PR 02-OCT-1998; 98US-0102954.
 XX PR 24-NOV-1998; 98US-0109869.
 XX PA (INCY-) INCYTE PHARM INC.
 XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
 XX PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;
 XX PI Au-Young J;
 XX DR WPI; 2000-072605/06.
 XX DR P-PSDB; AAY57947.

XX PT Proteins, polynucleotides, vectors, host cells and antibodies used to
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,
 PT neurological, gastrointestinal, developmental and cell proliferative
 PT disorders -
 PS Claim 9; Page 223; 229pp; English.
 XX CC AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
 CC transmembrane proteins designated HMPN-1 to HMPN-79, respectively.
 CC The transmembrane protein have immunospecific, antiproliferative and
 CC neuroprotective activities. The human transmembrane proteins,
 CC polynucleotides encoding them and other compositions and methods from
 CC the present invention, can be used for the diagnosis, treatment or
 CC prevention of immune, reproductive, smooth muscle, neurological,
 CC gastrointestinal, developmental and cell proliferative disorders. The
 CC HMPN's can be used to treat or prevent disorders associated with a
 CC decreased expression or activity of HMPN.

XX SQ Sequence 535 BP; 181 A; 93 C; 104 G; 157 T; 0 other;
 Query Match 60.0%; Score 15; DB 21; Length 535;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AGGACCCAGAAATTT 21
 DB 2 AGGACCCAGAAATTT 16
 RESULT 17
 ABK62291
 ID ABK62291 standard; cDNA; 569 BP.
 XX AC ABK62291;
 XX XX
 XX DT 18-JUN-2002 (first entry)
 XX DE Rat sequence differentially expressed in response to a hepatotoxin #198.
 XX KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 XX OS Rattus norvegicus.
 XX XX
 XX PN WO200210453-A2.
 XX XX
 XX PD 07-FEB-2002.

XX PF 30-JUL-2001; 2001WO-US23872.
 XX PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-250029P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX PA (GENE-) GENE LOGIC INC.
 XX PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 XX PI WPI; 2002-241625/29.

XX PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 PS Claim 1; Seq ID No 198; 239pp; English.

XX CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilize a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridizes to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information,
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterized by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.

XX SQ Sequence 569 BP; 146 A; 141 C; 132 G; 150 T; 0 other;

Query Match 60.0%; Score 15; DB 24; Length 569;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCCAGAAA 18
 |||||
 DB 240 GCCAGGACCCAGAAA 254

RESULT 18
 ABL26995
 ID ABL26995 standard; DNA; 591 BP.
 XX XX
 XX AC ABL26995;

XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32458.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX CC New isolated nucleic acid detection reagent for detecting 1000 or more
 CC genes from Drosophila and for elucidating cell signalling and cell-cell
 CC interactions.
 CC PS Claim 1; SEQ ID NO 32458; 21pp + Sequence Listing; English.
 CC CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).
 CC CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 591 BP; 167 A; 134 C; 175 G; 115 T; 0 other;
 Query Match 60.0%; Score 15; DB 23; Length 591;
 Best Local Similarity 100.0%; Pred. NO. 56;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GCCAGGACCCAGAAA 18
 Db 501 GCCAGGACCCAGAAA 515
 ||||||||||||
 RESULT 19
 AAS56010
 ID AAS56010 standard; DNA; 1302 BP.
 XX AC AAS56010;
 XX AC AAS56010;
 XX DT 13-FEB-2002 (first entry)
 XX DE Salmonella typhi DNA for cellular proliferation protein #43.
 XX KW Antisense; ds; prokaryotic cellular proliferation gene;
 XX KW antibiotic; antibacterial; drug design.
 XX OS Salmonella typhi.
 XX PN WO200170955-A2.
 XX PD 27-SEP-2001.
 XX XX

PF 21-MAR-2001; 2001WO-US09180.
 XX XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX XX
 PA (ELIT-) ELITRA PHARM INC.
 XX XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX XX
 DR WPI; 2001-611495/70.
 DR P-PSDB; AAU38151.
 XX XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX XX
 PS Claim 27; Seq ID No 9647; 511pp; English.
 XX CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 1302 BP; 322 A; 291 C; 352 G; 337 T; 0 other;
 Query Match 60.0%; Score 15; DB 23; Length 1302;
 Best Local Similarity 100.0%; Pred. NO. 57;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GGAACCCAGAAATTTA 22
 Db 735 GGAACCCAGAAATTTA 749
 ||||||||||||
 RESULT 20
 AAS90113
 ID AAS90113 standard; cDNA; 2433 BP.
 XX AC AAS90113;
 XX AC AAS90113;
 XX DT 13-FEB-2002 (first entry)
 XX DE DNA encoding novel human diagnostic protein #25917.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX XX

```
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG25926.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 25917; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2433 BP; 654 A; 605 C; 620 G; 554 T; 0 other;
Query Match 60.0%; Score 15; DB 23; Length 2433;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGAACACGAAATTTA 22
Db 1066 GGAACACGAAATTTA 1080
RESULT 21
AAS91291
ID AAS91291 standard; cDNA; 2433 BP.
XX
AC AAS91291;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #27095.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
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```
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ABG27104.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID NO 27095; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2433 BP; 654 A; 605 C; 620 G; 554 T; 0 other;
Query Match 60.0%; Score 15; DB 23; Length 2433;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGAACACGAAATTTA 22
Db 1066 GGAACACGAAATTTA 1080
RESULT 22
ABL26994
ID ABL26994 standard; DNA; 2649 BP.
XX
AC ABL26994;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32455.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
```

XX (PEXE) PE CORP NY.
XX
PI Venter JC, Adams M, Li FWD, Myers EW;
XX WPI; 2001-656860/75.
XX
DR New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 32455; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins
CC (AB157737-AB172072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2649 BP; 657 A; 596 C; 627 G; 769 T; 0 other;

Query Match 60.0%; Score 15; DB 23; Length 2649;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCAGAAA 18
|||||
Db 1559 GCCAGGACCAGAAA 1573

RESULT 23
AAL36492
ID AAL36492 standard; DNA; 11821 BP.
XX
AC AAL36492;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2857.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.
OS
XX Homo sapiens.
XX
FN W0200155367-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01338.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0228868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 05-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 25-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 26-SEP-2000; 2000US-0234998.
PR 27-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249219.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI: 2001-451937/48.
XX
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
XX
PS Example 2; SEQ ID NO 2857; 781pp + Sequence Listing; English.
XX

CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,

CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pot_sequences.
XX

SO Sequence 11821 BP; 3068 A; 2740 C; 2786 G; 3227 T; 0 other;

Query Match 60.0%; Score 15; DB 22; Length 11821;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAAACACG 15
|||||
DB 3694 TGTGCCAGGAAACACG 3708

RESULT 24

AAK74325
ID AAK74325 standard; DNA; 13395 BP.

XX AAK74325;

DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29137.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.

OS Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US01354.

XX 31-JAN-2000; 2000US-0179065.

XX 04-FEB-2000; 2000US-0180628.

XX 24-FEB-2000; 2000US-0184664.

XX 02-MAR-2000; 2000US-0186350.

XX 16-MAR-2000; 2000US-0189874.

XX 17-MAR-2000; 2000US-0190076.

XX 18-APR-2000; 2000US-0198123.

XX 19-MAY-2000; 2000US-0205515.

XX 07-JUN-2000; 2000US-0209467.

XX 28-JUN-2000; 2000US-0215135.

XX 30-JUN-2000; 2000US-0214886.

XX 07-JUL-2000; 2000US-0216647.

XX 07-JUL-2000; 2000US-0216980.

XX 11-JUL-2000; 2000US-0217487.

XX 11-JUL-2000; 2000US-0217496.

XX 14-JUL-2000; 2000US-0218290.

XX 26-JUL-2000; 2000US-0220963.

XX 26-JUL-2000; 2000US-0220964.

XX 14-AUG-2000; 2000US-0224518.

XX 14-AUG-2000; 2000US-0224519.

XX 14-AUG-2000; 2000US-0225213.

XX 14-AUG-2000; 2000US-0225214.

XX 14-AUG-2000; 2000US-0225266.

XX 14-AUG-2000; 2000US-0225267.

XX 14-AUG-2000; 2000US-0225268.

XX 14-AUG-2000; 2000US-0225270.

XX 14-AUG-2000; 2000US-0225447.

XX 14-AUG-2000; 2000US-0225757.

XX 14-AUG-2000; 2000US-0225758.

Db 3698 TGTGCCAGGACCAG 3712

RESULT 25
AAL36490

ID AAL36490 standard; DNA; 15535 BP.
XX
AC AAL36490;
XX
DT 08-JAN-2002 (first entry)
XX
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2855.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein;
KW musculoskeletal system; ds.
XX
OS Homo sapiens.
XX
PN WO200155367-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01338.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214986.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-451937/48.
DR
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
XX Example 2; SEQ ID NO 2855; 781pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (AB03087-AB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
CC healing; (e) neurological diseases such as cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 15535 BP; 3779 A; 3966 C; 3788 G; 4002 T; 0 other;
Query Match 60.0%; Score 15; DB 22; Length 15535;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCGAGGACGAC 15
Db 3783 TGTGCGAGGACGAC 3797
|||||
RESULT 26
ABAL6222
ID ABAL6222 standard; DNA; 26241 BP.
XX
AC ABAL6222;
XX
XX 23-JAN-2002 (first entry)
DT
XX
XX Human nervous system related polynucleotide SEQ ID NO 8553.
DE
XX

KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW antiparkinsonian; antiskilling; antianaemic; antiarthritic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX Homo sapiens.
OS
XX WO200159063-A2.
PN
XX
XX 16-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01334.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.

PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 02-OCT-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 20-OCT-2000; 2000US-0242221.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251160.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.

PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251889.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2000US-0254097.
XX 05-JAN-2001; 2001US-0259678.
PA (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-541565/60.
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
XX Disclosure; SEQ ID NO 8553; 1701pp + Sequence Listing; English.
XX The invention relates to novel genes (AB11004-ABA21534) and proteins
CC (AB114678-AB118001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 26241 BP; 7468 A; 5260 C; 5964 G; 7549 T; 0 other;

Query Match 60.0%; Score 15; DB 22; Length 26241;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACAC 15
Db 10724 TGTGCCAGGAACAC 10738
|||||

RESULT 27
AAV49655
ID AAV49655 standard; DNA: 28720 BP.
XX AAV49655;
AC AAV49655;
XX 23-OCT-1998 (first entry)
XX Human SC3 DNA.
DE
XX
KW Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
KW nervous system; medullo-blastoma; glioma; breast; detection; SC3;
KW autoantibody; ss.
XX
OS Homo sapiens.
XX
XX WO9830687-A2.
PN
XX
PD 16-JUL-1998.
XX
XX 09-JAN-1998; 98WO-DE00096.
PF
XX 18-JUL-1997; 97DE-1030997.
PR 09-JAN-1997; 97DE-1000519.

XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PI Mollenhauer J, Poustka A;
 XX XX WPI; 1998-399136/34.
 XX DR Proteins containing scavenger receptor, cysteine rich domain -
 XX PT useful for diagnosis and treatment of tumours
 XX PS Disclosure; Fig 5c; 54pp; German.
 XX CC This nucleotide sequence contains a fragment of a gene which is capable
 CC of encoding a protein which contains a SRCR (scavenger receptor,
 CC cysteine-rich) domain. The gene and encoded protein can be used to
 CC diagnose or treat tumours, particularly of the nervous system
 CC (medullo-blastoma or glioma) or breast. The DNA sequence and probes
 CC derived from it, are used to identify genes that express SRCR-domain
 CC containing proteins, to determine the form in which these proteins exist
 CC and to assess the significance of individual forms on cellular
 CC properties. The protein can be used to detect the presence of
 CC autoantibodies and antibodies which regulate its expression.
 XX SQ Sequence 28720 BP; 6956 A; 6728 C; 6982 G; 8054 T; 0 other;
 Query Match 60.0%; Score 15; DB 19; Length 28720;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 CAGGACCGAGAAATT 20
 Db 5047 CAGGACCGAGAAATT 5061
 RESULT 28
 ID AAA81502
 AC AAA81502 standard; DNA; 65632 BP.
 XX
 DT 04-DEC-2000 (first entry)
 DE N. meningitidis partial DNA sequence gnm_49 SEQ ID NO:49.
 XX
 DE Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW Meningococcus B; MenB; ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN W0200022430-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US23573.
 XX
 PR 09-OCT-1998; 98US-0103794.
 PR 30-APR-1999; 99US-0132068.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Massignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX
 DR WPI; 2000-318079/27.
 XX
 XX Isolated nucleotide sequences of Neisseria meningitidis which can be
 PT used in the diagnosis and treatment of N. meningitidis infection and
 PT other Neisserial infections, for example, N.gonorrhoea
 XX
 PS Claim 7; Page 1331-1350; 1760pp; English.
 XX

CC The present invention describes methods of obtaining immunogenic
 CC proteins from Neisseria genomic sequences. AAA81453 to AAA82414
 CC represent specifically claimed Neisseria meningitidis genomic DNA
 CC sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent
 CC Neisseria DNA sequences and their corresponding proteins; AAA81254 to
 CC AAA81259 and AAA81304 to AAA81321 represent PCR primers used in the
 CC isolation of Neisseria meningitidis DNA sequences; and AAA81322 to
 CC AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF
 CC sequences, which are all used in the exemplification of the present
 CC invention. The nucleic acid sequences, protein sequences, and antibodies
 CC against them, can be used in the manufacture of a composition. The
 CC composition can be used as a medicament (or in the manufacture of a
 CC medicament) for treating, preventing or diagnosing infection due to
 CC Neisserial bacteria. For example, some of the identified proteins could
 CC be components of vaccines against Meningococcus B; against all serotypes;
 CC and/or against all pathogenic Neisseriae. Identification of sequences
 CC from the bacterium will also facilitate production of biological probes,
 CC particularly organism-specific probes. Attempts to make efficacious
 CC Meningococcus B vaccines have failed mainly due to antigen tolerance.
 CC Multivalent vaccines have also been tried but none have successfully
 CC overcome antigenic variability. The provision of further, complete
 CC sequences may provide an opportunity to identify secreted or surface
 CC exposed proteins that may be presumed targets for the immune system and
 CC which are not antigenically variable or at least more conserved than
 CC other more variable regions.
 XX SQ Sequence 65632 BP; 16704 A; 16327 C; 15474 G; 17126 T; 1 other;
 Query Match 60.0%; Score 15; DB 21; Length 65632;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GAACGACGAAATTTAC 23
 Db 37275 GAACGACGAAATTTAC 37289
 RESULT 29
 ID AAA81544/c
 AC AAA81544 standard; DNA; 349980 BP.
 XX
 AC AAA81544;
 XX
 DT 13-MAR-2001 (first entry)
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:1.
 XX
 DE Neisseria meningitidis; Neisseria gonorrhoeae; immunogenic; vaccine;
 KW diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 KW ds.
 XX
 OS Neisseria meningitidis.
 XX
 PN W0200066791-A1.
 XX
 PD 09-NOV-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05928.
 XX
 PR 30-APR-1999; 99US-0132068.
 PR 08-OCT-1999; 99WO-US23573.
 PR 28-FEB-2000; 2000GB-0004695.
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC, Massignani V;
 PI Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V, Rappuoli R;
 PI Frazer CM, Grandi G;
 XX
 DR WPI; 2000-647603/62.
 XX
 PT Neisseria meningitidis B full length genome sequence and open reading

PT frames are used to detect, treat and prevent Neisserial infections -
 PS Claim 7; Appendix A; 692pp; English.
 XX
 CC The present invention describes the full length genome of
 CC Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607
 CC to AAF21613 represent fragments of the NMB genomic sequence, as the
 CC sequence was too long to go in a record on its own it was split into 8
 CC sequences which overlap each other at the beginning and end of each
 CC sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at
 CC the beginning of AAF21607, the last 49980 bp of AAF21607 is repeated at
 CC the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
 CC Neisseria proteins given in AAF21589 to AAF21593, and AAF21598 to
 CC AAF21606 represent PCR primers which are used in the amplification of
 CC the present invention. The NMB genome and fragments from it have
 CC antibacterial activity, and can be used in vaccines and gene therapy.
 CC Neisseria nucleic acids, proteins and/or antibodies which binds to the
 CC proteins can be used in compositions for treating or preventing infection
 CC due to Neisserial bacteria or as a diagnostic reagent for detecting the
 CC presence of Neisserial bacteria or of antibodies raised to Neisserial
 CC bacteria. Computers, computer memory, computer storage medium or computer
 CC databases can be used in a search to identify open reading frames (ORFs)
 CC or coding sequences within the NMB genome. The DNA sequences provide
 CC further opportunities to find antigenic or immunogenic proteins which are
 CC more effective in vaccines than the outer membrane proteins currently
 CC used.
 XX
 SQ Sequence 349980 BP; 83241 A; 85091 C; 95206 G; 86442 T; 0 other;
 Query Match 60.0%; Score 15; DB 21; Length 349980;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 GAACGAGAAATTAC 23
 Db 96883 GAACGAGAAATTAC 96869
 |||||
 RESULT 30
 AAC1935
 ID AAC1935 standard; cDNA; 123 BP.
 AC AAC1935;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein 5' EST, SEQ ID NO: 36010.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-500381/45.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 1; SEQ ID 36010; 71pp + CD-ROM; English.
 XX

CC The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA
 CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX
 SQ Sequence 123 BP; 44 A; 24 C; 17 G; 38 T; 0 other;
 Query Match 56.0%; Score 14; DB 21; Length 123;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 ACCAGAAATTAC 24
 Db 32 ACCAGAAATTAC 45
 |||||
 RESULT 31
 AAZ43073/c
 ID AAZ43073 standard; cDNA; 246 BP.
 XX
 AC AAZ43073;
 XX
 DT 01-FEB-2000 (first entry)
 XX
 DE Human 5' EST isolated from a cDNA library SEQ ID NO:1620.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9953051-A2.
 XX
 PD 21-OCT-1999.
 XX
 PF 09-APR-1999; 99WO-IB00712.
 XX
 PR 09-APR-1998; 98US-0057719.
 XX
 PR 28-APR-1998; 98US-0069047.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX WPI; 2000-038446/03.
 XX
 DR Novel secreted protein 5' expressed sequence tag sequences used in
 XX diagnostic, forensic, gene therapy, and chromosome mapping procedures
 XX
 PS Claim 1; Page 836; 837pp; English.
 XX
 CC AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
 CC sequences, corresponding to human secreted proteins. AAY64651 to
 CC AAY6438 represent the EST-related proteins corresponding to AAZ42265 to
 CC AAZ43052. The 5' ESTs can be used for producing secreted human gene
 CC products. They can be used to identify and isolate 5' untranslated
 CC regions (UTRs) and upstream regulatory regions which control the
 CC location, development stage, rate, and quantity of protein synthesis, as
 CC well as stability of mRNA. The ESTs are also useful as probes for
 CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can
 CC also be used in forensic procedures to identify individuals, or in

CC diagnostic procedures to identify individuals having genetic diseases
 CC resulting from abnormal gene expression. The products may also be used in
 CC gene therapy protocols. The nucleic acids encoding signal peptides can be
 CC used for directing extracellular secretion of a polypeptide or the
 CC insertion of a polypeptide into a membrane, or importing a polypeptide
 CC into a cell. The proteins encoded by the EST sequences may be useful in
 CC treating a variety of human conditions. Secreted proteins have
 CC therapeutic value, and the identification of new secreted proteins is
 CC valuable. AA242249 to AA242264 and AA242264 to AA242265 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 246 BP; 64 A; 40 C; 38 G; 102 T; 2 other;

Query Match 56.0%; Score 14; DB 21; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
 |||||
 DB 175 TGTGCCAGGAACCA 162

RESULT 32

ABN24228/c

ID ABN24228 standard; cDNA; 318 BP.

AC ABN24228;

DT 24-JUN-2002 (first entry)

XX Human ORFX polynucleotide sequence SEQ ID NO:16933.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.

XX Homo sapiens.
 XX WO200192523-A2.
 XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.
 XX 30-MAY-2000; 2000US-206132P.
 XX 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.
 XX Shinketsu RA, Leach MD;

XX WPI; 2002-106308/14.
 XX P-PSDB; ABP08476.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders
 XX Disclosure; SEQ ID 16933; 1037pp; English.

XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the

CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative diseases, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 318 BP; 41 A; 103 C; 112 G; 62 T; 0 other;

Query Match 56.0%; Score 14; DB 24; Length 318;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGAACCA 17
 |||||
 DB 195 GCCAGGAACCA 182

XX RESULT 33
 XX ABV01847/c

XX ID ABV01847 standard; cDNA; 350 BP.

XX AC ABV01847;

XX DT 13-SEP-2002 (first entry)

XX DE Human prostate expression marker cDNA 1838.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 XX WO200160860-A2.
 XX 23-AUG-2001.

XX 20-FEB-2001; 2001WO-US05171.

XX 17-FEB-2000; 2000US-183319P.

XX 16-MAR-2000; 2000US-189862P.

XX 25-MAY-2000; 2000US-207454P.

XX 09-JUN-2000; 2000US-211314P.

XX 18-JUL-2000; 2000US-219007P.

XX 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX Claim 1; Page 378; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;

CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 350 BP; 76 A; 71 C; 81 G; 122 T; 0 other;
 Query Match 56.0%; Score 14; DB 23; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTAC 24
 DB 311 ACCAGAAATTAC 298
 |||||

RESULT 34
 ABV11016/c
 ID ABV11016 standard; cDNA; 351 BP.
 XX
 AC ABV11016;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 11007.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PS Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 Claim 1; Page 1783; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 351 BP; 76 A; 71 C; 81 G; 123 T; 0 other;
 Query Match 56.0%; Score 14; DB 23; Length 351;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTAC 24
 DB 311 ACCAGAAATTAC 298
 |||||

RESULT 35
 ABV02282/c
 ID ABV02282 standard; cDNA; 353 BP.
 XX
 AC ABV02282;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 2273.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PS Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 Claim 1; Page 441; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.


```
SQ Sequence 353 BP; 89 A; 83 C; 73 G; 108 T; 0 other;
Query Match 56.0%; Score 14; DB 23; Length 353;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCA 14
    |||||
Db 210 TGTGCCAGGACCA 197

RESULT 37
ABV27268/c
ID ABV27268 standard; cDNA; 365 BP.
XX
AC ABV27268;
XX
XX 16-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 27259.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 5536; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 365 BP; 92 A; 78 C; 69 G; 123 T; 3 other;
Query Match 56.0%; Score 14; DB 23; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCA 14
    |||||
Db 210 TGTGCCAGGACCA 197

RESULT 38
ABV21450/c
ID ABV21450 standard; cDNA; 365 BP.
XX
AC ABV21450;
XX
XX 13-SEP-2002 (first entry)
XX
XX Human prostate expression marker cDNA 21441.
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200160860-A2.
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
XX PR 16-MAR-2000; 2000US-189862P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3576; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 365 BP; 92 A; 78 C; 69 G; 123 T; 3 other;
Query Match 56.0%; Score 14; DB 23; Length 365;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

AAH30937/c
 ID AAH30937 standard; cDNA; 388 BP.
 AC AAH30937;
 XX
 DT 27-JUL-2001 (first entry)
 XX
 DE Human colon cancer cell line Kml2L4-A cDNA library derived sequence #871.
 XX
 KW Human; diagnosis; colon cancer; cancer; malignant; chromosome mapping;
 KW detection; colon cancer cell line Kml2L4-A; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200018916-A2.
 XX
 PD 06-APR-2000.
 XX
 PF 23-SEP-1999; 99WO-US22226.
 XX
 PR 28-SEP-1998; 98US-0102161.
 PR 28-SEP-1998; 98US-0102180.
 PR 29-SEP-1998; 98US-0102380.
 PR 08-OCT-1998; 98US-0103815.
 PR 27-OCT-1998; 98US-0105877.
 XX
 PA (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX
 PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
 PI Reinhard C, Glese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
 PI Lamson G, Drmanac R, Crikvenjakov R, Dickson M, Drmanac S, Labat I;
 PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Grain B;
 DR WPI; 2000-293155/25.
 XX
 PT Polynucleotide library comprising 1079 defined sequences, useful in
 PT the form of an array to detect cancer or susceptibility to cancer -
 XX
 PS Claim 1; Page 433; 502pp; English.
 XX
 CC The present invention describes a library of polynucleotides comprising
 CC 1079 nucleotide sequences (given in AAH30067 to AAH31145). Also described
 CC are: (1) an isolated polynucleotide (I) having at least 90% identity to
 CC one of the 1079 sequences; (2) a recombinant host cell containing (1);
 CC (3) an isolated polypeptide (II) encoded by (1); (4) an antibody that
 CC specifically binds to (II); (5) a vector comprising (1); and (6) a method
 CC of detecting differentially expressed genes correlated with a cancerous
 CC state of a mammalian cell comprising detecting a gene product encoded by
 CC 65 of the 1079 sequences given in the specification. The polynucleotides
 CC are used to monitor patients having (or susceptible) to cancer to detect
 CC potentially malignant events at a molecular level before they are
 CC detectable at a gross morphological level. The polynucleotides are also
 CC useful for monitoring the efficacy of various therapies and preventive
 CC interventions. Polynucleotide probes based on the disclosed sequences
 CC are useful for chromosome mapping and detection of transcription levels.
 CC The 1079 polynucleotide sequences were derived from a human colon cancer
 CC cell line Kml2L4-A cDNA library.
 XX
 SQ Sequence 388 BP; 87 A; 97 C; 51 G; 153 T; 0 other;
 Query Match 56.0%; Score 14; DB 21; Length 388;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 GGAACCAAGAAATTT 21
 DB 370 GGAACCAAGAAATTT 357
 RESULT 39
 ABV32164/c
 ID ABV32164 standard; cDNA; 396 BP.

XX
 AC ABV32164;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 32155.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 6877; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 396 BP; 85 A; 85 C; 97 G; 129 T; 0 other;
 Query Match 56.0%; Score 14; DB 23; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 ACCAGAAATTTACA 24
 DB 357 ACCAGAAATTTACA 344
 RESULT 40
 ABV41096/c
 ID ABV41096 standard; cDNA; 396 BP.
 XX
 AC ABV41096;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 41087.

XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS
 PN WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 8268; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 396 BP; 85 A; 85 C; 97 G; 129 T; 0 other;
 SQ
 Query Match 56.0%; Score 14; DB 23; Length 396;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 ACCAGAAATTTCAC 24
 Db 357 ACCAGAAATTTCAC 344
 RESULT 41
 ABV32596/C
 ID ABV32596 standard; cDNA; 408 BP.
 XX
 AC ABV32596;
 XX 16-SEP-2002 (first entry)
 DT Human prostate expression marker cDNA 32587.
 DE
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS

PN WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 PA Schlegel R, Endege WO, Monahan JE;
 XX WPI; 2001-662795/76.
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX Claim 1; Page 6948; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX Sequence 408 BP; 98 A; 92 C; 89 G; 129 T; 0 other;
 SQ
 Query Match 56.0%; Score 14; DB 23; Length 408;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGAACCA 14
 Db 253 TGTGCCAGGAACCA 240
 RESULT 42
 ABV41521/C
 ID ABV41521 standard; cDNA; 408 BP.
 XX
 AC ABV41521;
 XX 16-SEP-2002 (first entry)
 DT Human prostate expression marker cDNA 41512.
 DE
 XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 OS
 PN WO200160860-A2.
 XX 23-AUG-2001.
 XX 20-FEB-2001; 2001WO-US05171.
 XX

PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WO, Monahan JE;
 PI
 XX WPI; 2001-662795/76.
 DR
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 8341; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 408 BP; 98 A; 92 C; 89 G; 129 T; 0 other;
 Query Match 56.0%; Score 14; DB 23; Length 408;
 Best Local Similarity 100.0%; Pred. NO. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGAACCA 14
 Db 253 TGTGCCAGGAACCA 240
 RESULT 43
 ABV11451/c
 ID ABV11451 standard; cDNA; 435 BP.
 XX
 AC ABV11451;
 XX
 DT 13-SEP-2002 (first entry)
 DE
 DE Human prostate expression marker cDNA 11442.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 KW Homo sapiens.
 OS
 XX WO200160860-A2.
 PN
 XX 23-AUG-2001.
 PD
 XX
 XX 20-FEB-2001; 2001WO-US05171.
 PF
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 PR

XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Schlegel R, Endege WO, Monahan JE;
 PI
 XX WPI; 2001-662795/76.
 DR
 XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 1865; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 435 BP; 107 A; 100 C; 88 G; 140 T; 0 other;
 Query Match 56.0%; Score 14; DB 23; Length 435;
 Best Local Similarity 100.0%; Pred. NO. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGAACCA 14
 Db 218 TGTGCCAGGAACCA 205
 RESULT 44
 ABN75835/c
 ID ABN75835 standard; cDNA; 439 BP.
 XX
 AC ABN75835;
 XX
 DT 08-JUL-2002 (first entry)
 DE
 DE Human ORF782 cDNA, SEQ ID NO:1563.
 XX
 KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
 OS
 XX Homo sapiens.
 XX
 PN WO200190366-A2.
 XX
 XX 29-NOV-2001.
 PD
 XX
 XX 24-MAY-2001; 2001WO-US17076.
 PF
 XX
 XX 24-MAY-2000; 2000US-206690P.
 PR

(CURA-) CURAGEN CORP.
 Leach MD, Shinkets RA;
 WPL: 2002-106200/14.
 P-PSDB; ABP31809.
 Novel human polypeptides and polynucleotides useful for diagnosing,
 preventing and treating cardiovascular disease, neurodegenerative,
 hyperproliferative disorders and disorders related to organ
 transplantation
 Claim 1; Page 656; 2508pp; English.
 Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 ABN79587 represent cDNAs encoding them. The invention also encompasses
 polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 referred to as ORFX) proteins, polynucleotides at least 85% identical to
 the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 polynucleotides, the recombinant production of ORFX proteins, antibodies
 specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 polypeptides, methods of screening for modulators of ORFX expression or
 activity, and methods of screening individuals for a predisposition to an
 ORFX-associated disorder. The ORFX proteins of the invention have a wide
 range of biological activities, such as cytokine, cell proliferation,
 cell differentiation, immune modulation, haematopoiesis regulation,
 tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 chemokinetic activity, haemostatic activity, thrombolytic activity,
 receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 and antineoplastic activity, and may also be involved in the determination
 of bodily characteristics, fertility and behaviour. ORFX proteins,
 nucleic acids and antibodies may be used in the treatment of cancers,
 other proliferative disorders such as psoriasis and benign tumours,
 neurological disorders such as epilepsy and Alzheimer's disease,
 cardiovascular diseases, immune system disorders, disorders related to
 organ transplantation, disorders of tissue growth and regeneration,
 diseases such as diabetes mellitus, hypothyroidism, and cholesterol
 storage disease, and infectious diseases caused by viral, bacterial,
 fungal and other pathogens. ORFX nucleic acids may also be used as a
 source of primers and probes, in the detection of ORFX genomic sequences
 or transcripts, in the identification and cloning of homologous
 sequences, in genetic diagnosis, and in forensic biology. The ORFX
 nucleic acids may additionally be used to produce transgenic animals
 which may be useful for studying the function and/or activity of ORFX
 protein, and in drug screening. The ORFX proteins may also be used as
 immunogens to generate specific antibodies, which are useful in the
 diagnosis, treatment and monitoring of ORFX-associated diseases.

Query Match 56.0%; Score 14; DB 24; Length 439;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 TGCAGGAACACAGA 16
 |||||
 Db 250 TGCAGGAACACAGA 237
 RESULT 45
 AAK60019/c
 ID AAK60019 standard; cDNA; 454 BP.
 XX
 AC AAK60019;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:5079.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis; ss.

XX Homo sapiens.
 OS WO200157182-A2.
 PN 09-AUG-2001.
 PD 17-JAN-2001; 2001WO-US01354.
 XX
 PF 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 PR 02-MAR-2000; 2000US-0186350.
 PR 16-MAR-2000; 2000US-0189874.
 PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0216880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 14-JUL-2000; 2000US-0217496.
 PR 26-JUL-2000; 2000US-0220693.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 18-AUG-2000; 2000US-0225759.
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 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0227009.
 PR 01-SEP-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 21-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.

PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 01-NOV-2000; 2000US-0241826.
 PR 08-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 17-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
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 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-483426/52.
 XX P-PSDB; AAM87238.
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 XX useful for preventing, diagnosing and/or treating cancers and
 XX metastasis -
 PS Claim 1; SEQ ID NO 5079; 3071pp + Sequence Listing; English.
 XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 454 BP; 142 A; 70 C; 121 G; 118 T; 3 other;
 Query Match 56.0%; Score 14; DB 22; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GTGCCAGGAACCCAG 15
 Db 303 GTGCCAGGAACCCAG 290
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 Search completed: November 24, 2002, 13:27:16
 Job time : 855.5 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 12:31:33 ; Search time 1611.5 Seconds
(without alignments)
451.486 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTCCAGGACCAAGAAATTACAG 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:

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2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
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31: em.htg_inv.*
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34: em.htg_pin.*
35: em.htg_rod.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	ARI54075
c 2	25	100.0	1000	6	ARI53982
c 3	25	100.0	62102	2	AC104363
c 4	25	100.0	69964	9	HS496C20
c 5	25	100.0	138459	2	AC090795
c 6	19	76.0	124427	9	AC048344
c 7	19	76.0	157395	9	CNS07EF8
c 8	19	76.0	159767	2	AC023529
c 9	19	76.0	227611	2	AC023766
c 10	19	76.0	322058	2	AC068887
c 11	18	72.0	133337	2	AC016231
c 12	18	72.0	146310	9	AC090459
c 13	18	72.0	169013	2	AC111142
c 14	18	72.0	181380	10	AC115123
c 15	18	72.0	182416	2	AC023044
c 16	18	72.0	185787	2	AC090215
c 17	18	72.0	191197	2	AP001779
c 18	17	68.0	14333	8	CPA277161
c 19	17	68.0	40740	9	AC027349
c 20	17	68.0	55252	2	AC119489_3
c 21	17	68.0	104934	2	AC128098
c 22	17	68.0	107361	2	AC118386
c 23	17	68.0	110000	2	CEY111B2_2
c 24	17	68.0	129151	9	AL365204
c 25	17	68.0	145481	9	AL356862
c 26	17	68.0	160538	2	AC018586
c 27	17	68.0	174736	9	AL355478
c 28	17	68.0	176861	9	AC097065
c 29	17	68.0	185473	9	AL136090
c 30	17	68.0	217873	9	HUAC004382
c 31	17	68.0	220388	2	AC122476
c 32	17	68.0	231923	2	AC122295
c 33	17	68.0	257703	3	CEY111B2A
c 34	16	64.0	286	8	OMI007725
c 35	16	64.0	320	8	CHZM05
c 36	16	64.0	585	6	AX017232
c 37	16	64.0	1147	8	SOTRNAPLE
c 38	16	64.0	1268	8	TOBCPLB3
c 39	16	64.0	1358	8	PVTRPHE
c 40	16	64.0	1608	8	MITATRSF
c 41	16	64.0	1700	4	AF232699
c 42	16	64.0	4894	8	RICMT16
c 43	16	64.0	12558	8	AF072704
c 44	16	64.0	15783	8	AF434192
c 45	16	64.0	21941	9	HSDJ69001

ALIGNMENTS

RESULT 1	ARI54075	Sequence 125 from patent US 6238863.	25 bp	DNA	linear	PAT 08-AUG-2001
ARI54075	LOCUS					
DEFINITION	Sequence 125 from patent US 6238863.					
ACCESSION	ARI54075					
VERSION	ARI54075.1	GI:15122128				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Schumm,J.W. and Bacher,J.W.					
TITLE	Materials and methods for indentifying and analyzing intermediate tandem repeat DNA markers					
JOURNAL	Patent: US 6238863-A 125 29-MAY-2001;					

FEATURES

Source Location/Qualifiers
1. .25
/organism="unknown"
BASE COUNT 9 a 5 c 6 g 5 t
ORIGIN

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGGACCAAGAAATTTACAG 25
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Db 1 TGTGCCAGGACCAAGAAATTTACAG 25

RESULT 2

AR153982/c
LOCUS AR153982 1000 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 32 from patent US 6238863.
ACCESSION AR153982
VERSION AR153982.1 GI:15122035
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1000)
Schumm, J.W. and Bacher, J.W.
Materials and methods for indentifying and analyzing intermediate
TITLE tandem repeat DNA markers
JOURNAL Patent: US 6238863-A 32 29-MAY-2001;
FEATURES Location/Qualifiers
source 1. .1000
/organism="unknown"

BASE COUNT

302 a 240 c 231 g 226 t 1 others
ORIGIN

Query Match

Best Local Similarity 100.0%; Score 25; DB 6; Length 1000;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTTACAG 25
|||||
Db 726 TGTGCCAGGACCAAGAAATTTACAG 702

RESULT 3

AC104363/c
LOCUS AC104363 62102 bp DNA linear HTG 08-DEC-2001
DEFINITION Homo sapiens chromosome 18 clone RP11-42N11 map 18, LOW-PASS
SEQUENCE SAMPLING.

ACCESSION

AC104363
VERSION AC104363.1 GI:17426352

KEYWORDS

HTG: HTGS_PHASE0.

SOURCE

Homo sapiens.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 62102)

AUTHORS

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Canarata, J., Campopiano, A., Chang, J., Chazaro, B.,

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Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,

Glode, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,

Jones, C., Kanat, A., Karatas, A., Kells, C., LaRocque, K.,

Lamazares, R., Landers, J., Lehoczy, J., Levine, R., Liu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Ramon, J., Retta, R., Rieback, M., Riley, K., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (08-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L22094

Center Clone name: 42_N_11

* NOTE: This record contains 81 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

* be preserved.

* 1 665: contig of 665 bp in length

* 666 765: gap of 100 bp

* 766 1454: contig of 689 bp in length

* 1455 1554: gap of 100 bp

* 1555 2232: contig of 678 bp in length

* 2233 2332: gap of 100 bp

* 2333 3028: contig of 696 bp in length

* 3029 3128: gap of 100 bp

* 3129 3753: contig of 625 bp in length

* 3754 3853: gap of 100 bp

* 3854 4459: contig of 606 bp in length

* 4460 4559: gap of 100 bp

* 4560 5225: contig of 666 bp in length

* 5226 5325: gap of 100 bp

* 5326 5979: contig of 654 bp in length

* 5980 6079: gap of 100 bp

* 6080 6752: contig of 673 bp in length

* 6753 6852: gap of 100 bp

* 6853 7526: contig of 674 bp in length

* 7527 7626: gap of 100 bp

* 7627 8307: contig of 681 bp in length

* 8308 8407: gap of 100 bp

* 8408 9090: contig of 683 bp in length

* 9091 9190: gap of 100 bp

* 9191 9880: contig of 690 bp in length

* 9881 9980: gap of 100 bp

* 9981 10667: contig of 687 bp in length

* 10668 10767: gap of 100 bp

* 10768 11436: contig of 669 bp in length

* 11437 11536: gap of 100 bp

* 11537 12157: contig of 621 bp in length

* 12158 12257: gap of 100 bp

* 12258 12913: contig of 656 bp in length

* 12914 13013: gap of 100 bp

* 13014 13667: contig of 654 bp in length

* 13668 13767: gap of 100 bp


```

* 13768 14429: contig of 662 bp in length
* 14430 14529: gap of 100 bp
* 14530 15189: contig of 660 bp in length
* 15190 15289: gap of 100 bp
* 15290 15950: contig of 661 bp in length
* 15951 16050: gap of 100 bp
* 16051 16724: contig of 674 bp in length
* 16725 16824: gap of 100 bp
* 16825 17505: contig of 681 bp in length
* 17506 17605: gap of 100 bp
* 17606 18290: contig of 685 bp in length
* 18291 18390: gap of 100 bp
* 18391 19050: contig of 660 bp in length
* 19051 19150: gap of 100 bp
* 19151 19807: contig of 657 bp in length
* 19808 19907: gap of 100 bp
* 19908 20568: contig of 661 bp in length
* 20569 20668: gap of 100 bp
* 20669 21322: contig of 654 bp in length
* 21323 21422: gap of 100 bp
* 21423 22079: contig of 657 bp in length
* 22080 22179: gap of 100 bp
* 22180 22852: contig of 673 bp in length
* 22853 22952: gap of 100 bp
* 22953 23621: contig of 669 bp in length
* 23622 23721: gap of 100 bp
* 23722 24386: contig of 665 bp in length
* 24387 24486: gap of 100 bp
* 24487 25174: contig of 688 bp in length
* 25175 25274: gap of 100 bp
* 25275 25957: contig of 683 bp in length
* 25958 26057: gap of 100 bp
* 26058 26729: contig of 672 bp in length
* 26730 26829: gap of 100 bp
* 26830 27478: contig of 649 bp in length
* 27479 27578: gap of 100 bp
* 27579 28237: contig of 659 bp in length
* 28238 28337: gap of 100 bp
* 28338 29002: contig of 665 bp in length
* 29003 29102: gap of 100 bp
* 29103 29764: contig of 662 bp in length
* 29765 29864: gap of 100 bp
* 29865 30544: contig of 680 bp in length
* 30545 30644: gap of 100 bp
* 30645 31330: contig of 686 bp in length
* 31331 31430: gap of 100 bp
* 31431 32107: contig of 677 bp in length
* 32108 32207: gap of 100 bp
* 32208 32887: contig of 680 bp in length
* 32888 32987: gap of 100 bp
* 32988 33679: contig of 692 bp in length
* 33680 33779: gap of 100 bp
* 33780 34451: contig of 672 bp in length
* 34452 34551: gap of 100 bp
* 34552 35216: contig of 665 bp in length
* 35217 35316: gap of 100 bp
* 35317 35978: contig of 662 bp in length
* 35979 36078: gap of 100 bp
* 36079 36731: contig of 653 bp in length
* 36732 36831: gap of 100 bp
* 36832 37486: contig of 655 bp in length
* 37487 37586: gap of 100 bp
* 37587 38249: contig of 663 bp in length
* 38250 38349: gap of 100 bp
* 38350 39032: contig of 683 bp in length
* 39033 39132: gap of 100 bp
* 39133 39815: contig of 683 bp in length
* 39816 39915: gap of 100 bp
* 39916 40576: contig of 661 bp in length
* 40577 40676: gap of 100 bp
* 40677 41356: contig of 680 bp in length
* 41357 41456: gap of 100 bp
* 41457 42141: contig of 665 bp in length

```

```

* 42142 42241: gap of 100 bp
* 42242 42899: contig of 658 bp in length
* 42900 42999: gap of 100 bp
* 43000 43650: contig of 651 bp in length
* 43651 43750: gap of 100 bp
* 43751 44412: contig of 662 bp in length
* 44413 44512: gap of 100 bp
* 44513 45169: contig of 657 bp in length
* 45170 45269: gap of 100 bp
* 45270 45925: contig of 656 bp in length
* 45926 46025: gap of 100 bp
* 46026 46695: contig of 670 bp in length
* 46696 46795: gap of 100 bp
* 46796 47481: contig of 686 bp in length
* 47482 47581: gap of 100 bp
* 47582 48185: contig of 604 bp in length
* 48186 48285: gap of 100 bp
* 48286 48964: contig of 679 bp in length
* 48965 49064: gap of 100 bp
* 49065 49751: contig of 687 bp in length
* 49752 49851: gap of 100 bp
* 49852 50518: contig of 667 bp in length
* 50519 50618: gap of 100 bp
* 50619 51290: contig of 672 bp in length
* 51291 51390: gap of 100 bp
* 51391 52048: contig of 658 bp in length
* 52049 52148: gap of 100 bp
* 52149 52826: contig of 678 bp in length

```

```

Query Match      100.0%; Score 25; DB 2; Length 62102;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TGTGCCAGCAGCAGCAATTTACAG 25
      |||||
Db 55346 TGTGCCAGCAGCAGCAATTTACAG 55322

```

```

RESULT 4
HS496C20
LOCUS

```

```

DEFINITION
Human DNA sequence from clone RP3-496C20 on chromosome 22 Contains
STSs, GSSs and two putative CpG islands, complete sequence.
ACCESSION
283847
VERSION
283847.1 GI:3550060
KEYWORDS
HTG; CpG island.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
1 (bases 1 to 69964)
AUTHORS
Clark G.
JOURNAL
Direct Submission
Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

```

```

COMMENT
On Sep 8, 1998 this sequence version replaced gi:3413284.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 22, constructed by the Sanger Centre Chromosome 22
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr22
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

```

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
 Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-496C20 is from the library RP3-3 constructed at the Roswell Park Cancer Institute by the group of Pietter de Jong. For further details see <http://bacpac.med.buffalo.edu/>
 VECTOR: pCYPAC2

This sequence is the entire insert of clone RP3-496C20. The true left end of clone RP3-340K22 is at 21972 in this sequence. The true right end of clone RP1-140N12 is at 41206 in this sequence. The start of this sequence overlaps with sequence 282206. The end of this sequence overlaps with sequence AL022238.

FEATURES

```

    Location/Qualifiers
      1..69964
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="22"
        /clone="RP3-496C20"
        /clone_lib="RPCI-3"
        24..186
      /note="match: STS: Em:HS496C20S; match: STS: Em:AL021673"
    repeat_region
      169..311
      /note="MIR repeat: matches 71..211 of consensus"
    repeat_region
      551..600
      /note="10 copies 5 mer ttttt 76 conserved"
    repeat_region
      2394..2462
      /note="L2 repeat: matches 2626..2696 of consensus"
    repeat_region
      3060..3221
      /note="MIR repeat: matches 21..192 of consensus"
    repeat_region
      3226..3535
      /note="AluJb repeat: matches 5..312 of consensus"
    repeat_region
      4446..4662
      /note="MIR repeat: matches 35..236 of consensus"
    repeat_region
      5924..5970
      /note="L2 repeat: matches 2701..2748 of consensus"
    misc_feature
      6015..6330
      /note="match: GSS: Em:AQ356083"
    repeat_region
      6149..6461
      /note="AluX repeat: matches 1..312 of consensus"
    repeat_region
      6462..6536
      /note="AluSq/x repeat: matches 1..135 of consensus"
    repeat_region
      6632..6695
      /note="MIR repeat: matches 70..146 of consensus"
    repeat_region
      7617..8113
      /note="AluX repeat: matches 1..297 of consensus"
    misc_feature
      complement(8207..8891)
      /note="match: GSS: Em:AQ344529"
    repeat_region
      8840..8926
      /note="MIR repeat: matches 80..191 of consensus"
    repeat_region
      9079..9606
      /note="264 copies 2 mer cc 58 conserved"
    misc_feature
      9187..9189
      /note="forced join; gap estimated as 1kb by restriction digest data"
    misc_feature
      complement(9187..9189)
      /note="Forced join. Gap estimated as 1kb by restriction digest data."
    repeat_region
      9481..9605
      /note="25 copies 5 mer ctctt 62 conserved"
    repeat_region
      10240..10395
      /note="MIR repeat: matches 76..255 of consensus"
    repeat_region
      10502..10587
      /note="MER5A repeat: matches 57..150 of consensus"
    repeat_region
      10511..10643
      /note="MER5A repeat: matches 57..185 of consensus"
    repeat_region
      11303..11539
      /note="L2 repeat: matches 1865..2127 of consensus"
    repeat_region
      13046..13314
      /note="AluX repeat: matches 28..305 of consensus"
    repeat_region
      13527..13983
      /note="L1A8 repeat: matches 5393..5854 of consensus"
    repeat_region
      13984..14293
      /note="AluSq repeat: matches 1..310 of consensus"
    repeat_region
      14294..14347
      /note="L1A8 repeat: matches 5340..5393 of consensus"
    repeat_region
      14348..14649
      /note="AluX repeat: matches 2..304 of consensus"
    repeat_region
      14651..14966
      /note="AluY repeat: matches 1..306 of consensus"
    repeat_region
      14967..15007
      /note="L1A8 repeat: matches 5352..5341 of consensus"
    repeat_region
      15024..16371
      /note="L1A4 repeat: matches 3784..5097 of consensus"
    repeat_region
      16413..16611
      /note="L1 repeat: matches 3186..3382 of consensus"
    repeat_region
      16662..16875
      /note="MIR repeat: matches 29..256 of consensus"
    repeat_region
      16891..17310
      /note="MLT2FB repeat: matches 2..414 of consensus"
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      17137..17686
      /note="match: GSS: Em:AQ551353"
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      17359..17438
      /note="MER91A repeat: matches 114..193 of consensus"
    repeat_region
      17825..18044
      /note="LTR23 repeat: matches 210..437 of consensus"
    repeat_region
      18046..18357
      /note="AluSq repeat: matches 1..309 of consensus"
    repeat_region
      18511..18822
      /note="AluSq repeat: matches 1..313 of consensus"
    repeat_region
      18830..18897
      /note="BUR1 repeat: matches 6300..6367 of consensus"
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      19044..19080
      /note="MIR repeat: matches 207..245 of consensus"
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      19081..19391
      /note="AluSq repeat: matches 1..307 of consensus"
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      19392..19492
      /note="MIR repeat: matches 117..207 of consensus"
    repeat_region
      19581..19801
      /note="MIR repeat: matches 29..261 of consensus"
    repeat_region
      20302..20464
      /note="AluSq/x repeat: matches 134..302 of consensus"
    repeat_region
      20465..20747
      /note="AluSq repeat: matches 1..296 of consensus"
    repeat_region
      22217..22508
      /note="AluX repeat: matches 14..305 of consensus"
    repeat_region
      22764..22848
      /note="MIR repeat: matches 164..249 of consensus"
    misc_feature
      23209..23725
      /note="CpG island"
    repeat_region
      23946..24063
      /note="MIR repeat: matches 21..140 of consensus"
    repeat_region
      25053..25142
      /note="MIR repeat: matches 21..119 of consensus"
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      25207..25233
      /note="9 copies 3 mer gct 96 conserved"
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      25401..26038
      /note="match: GSS: Em:B54652"
    repeat_region
      25877..26155
      /note="AluJb repeat: matches 1..296 of consensus"
    repeat_region
      26997..27304
      /note="AluJb repeat: matches 1..311 of consensus"
    repeat_region
      27326..27595
      /note="AluX repeat: matches 37..311 of consensus"
    repeat_region
      28098..28406
      /note="AluSq repeat: matches 1..311 of consensus"
    repeat_region
      28847..29128
      /note="L2 repeat: matches 2362..2745 of consensus"
    misc_feature
      complement(29031..29545)
      /note="match: GSS: Em:AQ528941"
    repeat_region
      30940..30989
      /note="25 copies 2 mer gt 100 conserved"
    repeat_region
      30990..31054
      /note="MER41A repeat: matches 400..464 of consensus"

```

```

misc_feature      31120..31339
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repeat_region     34416..34721
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repeat_region     34776..34821
                    /note="L2 repeat: matches 2688..2733 of consensus"
repeat_region     34944..35243
                    /note="AluX repeat: matches 1..300 of consensus"
repeat_region     35351..35551
                    /note="MER20 repeat: matches 1..204 of consensus"
repeat_region     36460..36544
                    /note="L2 repeat: matches 2665..2749 of consensus"
repeat_region     37480..37620
                    /note="MIR repeat: matches 4..150 of consensus"
repeat_region     37861..38188
                    /note="AluJo repeat: matches 1..312 of consensus"
                    complement(38024..38419)
misc_feature       /note="match: STS: Em:G28177; match: STS: Em:R54672"
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repeat_region     38802..38948

```

```

Query Match      100.0%; Score 25; DB 9; Length 69964;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCGACGACACCAAAATTTACAG 25
    |||||
Db 5959 TGTCGACGACACCAAAATTTACAG 5983

```

```

RESULT 5
AC090795/c
LOCUS             AC090795             138459 bp    DNA        linear    HTG 11-JUN-2001
DEFINITION       Homo sapiens chromosome 8 clone RP11-254K5 map 8, WORKING DRAFT
SEQUENCE         AC090795             12 unordered pieces.
ACCESSION        AC090795
VERSION          AC090795.2   GT:14336499
KEYWORDS         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE           Homo sapiens
ORGANISM         Homo sapiens
REFERENCE        1 (bases 1 to 138459)
AUTHORS          Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
                  Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
                  Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
                  Collamore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S.,
                  Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
                  Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
                  Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
                  Jones,C., Karatas,A., LaRoque,K., Lamazares,R., Landers,T.,
                  Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
                  Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
                  McPheeters,R., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V.,
                  Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
                  O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
                  Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
                  Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
                  Roy,A., Santos,R., Schauer,S., Schuppback,R., Seaman,S., Severy,P.,
                  Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
                  Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
                  Travers,M., Travis,N., Triggilio,J., Vassiliev,H., Viel,R., Vo,A.,
                  Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
                  Zembek,L., Zimmer,A. and Zody,M.
DIRECT SUBMISSION
TITLE            Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome
JOURNAL          Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT          On Jun 11, 2001 this sequence version replaced gi:13270664.

```

```

All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L12790
Center clone name: 254_K_5
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 133567 bases at least Q40
Consensus quality: 135811 bases at least Q30
Consensus quality: 136678 bases at least Q20
Insert size: 139000; agarose-fp
Quality coverage: 6.5 in Q20 bases; agarose-fp
Quality coverage: 6.6 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1411: contig of 1411 bp in length
* 1412 1511: gap of 100 bp
* 1512 2165: contig of 654 bp in length
* 2166 2265: gap of 100 bp
* 2266 3074: contig of 809 bp in length
* 3075 3174: gap of 100 bp
* 3175 4763: contig of 1589 bp in length
* 4764 4863: gap of 100 bp
* 4864 6161: contig of 1298 bp in length
* 6162 6261: gap of 100 bp
* 6262 8601: contig of 2340 bp in length
* 8602 8701: gap of 100 bp
* 8702 13139: contig of 4438 bp in length
* 13140 13239: gap of 100 bp
* 13240 17613: contig of 4374 bp in length
* 17614 17713: gap of 100 bp
* 17714 30894: contig of 13181 bp in length
* 30895 30994: gap of 100 bp
* 30995 40051: contig of 9057 bp in length
* 40052 40151: gap of 100 bp
* 40152 95859: contig of 55708 bp in length
* 95860 95959: gap of 100 bp
* 95960 138459: contig of 42500 bp in length.
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* Location/Qualifiers
* 1. 138459
* /organism="Homo sapiens"
* /db_xref="taxon:9606"
* /chromosome="8"
* /map="8"
* /clone="RP11-254K5"
* /clone_lib="RPC1-11 Human Male BAC"
*
* 1. 1411
* /note="assembly_fragment"
* clone_end:Sp6
* vector_side:left
* 1512..2165
* /note="assembly_fragment"
* 2266..3074
* /note="assembly_fragment"
* 3175..4763
* /note="assembly_fragment"
* 4864..6161

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```

misc_feature /note="assembly_fragment"
6262..8601
misc_feature /note="assembly_fragment"
8702..13139
misc_feature /note="assembly_fragment"
13240..17613
misc_feature /note="assembly_fragment"
17714..30894
misc_feature /note="assembly_fragment"
30995..40051
misc_feature /note="assembly_fragment"
40152..95859
misc_feature /note="assembly_fragment"
95960..138459
/note="assembly_fragment"
clone_end:t7
vector_slide:right"
BASE COUNT 38140 a 31260 c 30041 g 37914 t 1104 others
ORIGIN

Query Match 100.0%; Score 25; DB 2; Length 138459;
Best Local Similarity 100.0%; Pred. NO. 0.00016;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGACACCAAGAAATTACAG 25
|||||
Db 34265 TGTGCCAGGACACCAAGAAATTACAG 34241

RESULT 6
AC048344/c
LOCUS Homo sapiens 124427 bp DNA linear PRI 27-JUN-2002
DEFINITION Human BAC Library) complete sequence.
ACCESSION AC048344
VERSION AC048344.44 GI:21553132
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Binage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,F.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Devilla,M.L., Davis,C., Davy-Carroll,J., Dederich,D.A.,
Douthwaite,K.J., Draper,H., Dunn,A.L., Ding,Y., Dinh,H.H.,
Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S.,
Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P.,
Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N.,
Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,
Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Haviak,P.,
Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M.,
Holloway,C., Hollins,B., Homsli,F., Howard,S., Huber,J., Hulyk,S.,
Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y.,
Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,J.,
King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N.,
Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O.,
Lieu,C., Liu,J., Liu,W., Louisgied,H., Lozado,R.J., Lu,X.,
Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P.,
Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E.,
Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S.,
Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T.,
Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M.,
Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,

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Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I., Sodergren,B., Sonaika,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.

TITLE JOURNAL REFERENCE AUTHORS

Direct Submission
Unpublished
2 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (14-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (17-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (25-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (27-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2002 this sequence version replaced gi:21426084.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

TITLE JOURNAL REFERENCE AUTHORS

Direct Submission
Unpublished
2 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (14-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (17-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 124427)
Worley,K.C.
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5 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (27-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2002 this sequence version replaced gi:21426084.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

TITLE JOURNAL REFERENCE AUTHORS

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Submitted (14-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
Submitted (17-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (25-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 124427)
Worley,K.C.
Direct Submission
Submitted (27-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2002 this sequence version replaced gi:21426084.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot>

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FEATURES          ation.html.
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  148. 488
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  825. 1055
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  1340. 1644
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  /rpt_family="AluSp"
  1369. 1503
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  /rpt_family="L1MA9"
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  /rpt_family="FLAM_C"
  1940. 1992
  repeat_region
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  complement(1993..2272)
  /rpt_family="AluY"
  repeat_region
  complement(2276..2572)
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  2576. 2602
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  /rpt_family="AT-rich"
  2689. 2806
  repeat_region
  /rpt_family="FLAM_C"
  2817. 2838
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  /rpt_family="AT-rich"
  2839. 3137
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  /rpt_family="AluSc"
  3817. 3922
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  /rpt_family="MER113"
  complement(3950..4047)
  /rpt_family="MIR"
  4048. 4331
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  /rpt_family="AluSx"
  complement(4398..4458)
  /rpt_family="MIR"
  4458. 4839
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  complement(4541..4839)
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  4912. 5306
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  /rpt_family="MER4A2"
  5307. 5587
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  5588. 5666
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  /rpt_family="MER4A2"
  5799. 6087
  repeat_region
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  complement(6100..6180)
  /rpt_family="MER34"
  complement(6241..6419)
  /rpt_family="MER34B"
  6489. 6670
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  /rpt_family="CT-rich"
  complement(6674..6755)
  /rpt_family="MER34B"
  7008. 7139
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  /rpt_family="FLAM_C"
  7147. 7449
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  7450. 7494
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repeat_region      /rpt_family="AluJo"
                    complement(8678..8806)
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repeat_region      /rpt_family="AluY"
                    complement(9179..9328)

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Query Match 76.08; Score 19; DB 9; Length 124427;
 Best Local Similarity 100.0%; Pred. No. 0.65;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 7 AGGAACCCAGAAATTTACAG 25
|||||
Db 101453 AGGAACCCAGAAATTTACAG 101435
|||||

```

```

RESULT 7
CNS07EF8/c      157395 bp DNA linear PRI 04-MAY-2001
LOCUS           Human chromosome 14 DNA sequence BAC R-286B5 of library RPT-11
DEFINITION      from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION       AL512359
VERSION         AL512359.2 GI:13992194
KEYWORDS        HTG.
SOURCE          human.
ORGANISM        Homo sapiens

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```

REFERENCE
AUTHORS         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
                  Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
                  Levy, M., Eckenberg, R., Bruls, T., Deserardinis, V., Cruaud, C.,
                  Sygpay, G., Saurin, W. and Weissbach, J.
                  Sequencing of the human chromosome 14
                  Unpublished
                  2 (bases 1 to 157395)
                  Genoscope.

```

```

TITLE           JOURNAL
REFERENCE       Submitted (04-MAY-2001) Genoscope - Centre National de Sequençage :
                  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                  - Web : www.genoscope.cns.fr)
                  On May 8, 2001 this sequence version replaced gi:11990874.
                  ----- Genoscope Center
                  Center: Genoscope / Centre National de Sequençage
                  Center code: GS
                  Web site: http://www.genoscope.cns.fr/
                  Contact: SeqRef@genoscope.cns.fr
                  -----

```

```

COMMENT
The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-2G1
Downstream BAC (overlapping the SP6 end) : R-1109N18_PCR1
(AC-AL583762) ----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 6.59x in Q20 bases; sum-of-contigs

```

```

-----
Overall quality chart :
Range : bases
0 : 11
1 - 9 : 10
10 - 19 : 145
20 - 29 : 279
30 - 39 : 660
40 - 49 : 4075
50 - 59 : 7108
60 - 69 : 11941
70 - 79 : 27134

```

```

80 - 89 : 50220
90 - 99 : 55812
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Percentage of bases with a quality value >= 40 : 99 %
-----
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        /db_xref="taxon:9606"
        /chromosome="14"
        /clone="R-286B5"
        /clone_lib="RPCI-11"
BASE COUNT 52242 a 27541 c 27367 g 50245 t
ORIGIN
Query Match 76.0%; Score 19; DB 9; Length 157395;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGCAACCAAGAAAT 19
|||||
Db 46581 TGTGCCAGCAACCAAGAAAT 46563

RESULT 8
AC023529 Homo sapiens clone RP11-27P2, WORKING DRAFT SEQUENCE, 14 unordered
LOCUS pieces
DEFINITION AC023529 Homo sapiens clone RP11-27P2, WORKING DRAFT SEQUENCE, 14 unordered
pieces
ACCESSION AC023529
VERSION AC023529.3 GI:10047793
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159767)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-27P2
Unpublished
2 (bases 1 to 159767)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burnett,G., Campopiano,A., Castle,A.,
Choei,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheters,R., Meldrum,J.,
Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,K., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.
Direct Submission
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 10, 2000 this sequence version replaced gi:7209947.
All repeats were identified using RepeatMasker:
Snit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

```

```

----- Project Information
Center project name: L4732
Center clone name: 27_P_2
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 147596 bases at least Q40
Consensus quality: 154530 bases at least Q30
Consensus quality: 156916 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 158467; sum-of-ctnigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 3.9 in Q20 bases; sum-of-ctnigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 ctnigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the ctnigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 38585: contig of 38585 bp in length
* 38586 38685: gap of 100 bp
* 38686 40414: contig of 1729 bp in length
* 40415 40514: gap of 100 bp
* 40515 44702: contig of 4188 bp in length
* 44703 44802: gap of 100 bp
* 44803 49260: contig of 4458 bp in length
* 49261 49360: gap of 100 bp
* 49361 54772: contig of 5412 bp in length
* 54773 54872: gap of 100 bp
* 54873 61094: contig of 6222 bp in length
* 61095 61194: gap of 100 bp
* 61195 69615: contig of 8421 bp in length
* 69616 69715: gap of 100 bp
* 69716 76018: contig of 6303 bp in length
* 76019 76118: gap of 100 bp
* 76119 84944: contig of 8826 bp in length
* 84945 85044: gap of 100 bp
* 85045 94808: contig of 9764 bp in length
* 94809 94908: gap of 100 bp
* 94909 105344: contig of 10436 bp in length
* 105345 105444: gap of 100 bp
* 105445 117738: contig of 12294 bp in length
* 117739 117838: gap of 100 bp
* 117839 153494: contig of 35656 bp in length
* 153495 153594: gap of 100 bp
* 153595 159767: contig of 6173 bp in length.
FEATURES
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        44803..49260
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85045..94808
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105445..117738
/misc_feature      /note="assembly_fragment"
117839..153494
/misc_feature      /note="assembly_fragment"
153595..159767
/misc_feature      /note="assembly_fragment"
clone_end:17
vector_side:right"
BASE COUNT      50843 a 28235 c 28248 g 51140 t 1301 others
ORIGIN
Query Match      76.0%; Score 19; DB 2; Length 159767;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGGACACAGAAAT 19
|||||
Db 38092 TGTGCCAGGACACAGAAAT 38110

RESULT 9
AC023766/c
LOCUS      AC023766      227611 bp      DNA      linear      HTG 24-AUG-2002
DEFINITION Homo sapiens chromosome 12 clone RP11-459A22 map 12, WORKING DRAFT
SEQUENCE      AC023766      62 unordered pieces.
ACCESSION      AC023766
VERSION      AC023766.2      GI:7767814
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 227611)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens chromosome 12, clone RP11-459A22
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 227611)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavskiy,L.,
Bouckgaalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczkv,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 227611)
REFERENCE      3 (bases 1 to 227611)
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Bouckgaalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,

```

Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRoque,K., Lamazares,R., Landers,T., Lehoczkv,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 10, 2000 this sequence version replaced gi:6984473.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6351

Center clone name: 459_A.22

----- Summary Statistics

Sequencing vector: M13; M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 161281 bases at least Q40

Consensus quality: 183874 bases at least Q30

Consensus quality: 202702 bases at least Q20

Insert size: 162000; agarose-fp

Insert size: 221511; sum-of-contigs

Quality coverage: 4.9 in Q20 bases; agarose-fp

Quality coverage: 3.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 62 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1178: contig of 1178 bp in length

1179 1278: gap of 100 bp

1279 2325: contig of 1047 bp in length

2326 2425: gap of 100 bp

2426 3504: contig of 1079 bp in length

3505 3604: gap of 100 bp

3605 4812: contig of 1208 bp in length

4813 4912: gap of 100 bp

4913 6336: contig of 1424 bp in length

6337 6436: gap of 100 bp

6437 7606: contig of 1170 bp in length

7607 7706: gap of 100 bp

7707 9220: contig of 1514 bp in length

9221 9320: gap of 100 bp

9321 10404: contig of 1084 bp in length

10405 10504: gap of 100 bp

10505 11787: contig of 1283 bp in length

11788 11887: gap of 100 bp

11888 13396: contig of 1509 bp in length

13397 13496: gap of 100 bp

13497 14524: contig of 1028 bp in length

* 14525 14624: gap of 100 bp
 * 14625 15925: contig of 1301 bp in length
 * 15926 16025: gap of 100 bp
 * 16026 16427: contig of 402 bp in length
 * 16428 16527: gap of 100 bp
 * 16528 17984: contig of 1457 bp in length
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 * 18085 19857: contig of 1773 bp in length
 * 19858 19957: gap of 100 bp
 * 19958 21461: contig of 1504 bp in length
 * 21462 21561: gap of 100 bp
 * 21562 23157: contig of 1596 bp in length
 * 23158 23257: gap of 100 bp
 * 23258 24526: contig of 1269 bp in length
 * 24527 24626: gap of 100 bp
 * 24627 25955: contig of 1329 bp in length
 * 25956 26055: gap of 100 bp
 * 26056 27976: contig of 1921 bp in length
 * 27977 28076: gap of 100 bp
 * 28077 29874: contig of 1798 bp in length
 * 29875 29974: gap of 100 bp
 * 29975 31504: contig of 1530 bp in length
 * 31505 31604: gap of 100 bp
 * 31605 32976: contig of 1372 bp in length
 * 32977 33076: gap of 100 bp
 * 33077 34237: contig of 1161 bp in length
 * 34238 34337: gap of 100 bp
 * 34338 35654: contig of 1317 bp in length
 * 35655 35754: gap of 100 bp
 * 35755 37631: contig of 1877 bp in length
 * 37632 37731: gap of 100 bp
 * 37732 39294: contig of 1563 bp in length
 * 39295 39394: gap of 100 bp
 * 39395 41364: contig of 1970 bp in length
 * 41365 41464: gap of 100 bp
 * 41465 43336: contig of 1872 bp in length
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 * 47903 48002: gap of 100 bp
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 * 61917 62016: gap of 100 bp
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 * 64900 64999: gap of 100 bp
 * 65000 69476: contig of 4477 bp in length
 * 69477 69576: gap of 100 bp
 * 69577 74433: contig of 4857 bp in length
 * 74434 74533: gap of 100 bp
 * 74534 78765: contig of 4232 bp in length
 * 78766 78865: gap of 100 bp
 * 78866 83783: contig of 4918 bp in length
 * 83784 83883: gap of 100 bp
 * 83884 88554: contig of 4671 bp in length
 * 88555 88654: gap of 100 bp
 * 88655 92887: contig of 4233 bp in length
 * 92888 92987: gap of 100 bp
 * 92988 97174: contig of 4187 bp in length
 * 97175 97274: gap of 100 bp
 * 97275 101602: contig of 4328 bp in length
 * 101603 101702: gap of 100 bp
 * 101703 107534: contig of 5832 bp in length
 * 107535 107634: gap of 100 bp
 * 107635 112107: contig of 4473 bp in length
 * 112108 112207: gap of 100 bp

* 112208 117172: contig of 4965 bp in length
 * 117173 117272: gap of 100 bp
 * 117273 121060: contig of 3788 bp in length
 * 121061 121160: gap of 100 bp
 * 121161 124846: contig of 3686 bp in length
 * 124847 124946: gap of 100 bp
 * 124947 129670: contig of 4724 bp in length
 * 129671 129770: gap of 100 bp
 * 129771 134148: contig of 4378 bp in length
 * 134149 134248: gap of 100 bp

Query Match 76.0%; Score 19; DB 2; Length 227611;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACACAGAAATTACAG 25
 |||||
 Db 194040 AGGAACACAGAAATTACAG 194022

RESULT 10
 AC068887

LOCUS AC068887 322058 bp DNA linear HTG 29-JUN-2002
 DEFINITION Homo sapiens chromosome 12 clone RP11-392G11, WORKING DRAFT
 SEQUENCE, 12 unordered pieces.

AC068887 GI:21553130

HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 322058)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-ouman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayale,M., Banks,T.,
 Barbara,J., Benton,J., Blincoe,K., Blankenburg,K., Bonnin,D.,
 Bouck,J., Bowie,S., Brivna,M., Brown,E., Brown,M., Bryant,N.P.,
 Buhaq,C., Burck,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
 Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
 Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
 Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
 DeLunhwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
 Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
 Falls,T., Ferraguto,B., Flagg,N., Ford,J., Foster,P., Frantz,P.,
 Gabisi,A., Geo,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
 Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
 Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
 Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
 Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
 Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S.,
 Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
 Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
 Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulsegged,H.,
 Lozato,R.J., Lu,X., Lucier,A., Lucier,R., Iuna,R., Ma,J.,
 Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
 Massey,E., Mathiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
 Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
 Moser,N., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,S.,
 Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
 Oragunye,N., Oviado,R., Pace,A., Payton,B., Peery,J., Perez,L.,
 Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
 Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
 Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
 Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H.,
 Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
 Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
 Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K.,
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstein,G., and Gibbs,R.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
Unpublished
2 (bases 1 to 322058)
Worley, K.C.
Direct Submission
Submitted (11-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 322058)
Worley, K.C.
Direct Submission
Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 25, 2002 this sequence version replaced gi:21535845.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Drafting Center Code: BCM
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HAQU
Center clone name: RP11-392G11
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator; 1% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 314551 bases at least Q40
Consensus quality: 316234 bases at least Q30
Estimated insert size: 316974 bases at least Q20
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

COMMENT

RESULT 11
AC016231/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

AC016231
Homo sapiens clone RP11-27H13, WORKING DRAFT SEQUENCE, 39 unordered
pieces.
AC016231
AC016231.4 GI:13123345
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-27H13
Unpublished
2 (bases 1 to 133337)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Bozulavsky, L., Boukhalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
Cooke, P., DeRellano, K., Dewar, K., Domino, M., Donegan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funk, R., Gage, D.,
Galaan, J., Gardyna, S., Grant, G., Hago, B., Heaford, A., Horton, L.,
Howard, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lewandowski, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyma, D., Ye, W. J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 25, 2001 this sequence version replaced gi:12039543.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 14697
Center clone name: 27_H13
----- Summary Statistics
Sequencing vector: M13; M77815; 11% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 116391 bases at least Q40
Consensus quality: 125269 bases at least Q30
Consensus quality: 128158 bases at least Q20
Insert size: 153000; agarose-fp
Quality coverage: 2.6 in Q20 bases; agarose-fp
Quality coverage: 3.1 in Q20 ba.

TITLE
JOURNAL
COMMENT

2423: contig of 2423 bp in length
2424 2523: gap of unknown length
2524 8179: contig of 5656 bp in length
8180 8279: gap of unknown length
8280 22503: contig of 14224 bp in length
22504 22603: gap of unknown length
22604 35216: contig of 12613 bp in length
35217 35316: gap of unknown length
35317 42339: contig of 7023 bp in length
42340 42349: gap of unknown length
42400 62720: contig of 20281 bp in length
62721 62820: gap of unknown length
62821 71459: contig of 8639 bp in length
71460 71559: gap of unknown length
71560 109809: contig of 38249 bp in length
109809 134937: gap of unknown length
134938 135037: contig of 25029 bp in length
135038 164861: gap of unknown length
164862 164962: gap of unknown length
164963 235517: contig of 70556 bp in length
235518 235618: gap of unknown length
235619 322058: contig of 86441 bp in length.
Location/Qualifiers
1. 322058
/organism="Homo sapiens"

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
2423: contig of 2423 bp in length
2424 2523: gap of unknown length
2524 8179: contig of 5656 bp in length
8180 8279: gap of unknown length
8280 22503: contig of 14224 bp in length
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22604 35216: contig of 12613 bp in length
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35317 42339: contig of 7023 bp in length
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42400 62720: contig of 20281 bp in length
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71560 109809: contig of 38249 bp in length
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135038 164861: gap of unknown length
164862 164962: gap of unknown length
164963 235517: contig of 70556 bp in length
235518 235618: gap of unknown length
235619 322058: contig of 86441 bp in length.
Location/Qualifiers
1. 322058
/organism="Homo sapiens"

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 39 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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* 673 772: gap of 100 bp
* 773 1578: contig of 806 bp in length
* 1579 1678: gap of 100 bp
* 1679 13396: contig of 11718 bp in length
* 13397 13496: gap of 100 bp
* 13497 14553: contig of 1057 bp in length
* 14554 14653: gap of 100 bp
* 14654 15808: contig of 1155 bp in length
* 15809 15908: gap of 100 bp
* 15909 17297: contig of 1389 bp in length
* 17298 17397: gap of 100 bp
* 17398 18345: contig of 948 bp in length
* 18346 18445: gap of 100 bp
* 18446 19764: contig of 1319 bp in length
* 19765 19864: gap of 100 bp
* 19865 21198: contig of 1334 bp in length
* 21199 21298: gap of 100 bp
* 21299 22590: contig of 1292 bp in length
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* 22691 24188: contig of 1498 bp in length
* 24189 24288: gap of 100 bp
* 24289 25165: contig of 877 bp in length
* 25166 25265: gap of 100 bp
* 25266 27286: contig of 2021 bp in length
* 27287 27386: gap of 100 bp
* 27387 29216: contig of 1830 bp in length
* 29217 29316: gap of 100 bp
* 29317 32525: contig of 3209 bp in length
* 32526 32625: gap of 100 bp
* 32626 34252: contig of 1627 bp in length
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* 34353 37416: contig of 3064 bp in length
* 37417 37516: gap of 100 bp
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* 40515 40614: gap of 100 bp
* 40615 44387: contig of 3773 bp in length
* 44388 44487: gap of 100 bp
* 44488 46779: contig of 2292 bp in length
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* 63111 66323: contig of 3213 bp in length
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* 69941 70040: gap of 100 bp
* 70041 74249: contig of 4209 bp in length
* 74250 74349: gap of 100 bp
* 74350 77988: contig of 3639 bp in length
* 77989 82061: contig of 3973 bp in length
* 82062 82161: gap of 100 bp
* 82162 87385: contig of 5224 bp in length
* 87386 87485: gap of 100 bp
* 87486 92662: contig of 5177 bp in length
* 92663 92762: gap of 100 bp
* 92763 99121: contig of 6359 bp in length

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* 99122 99221: gap of 100 bp
* 99222 104889: contig of 5668 bp in length
* 104890 104989: gap of 100 bp
* 104990 110282: contig of 5293 bp in length
* 110283 110382: gap of 100 bp
* 110383 118167: contig of 7785 bp in length
* 118168 118267: gap of 100 bp
* 118268 126038: contig of 7771 bp in length
* 126039 126138: gap of 100 bp
* 126139 132808: contig of 6670 bp in length
* 132809 132908: gap of 100 bp
* 132909 133337: contig of 429 bp in length.
FEATURES
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      /db_xref="taxon:9606"
      /clone_RP11="27H13"
      /clone_lib="RPC1-11 Human Male BAC"
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Query Match

72.0%; Score 18; DB 2; Length 133337;

Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAAACAGAGAA 18
|||||
Db 58416 TGTGCCAGGAAACAGAGAA 58399

RESULT 12 AC090459/c

LOCUS Homo sapiens chromosome 18, clone RP11-125B6, complete sequence.
DEFINITION AC090459
ACCESSION AC090459.6 GI:21955087
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

AC090459 146310 bp DNA linear PRI 25-JUL-2002
Homo sapiens chromosome 18, clone RP11-125B6, complete sequence.
AC090459
HTG.
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 146310)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-125B6
2 (bases 1 to 146310)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Karatas,A., Lakoque,K., Lamazares,R., Landers,T.,
Lehocky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
Rieback,N., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Sougnuez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (23-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146310)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Bouckgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehocky,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,N., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 146310)

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Bouckgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
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Pollara,V., Raymond,C., Retta,R., Rieback,N., Riley,R., Rise,C.,
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Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (20-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE AUTHORS

Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 146310)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bouckgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collamore,A.,
Cooke,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schupback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

TITLE JOURNAL

COMMENT

Submitted (25-JUL-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 25, 2002 this sequence version replaced gi:21490275.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

FEATURES source

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu

Location/Qualifiers

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 DB 51137 TGTCCAGGACAGAAA 51120

RESULT 13 AC111142/c LOCUS DEFINITION

AC111142 169013 bp DNA linear HTG 24-MAY-2002
 Mus musculus clone RP23-370L24, WORKING DRAFT SEQUENCE, 7 ordered
 pieces.

AC111142 VERSION HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. KEYWORDS SOURCE ORGANISM

AC111142.3 GI:21166275

Mus musculus

REFERENCE

1 (bases 1 to 169013)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Mus musculus, clone RP23-370L24

Unpublished

2 (bases 1 to 169013)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepe, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fero, S.,

Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardina, S.,

Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

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Landers, T., Lehoczy, J., Levine, R., Liu, G., MacLean, C.,

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McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T.,

Norman, C. H., O'Connor, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,

Mlene, V., Murphy, T., O'Donnell, P., O'Neill, D., Oliver, J.,

Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,

Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S.,

Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,

Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (18-FEB-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 169013)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,

Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,

Chazaro, B., Choepe, Y., Colangelo, M., Collins, S., Collamore, A.,

Cooke, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,

Fero, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,

Galagan, J., Gardina, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,

Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K.,

Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K.,

Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,

Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,

Meneus, L., Mihova, T., Mlene, V., Murphy, T., Naylor, J., Nguyen, C.,

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,

Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,

Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,

Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,

Theodore, J., Topham, K., Travers, M., Travis, N., Triglio, J.,

Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,

Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (24-MAY-2002) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 24, 2002 this sequence version replaced gi:21070739.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Direct Submission

Submitted (24-MAY-2002) Whitehead Institute/MIT Center for Genome

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RESULT 16

AC090215

LOCUS

DEFINITION

AC090215 Homo sapiens chromosome 18 clone RP11-810C2 map 18, *** SEQUENCING

ACCESSION

AC090215.3 GI:22123621

VERSION

HTG: HTGS_PHASE1.

KEYWORDS

human.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

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AUTHORS

DEFINITION Homo sapiens chromosome 18 clone RP11-810C2 map 18q12, WORKING
DRAFT SEQUENCE, 13 unordered pieces.
ACCESSION AP001779
VERSION AP001779.3 GI:9188516
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens DNA, clone:RP11-810C2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 191197)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens 191,197 genomic DNA of 18q12
JOURNAL Published Only in DataBase (2000)
REFERENCE 2 (bases 1 to 191197)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (07-APR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
COMMENT (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
 On Jul 14, 2000 this sequence version replaced gi:8117451.
 ----- Genome Center
 Center: RIKEN Genomic Sciences Center (GSC)
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp
 ----- Project Information
 Center project name: HumDrafl18
 Center clone name: RP11-810C2
 ----- Summary Statistics
 Sequencing vector: PCR products; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 100% of reads
 Assembly program: Phrap; version 0.990329
 Consensus quality: 186784 bases at least Q40
 Consensus quality: 188417 bases at least Q30
 Consensus quality: 189158 bases at least Q20
 Insert size: 189997; sum-of-contigs
 Quality coverage: 9.58x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

1 52211 contig of 52211 bp in length
 52312 95959 contig of 43648 bp in length
 96060 129191 contig of 33132 bp in length
 129292 144917 contig of 15626 bp in length
 145018 154847 contig of 9830 bp in length
 154948 165265 contig of 10318 bp in length
 165366 173461 contig of 8096 bp in length
 173562 177237 contig of 3676 bp in length
 177338 181320 contig of 3983 bp in length
 181421 183769 contig of 2349 bp in length
 183870 186900 contig of 3031 bp in length
 187001 189395 contig of 2395 bp in length
 189496 191197 contig of 1702 bp in length
 NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 52211: contig of 52211 bp in length
 * 52212 52312: gap of 100 bp
 * 52312 95959: contig of 43648 bp in length

* 95960 96059: gap of 100 bp
 * 96060 129191: contig of 33132 bp in length
 * 129192 129291: gap of 100 bp
 * 129292 144917: contig of 15626 bp in length
 * 144918 145017: gap of 100 bp
 * 145018 154847: contig of 9830 bp in length
 * 154848 154947: gap of 100 bp
 * 154948 165265: contig of 10318 bp in length
 * 165266 165365: gap of 100 bp
 * 165366 173461: contig of 8096 bp in length
 * 173462 173561: gap of 100 bp
 * 173562 177237: contig of 3676 bp in length
 * 177238 177337: gap of 100 bp
 * 177338 181320: contig of 3983 bp in length
 * 181321 181420: gap of 100 bp
 * 181421 183769: contig of 2349 bp in length
 * 183770 183869: gap of 100 bp
 * 183870 186900: contig of 3031 bp in length
 * 186901 187000: gap of 100 bp
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 * 189396 189495: gap of 100 bp
 * 189496 191197: contig of 1702 bp in length.
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 Best Local Similarity 100.0%; Pred.No. 2.5;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 TGTGCCAGGACACAGAAA 18
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 Db 111130 TGTGCCAGGACACAGAAA 111147
 RESULT 18
 CPA277161
 LOCUS CPA277161 1433 bp DNA linear PLN 04-APR-2000
 DEFINITION Carica papaya partial paccs1B gene for
 1-aminocyclopropane-1-carboxylate synthase, exons 1-4.
 ACCESSION AJ277161


```

VERSION      AJ277161.1 GI:7413855
KEYWORDS     1-aminocyclopropane-1-carboxylate synthase; paccs1b gene.
SOURCE       Carica papaya.
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Rosidae; eurosids II; Brassicales; Caricaceae; Carica.
REFERENCE    1 (bases 1 to 1433)
AUTHORS      Lam, P.F. and Abubakar, U.K.
TITLE        Nucleotide sequence of a partial DNA (PACCS1B) encoding ACC
              synthase from ripe papaya fruit
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 1433)
AUTHORS      Lam, P.F.
TITLE        Direct Submission
JOURNAL      Submitted (03-APR-2000) Lam P.F., Biotechnology Programme,
              Malaysian Agricultural Research and Development Institute, GPO Box
              12301, 50774 Kuala Lumpur, MALAYSIA
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                /tissue_type="ripe fruit"
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                PLGITIPRHVLEQLDFTVLKTHLISDETSQSVTSDFTSVVAEILHRRNNVAECA
                ERHVIVLSKDLGLGFRVGTIYNKYVITARRMSSFTLIFSQTQHLHLSMLSNQ
                KFTENVINTNRDLRRRYENIVEGLRSAGIECLAGNAGLCFWMNLSSFLEPTREAEI
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                265..373
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                Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                QY 3 TGCACGAGACCAAGAAAT 19
                DB 40194 TGCACGAGACCAAGAAAT 40210
                RESULT 20
                AC119489_3

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GAACACAGAAATTACAG 25
DB 1155 GAACACAGAAATTACAG 1171
RESULT 19
AC027349
LOCUS       AC027349
DEFINITION Homo sapiens chromosome 16 clone CTD-3083H4, complete sequence.
ACCESSION   AC027349
VERSION     AC027349.3 GI:22122874
KEYWORDS    HTG.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 40740)
AUTHORS     DOE Joint Genome Institute.
TITLE       Sequencing of Human Chromosome 16
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 40740)
AUTHORS     DOE Joint Genome Institute.
TITLE       Direct Submission
JOURNAL     Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
              (bases 1 to 40740)
REFERENCE   3 (bases 1 to 40740)
AUTHORS     DOE Joint Genome Institute.
TITLE       Direct Submission
JOURNAL     Submitted (06-AUG-2002) Production Sequencing Facility, DOE Joint
              Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
              On Aug 6, 2002 this sequence version replaced gi:9090640.
              Sequence Quality Assessment:
              This entry has been annotated with sequence quality
              estimates computed by the Phrap assembly program.
              All manually edited bases have been reduced to quality zero.
              Quality levels above 40 are expected to have less than
              1 error in 10,000 bp.
              Base-by-base quality values are not generally visible from the
              Genbank flat file format but are available as part
              of this entry's ASN.1 file.
              -----
              Sequence Quality Assessment:
              This entry has been annotated with sequence quality
              estimates computed by the Phrap assembly program.
              All manually edited bases have been reduced to quality zero.
              Quality levels above 40 are expected to have less than
              1 error in 10,000 bp.
              Base-by-base quality values are not generally visible from the
              Genbank flat file format but are available as part
              of this entry's ASN.1 file.
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                  Best Local Similarity 100.0%; Pred. No. 11;
                  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                  QY 3 TGCACGAGACCAAGAAAT 19
                  DB 40194 TGCACGAGACCAAGAAAT 40210
                  RESULT 20
                  AC119489_3

```

WPCOMMENT

Sequence split into 4 fragments LOCUS AC119489 Accession AC119489
Fragment Name Begin End
AC119489_0 1 110000
AC119489_1 100001 210000
AC119489_2 200001 310000
AC119489_3 300001 35252

Continuation (4 of 4) of AC119489 from base 300001 (AC119489 Rattus norvegicus clone CH2)

Query Match 68.0%; Score 17; DB 2; Length 55252;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCCAGAAATT 20

DB 54377 GCCAGGACCCAGAAATT 54393

RESULT 21

AC128098/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-322L19, *** SEQUENCING IN PROGRESS
***, 54 unordered pieces.

ACCESSION

AC128098.1 GI:21908696

VERSION HTG: HTGS PHASEL.

KEYWORDS Rattus norvegicus.

SOURCE Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE

AUTHORS

1 (bases 1 to 104934)
Murny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amarantunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbacia,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyte,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorelli,H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hoques,M., Holloway,C., Hollins,B.,
Honsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
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Lozad,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojibokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sodergren,E., Sonaikhe,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Taber,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tanner,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,I., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 104934)

Worley,K.C.

Direct Submission

Submitted (19-JUL-2002)

Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GZOM

Center clone name: CH230-322L19

----- Summary Statistics

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 58882 bases at least Q40

Consensus quality: 64470 bases at least Q30

Consensus quality: 68220 bases at least Q20

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 54 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 1190: contig of 1190 bp in length

* 1290: gap of unknown length

* 1291: contig of 1013 bp in length

* 2304: gap of unknown length

* 2404: contig of 1032 bp in length

* 3435: gap of unknown length

* 3536: contig of 1135 bp in length

* 4671: gap of unknown length

* 4771: contig of 1712 bp in length

* 6482: gap of unknown length

* 6583: contig of 1287 bp in length

* 7869: gap of unknown length

* 7970: contig of 1288 bp in length

* 9257: gap of unknown length

* 9358: contig of 1377 bp in length

* 10735: gap of unknown length

* 10835: contig of 1065 bp in length

* 11899: gap of unknown length

* 11900: contig of 1223 bp in length

* 13222: gap of unknown length

* 13223: contig of 1488 bp in length

* 13323: gap of unknown length

* 14811: contig of 1165 bp in length

* 16075: gap of unknown length

* 16176: contig of 1100 bp in length

* 17276: gap of unknown length

* 17376: contig of 1460 bp in length

* 18836: gap of unknown length

* 18936: contig of 1600 bp in length

* 20536: gap of unknown length

* 20636: contig of 1540 bp in length

* 22176: gap of unknown length

* 22276: contig of 2004 bp in length

* 24279: gap of unknown length

* 24380: contig of 1127 bp in length

* 25506: gap of unknown length

* 25607: contig of 1408 bp in length

* 27015: gap of unknown length

* 27115: contig of 1879 bp in length

* 28993: gap of unknown length

* 28994

TITLE

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 32328 32427: gap of unknown length
 32428 33824: contig of 1397 bp in length
 33825 33924: gap of unknown length
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 35528 37744: contig of 2117 bp in length
 37745 37844: gap of unknown length
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 39203 40775: contig of 1573 bp in length
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 42723 43932: contig of 1210 bp in length
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 49094 50421: contig of 1328 bp in length
 50422 50521: gap of unknown length
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 52713 54772: contig of 2060 bp in length
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 67458 70118: contig of 2661 bp in length
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 71979 73325: contig of 1347 bp in length
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FEATURES
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Location/Qualifiers
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 /db_xref="taxon:10116"
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BASE COUNT

30320 a 19586 c 20195 g 29489 t 5344 others

ORIGIN

Query Match 68.0%; Score 17; DB 2; Length 104934;
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAATTTAC 23
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RESULT 22

AC118386

LOCUS

AC118386 107361 bp DNA linear HTG 18-JUL-2002
 Rattus norvegicus clone CH230-397N16, *** SEQUENCING IN PROGRESS
 ***, 47 unordered clones.

ACCESSION

AC118386

VERSION

AC118386.2 GI:21746308

KEYWORDS

HTG; HTGS_PHASE1.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1. (bases 1 to 107361)

AUTHORS

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
 Albrooks, S.L., Amaral, H.C., Are, J.R., Ayale, M., Banks, T.,
 Barbara, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,
 Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
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 Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, C.,
 Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
 Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,
 Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,
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 Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
 Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
 Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M.,
 Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,
 Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
 Nguyen, N., Nickerson, E., Nwokenwo, S., Ogih, M., Okunolu, G.,
 Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L.,
 Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
 Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G.,
 Scherer, S., Scott, G., Shen, H., Shoshitari, N., Sisson, I.,
 Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
 Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
 Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
 Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,
 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.

Unpublished

2 (bases 1 to 107361)

AUTHORS

Worley, K.C.

JOURNAL

Direct Submission

Submitted (17-APR-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

3 (bases 1 to 107361)
Worley K.C.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20162749.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUEX
Center clone name: CH230-397N16
----- Summary Statistics
Sequencing vector: Plasmid
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 65518 bases at least Q40
Consensus quality: 68520 bases at least Q30
Consensus quality: 70855 bases at least Q20

COMMENT

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: this is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1201: contig of 1201 bp in length
1301: gap of unknown length
1302: 1302: contig of 1125 bp in length
2427 2526: gap of unknown length
3672: contig of 1146 bp in length
3673 3772: gap of unknown length
3773 4896: contig of 1124 bp in length
4897 6187: gap of unknown length
6188 6287: contig of 1191 bp in length
6288 7419: gap of unknown length
7419 8964: contig of 1131 bp in length
7519 8964: contig of 1446 bp in length
8965 9064: gap of unknown length
9065 10143: contig of 1079 bp in length
10144 10243: gap of unknown length
10244 11611: contig of 1368 bp in length
11612 11711: gap of unknown length
11712 12908: contig of 1197 bp in length
12909 13008: gap of unknown length
13009 14201: contig of 1193 bp in length
14202 14301: gap of unknown length
14302 15542: contig of 1241 bp in length
15543 15642: gap of unknown length
15643 17547: contig of 1904 bp in length
17547 17646: gap of unknown length
17647 19349: contig of 1703 bp in length
19350 19449: gap of unknown length
19450 20867: contig of 1418 bp in length
20868 20967: gap of unknown length
20968 22520: contig of 1553 bp in length
22521 24029: gap of unknown length
24030 24129: contig of 1409 bp in length
24130 25659: contig of 1530 bp in length
25660 25759: gap of unknown length
25760 27750: contig of 1991 bp in length
27751 27851: gap of unknown length
27851 28914: contig of 1064 bp in length
28915 29014: gap of unknown length

29015 31201: contig of 2187 bp in length
31202 31301: gap of unknown length
31302 32550: contig of 1258 bp in length
32560 32650: gap of unknown length
32650 33681: contig of 1022 bp in length
33682 33781: gap of unknown length
33782 35464: contig of 1683 bp in length
35465 35665: gap of unknown length
35665 36945: contig of 1380 bp in length
36945 37045: gap of unknown length
37045 39646: contig of 2602 bp in length
39647 39747: gap of unknown length
39747 41780: contig of 2034 bp in length
41781 41880: gap of unknown length
41881 44391: contig of 2511 bp in length
44392 44491: gap of unknown length
44492 46600: contig of 2109 bp in length
46601 46700: gap of unknown length
46701 48130: contig of 1430 bp in length
48131 48230: gap of unknown length
48231 51265: contig of 3035 bp in length
51266 51363: gap of unknown length
51366 54937: contig of 3571 bp in length
54937 55036: gap of unknown length
55037 57632: contig of 2596 bp in length
57633 57732: gap of unknown length
57733 59902: contig of 2170 bp in length
59903 60002: gap of unknown length
60003 62223: contig of 2227 bp in length
62223 62329: gap of unknown length
62330 64139: contig of 1810 bp in length
64140 64239: gap of unknown length
64240 67195: contig of 2956 bp in length
67196 67295: gap of unknown length
67296 71428: contig of 4133 bp in length
71429 71528: gap of unknown length
71529 74034: contig of 2506 bp in length
74035 74134: gap of unknown length
74135 77135: contig of 3001 bp in length
77136 77235: gap of unknown length
77236 81591: contig of 4356 bp in length
81592 81691: gap of unknown length
81692 85122: contig of 3431 bp in length
85123 85222: gap of unknown length
85223 88560: contig of 3338 bp in length
88561 92896: gap of unknown length
92897 92996: gap of unknown length
92997 97294: contig of 4298 bp in length
97295 97394: gap of unknown length
97395 102359: contig of 4964 bp in length
102359 107361: contig of 4903 bp in length.
102459 107361: contig of 4903 bp in length.

FEATURES
source

1. 107361
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-397N16"

BASE COUNT 26683 a 21519 c 21208 g 26730 t 11221 others
ORIGIN

Query Match 68.0%; Score 17; DB 2: Length 107361;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGACCAGAAATT 20

Db 9135 GCCAGGACCAGAAATT 9151

RESULT 23
CEYL11B2_2
WPCOMMENT

Sequence split into 7 fragments LOCUS CEY111B2 Accession Z98857

```

Fragment Name      Begin      End
CEY111B2_0        1      110000
CEY111B2_1        100001   210000
CEY111B2_2        200001   310000
CEY111B2_3        300001   410000
CEY111B2_4        400001   510000
CEY111B2_5        500001   610000
CEY111B2_6        600001   614429

```

Continuation (3 of 7) of CEY111B2 from base 200001 (Z98857 *Caenorhabditis elegans* chromosome 9)

```

Query Match      68.0%; Score 17; DB 2; Length 110000;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 6 CAGGAACCAAGAAATTTA 22

Db 74352 CAGGAACCAAGAAATTTA 74368

RESULT 24
AL365204/c

LOCUS Human DNA sequence from clone RP11-321L2 on chromosome 9, complete
DEFINITION

ACCESSION AL365204 AC073983
VERSION AL365204.11 GI:13810068
KEYWORDS HTG.
SOURCE human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 129191)
Griffiths/C.

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonesrequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
gi:8979993, gi:13396592.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; SW:
SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr9>
RP11-321L2 is from the library RPC1-11.2 constructed by the group
of Peter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-321L2. It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true right end of clone RP11-321L2 is at 129191 in this
sequence. The true right end of clone RP11-31K16 is at 100 in this
sequence.

FEATURES

Location/Qualifiers

```

source
1..129191
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone_lib="RPC1-11.2"
1262..1428
/repeat_region
/repeat_region repeat: matches 89..262 of consensus"
3496..3539
/repeat_region repeat: matches 11 copies 4 mer tgtg 84% conserved"
4371..4499
/repeat_region repeat: matches 11..146 of consensus"
6913..7101
/repeat_region repeat: matches 56..250 of consensus"
7125..7300
/repeat_region repeat: matches 6..178 of consensus"
10943..11213
/repeat_region repeat: matches 2460..2705 of consensus"
17072..17119
/repeat_region repeat: matches 16 copies 3 mer acc 79% conserved"
17572..17659
/repeat_region repeat: matches 44 copies 2 mer tc 88% conserved"
17574..17657
/repeat_region repeat: matches 21 copies 4 mer tctc 90% conserved"
17688..17717
/repeat_region repeat: matches 15 copies 2 mer ca 86% conserved"
17765..18376
/misc_feature
/note="OpG island"
/evidence-not_experimental
19301..19596
/repeat_region repeat: matches 1..295 of consensus"
21560..21624
/repeat_region repeat: matches 109..173 of consensus"
/note="MLT1J repeat: matches 109..173 of consensus"
21629..21925
/repeat_region repeat: matches 1..296 of consensus"
/note="AluSx repeat: matches 1..296 of consensus"
22007..22263
/repeat_region repeat: matches 228..482 of consensus"
/note="MLT1J repeat: matches 228..482 of consensus"
22749..22904
/repeat_region repeat: matches 7..157 of consensus"
/note="FRAM repeat: matches 7..157 of consensus"
23487..23712
/repeat_region repeat: matches 29..261 of consensus"
/note="MIR repeat: matches 29..261 of consensus"
24265..24320
/repeat_region repeat: matches 88..144 of consensus"
/note="MIR repeat: matches 88..144 of consensus"
24725..24971
/repeat_region repeat: matches 1..297 of consensus"
/note="AluJb repeat: matches 1..297 of consensus"
25030..25216
/repeat_region repeat: matches 1..189 of consensus"
/note="MER5A repeat: matches 1..189 of consensus"
25239..25622
/repeat_region repeat: matches 52..503 of consensus"
/note="MLT1H repeat: matches 52..503 of consensus"
26274..26572
/repeat_region repeat: matches 1..299 of consensus"
/note="AluY repeat: matches 1..299 of consensus"
27476..33907
/repeat_region repeat: matches 7..6141 of consensus"
/note="LIP7 repeat: matches 7..6141 of consensus"
34090..34561
/repeat_region repeat: matches 1..493 of consensus"
/note="MLT1D repeat: matches 1..493 of consensus"
36528..40748
/repeat_region repeat: matches 1814..6155 of consensus"
/note="LIP2 repeat: matches 1814..6155 of consensus"
40886..41065
/repeat_region repeat: matches 5947..6140 of consensus"
/note="LIMB8 repeat: matches 5947..6140 of consensus"
41064..41123
/repeat_region repeat: matches 5667..5727 of consensus"
/note="LIM4 repeat: matches 5667..5727 of consensus"
41344..41405
/repeat_region repeat: matches 3..59 of consensus"
/note="MIR repeat: matches 3..59 of consensus"
41406..41759
/repeat_region repeat: matches 1..370 of consensus"
/note="THELC repeat: matches 1..370 of consensus"
41760..41892
/repeat_region repeat: matches 59..212 of consensus"
/note="MIR repeat: matches 59..212 of consensus"
41948..42777
/repeat_region repeat: matches 5318..6165 of consensus"
/note="LIMB2 repeat: matches 5318..6165 of consensus"
42795..44704
/repeat_region repeat: matches 4140..6155 of consensus"
/note="LIP2 repeat: matches 4140..6155 of consensus"
44709..44898
/repeat_region repeat: matches 5144..5330 of consensus"
/note="L1 repeat: matches 5144..5330 of consensus"

```

repeat_region 46070..48455 /note="L1M45A repeat: matches 3961..6285 of consensus"
repeat_region 48474..48835 /note="THEIB repeat: matches 1..364 of consensus"
repeat_region 48836..50419 /note="THEIB-INTERNAL repeat: matches 1..1580 of consensus"
repeat_region 50420..50492 /note="THEIC repeat: matches 300..371 of consensus"
repeat_region 50514..51080 /note="L1M1 repeat: matches 1134..1658 of consensus"
repeat_region 51082..51578 /note="MLT2CB repeat: matches 12..501 of consensus"
repeat_region 51712..52013 /note="AluJo repeat: matches 1..296 of consensus"
repeat_region 52127..52211 /note="AluJ/FLAM repeat: matches 1..85 of consensus"
repeat_region 52315..52473 /note="FRAM repeat: matches 6..146 of consensus"
repeat_region 52492..52773 /note="AluX repeat: matches 1..282 of consensus"
repeat_region 52786..52819 /note="17 copies 2 mer at 85% conserved"
repeat_region 52788..52819 /note="8 copies 4 mer at 87% conserved"
repeat_region 53063..53888 /note="L1M4C repeat: matches 1242..1587 of consensus"
repeat_region 53960..54096 /note="L1M4C repeat: matches 1009..1143 of consensus"
repeat_region 54097..54513 /note="MSTA repeat: matches 1..426 of consensus"
repeat_region 54514..54596 /note="L1M4C repeat: matches 926..1009 of consensus"
repeat_region 55756..56074 /note="L1M4C repeat: matches 4154..4470 of consensus"
repeat_region 56084..56452 /note="L2 repeat: matches 2373..2747 of consensus"
repeat_region 56972..57204 /note="L1MD2 repeat: matches 5778..6001 of consensus"
repeat_region 57687..57976 /note="AluX repeat: matches 1..290 of consensus"
repeat_region 5830..59097 /note="L1M4A repeat: matches 6023..6295 of consensus"
repeat_region 59105..59416 /note="AluSq repeat: matches 1..313 of consensus"
repeat_region 59811..59910 /note="AluY repeat: matches 211..310 of consensus"
repeat_region 60755..62450 /note="L1FA5 repeat: matches 4445..6143 of consensus"
repeat_region 62558..62765 /note="MIR repeat: matches 52..260 of consensus"
repeat_region 64608..64706 /note="L1MC5 repeat: matches 7835..7939 of consensus"
repeat_region 64930..65232 /note="AluY repeat: matches 3..310 of consensus"
repeat_region 65234..65595 /note="MER57B repeat: matches 1..390 of consensus"
repeat_region 65596..66194 /note="L1TR29 repeat: matches 4..616 of consensus"
repeat_region 66277..66588 /note="L1ME3 repeat: matches 5655..5988 of consensus"
repeat_region 67535..67638 /note="MIR repeat: matches 47..150 of consensus"
repeat_region 67727..67925 /note="AluJo repeat: matches 83..309 of consensus"
repeat_region 69066..69174 /note="FLAM_A repeat: matches 1..131 of consensus"
repeat_region 69458..70040 /note="MLT2D repeat: matches 2..553 of consensus"
repeat_region 71046..71085 /note="MER5A repeat: matches 128..167 of consensus"
repeat_region 71047..71111 /note="MER5A repeat: matches 35..107 of consensus"

repeat_region 71368..71686 /note="MLT2E repeat: matches 3..330 of consensus"
repeat_region 71687..71848
Query Match 68.0%; Score 17; DB 9; Length 129191;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TGCCAGGAGCACAGAAAT 19
|||||
Db 120038 TGCCAGGAGCACAGAAAT 120022
RESULT 25
AL356862/c 145481 bp DNA linear PRI 19-JAN-2001
LOCUS Human DNA sequence from clone RP11-1M19 on chromosome q34.11-34.3,
DEFINITION complete sequence.
ACCESSION AL356862
VERSION AL356862.10 GI:12044598
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 145481)
AUTHORS Garner P.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jan 8, 2001 this sequence version replaced gi:11611012.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated repeat sequence elements. Where the sequence is
ambiguous, there is an annotation using the 'unsure' feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-1M19 is from the library RPI-11.1 constructed by the group of
Pierer de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone RP11-1M19 The true left
end of clone RP11-342E24 is at 59483 in this sequence. The true
right end of clone RP11-405C6 is at 27333 in this sequence.

FEATURES
Location/Qualifiers
Source
1..145481
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="q34.11-34.3"
/clone="RP11-1M19"
/clone_lib="RPI-11.1"

BASE COUNT 36669 a 33113 c 34164 g 41535 t
ORIGIN

Query Match 68.0%; Score 17; DB 9; Length 145481;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      4  GCCAGGAACCAAGAAAT 20
          |||||
Db 77828 GCCAGGAACCAAGAAAT 77812

RESULT 26
AC018586/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

160538 bp      DNA      linear      HTG 12-MAR-2000
Homo sapiens clone RP11-9L23, WORKING DRAFT SEQUENCE, 7 unordered
pieces
AC018586
AC018586.3 GI:7230039
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160538)
Birtten,B., Linton,L., Nusbaum,C. and Lander,E.
Unpublished
2 (bases 1 to 160538)
Birtten,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepei,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H.,
O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A.,
Santos,K., Severy,P., Spencer,B., Stange-Thomann,N., Stofanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Vassiliev,H., Viel,R., Vo.A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A.
and Zody,M.
Direct Submission
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L3018
Center clone name: 9_L23
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 150680 bases at least Q40
Consensus quality: 156181 bases at least Q30
Consensus quality: 158397 bases at least Q20
Insert size: 165000; agarose-fp
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

```

* as soon as it is available and the accession number will
* be preserved.

1 4906: contig of 4906 bp in length
* 4907 5006: gap of 100 bp
* 5007 12883: contig of 7877 bp in length
* 12884 12983: gap of 100 bp
* 12984 29048: contig of 16065 bp in length
* 29049 29148: gap of 100 bp
* 29149 59139: contig of 29991 bp in length
* 59140 59239: gap of 100 bp
* 59240 89099: contig of 29860 bp in length
* 89100 89199: gap of 100 bp
* 89200 121942: contig of 32743 bp in length
* 121943 122042: gap of 100 bp
* 122043 160538: contig of 38496 bp in length.

FEATURES
source
1..160538
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-9L23"
/clone_lib="RPC1-11 Human Male BAC"
misc_feature
1..4906
/note="assembly_fragment"
misc_feature
5007..12883
/note="assembly_fragment"
/note="assembly_fragment"
vector_side:right
12984..29048
/note="assembly_fragment"
misc_feature
29149..59139
/note="assembly_fragment"
vector_side:right
59240..89099
/note="assembly_fragment"
misc_feature
89200..121942
/note="assembly_fragment"
misc_feature
122043..160538
/note="assembly_fragment"

BASE COUNT 47831 a 29592 c 29049 g 53460 t 606 others
ORIGIN

Query Match 68.08; Score 17; DB 2; Length 160538;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGAACCAAGAAAT 19
|||||
Db 92137 TGCCAGGAACCAAGAAAT 92121

RESULT 27
AL355478/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL355478
Human DNA sequence from clone RP11-45J023 on chromosome 13,
complete sequence.
AL355478
AL355478.16 GI:11876038
HTG.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174736)
Oliver,K.
Direct Submission
Submitted (15-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Dec 17, 2000 this sequence version replaced gi:11544993.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: En.; EMBL; SW.; SWISSPROT; Tr.; TRMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/projects/C.elegans/wormpep> This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13> RP11-459J23 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBAC3.6

This sequence is the entire insert of clone RP11-459J23 The true left end of clone RP11-237E3 is at 120113 in this sequence. The true right end of clone RP11-501G6 is at 18764 in this sequence.

FEATURES

```

source
1..174736
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="13"
    /clone="RP11-459J23"
    /clone_lib="RP11-11.2"
    /note="16 copies 2 mer to 87% conserved"
repeat_region
853..880
    /note="14 copies 2 mer ac 89% conserved"
repeat_region
4826..5290
    /note="L1MA7 repeat: matches 5824..6283 of consensus"
repeat_region
5914..6070
    /note="L1MA7 repeat: matches 1994..2151 of consensus"
repeat_region
9261..9399
    /note="L2 repeat: matches 1283..1426 of consensus"
repeat_region
10111..10378
    /note="MIR repeat: matches 6..262 of consensus"
repeat_region
12261..12405
    /note="MIR repeat: matches 59..214 of consensus"
repeat_region
13124..13248
    /note="L2 repeat: matches 2371..2496 of consensus"
repeat_region
13326..13467
    /note="L2 repeat: matches 2601..2750 of consensus"
repeat_region
13949..13984
    /note="L2 copies 3 mer aa 86% conserved"
repeat_region
15107..15170
    /note="32 copies 2 mer tg 93% conserved"
repeat_region
15634..15806
    /note="FAM repeat: matches 1..167 of consensus"
repeat_region
16438..16509
    /note="36 copies 2 mer aa 66% conserved"
repeat_region
17539..17616
    /note="MIR repeat: matches 33..115 of consensus"
repeat_region
18506..18533
    /note="L4 copies 2 mer gt 92% conserved"
repeat_region
19491..19546
    /note="28 copies 2 mer tt 69% conserved"
repeat_region
20234..20520
    /note="AluSg repeat: matches 1..287 of consensus"
repeat_region
20945..21234
    /note="AluY repeat: matches 2..307 of consensus"
repeat_region
21679..21887
    /note="L1PA8 repeat: matches 5955..6163 of consensus"
repeat_region
21888..22683
    /note="L1P repeat: matches 3673..4469 of consensus"
repeat_region
23134..23182
    /note="HSMAR1 repeat: matches 1237..1286 of consensus"

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```

repeat_region
28857..28916
    /note="2 copies 30 mer 93% conserved"
repeat_region
29207..29650
    /note="MER5A repeat: matches 1..445 of consensus"
repeat_region
29651..29680
    /note="15 copies 2 mer tt 86% conserved"
repeat_region
29692..31011
    /note="MER65-internal repeat: matches 3513..4851 of consensus"
repeat_region
31100..31412
    /note="MER31-internal repeat: matches 5305..5593 of consensus"
repeat_region
31413..31707
    /note="AluY repeat: matches 1..295 of consensus"
repeat_region
31708..32405
    /note="MER31-internal repeat: matches 3077..5305 of consensus"
repeat_region
32398..32706
    /note="MER4-internal repeat: matches 3734..4021 of consensus"
repeat_region
32534..32712
    /note="MER83-internal repeat: matches 3136..3309 of consensus"
repeat_region
32761..32880
    /note="MER83-internal repeat: matches 3017..3136 of consensus"
repeat_region
33026..33262
    /note="MER4-internal repeat: matches 3170..3395 of consensus"
repeat_region
33396..33529
    /note="FLAM_C repeat: matches 10..143 of consensus"
repeat_region
33779..33985
    /note="AluY repeat: matches 106..310 of consensus"
repeat_region
34176..35049
    /note="MER65-internal repeat: matches 1647..2494 of consensus"
repeat_region
35078..35358
    /note="L1MA7 repeat: matches 5998..6279 of consensus"
repeat_region
35388..35980
    /note="L1 repeat: matches 2445..3040 of consensus"
repeat_region
35995..36050
    /note="14 copies 4 mer tatc 85% conserved"
repeat_region
36111..36254
    /note="36 copies 4 mer atat 70% conserved"
repeat_region
36129..36248
    /note="4 copies 30 mer 73% conserved"
repeat_region
36259..36385
    /note="MSRD repeat: matches 260..392 of consensus"
repeat_region
36533..36679
    /note="MSTC repeat: matches 9..155 of consensus"
repeat_region
36705..38179
    /note="L1M3e repeat: matches 1222..2794 of consensus"
repeat_region
38180..38564
    /note="MSRD repeat: matches 1..394 of consensus"
repeat_region
38565..39381
    /note="L1M3e repeat: matches 474..1222 of consensus"
repeat_region
39987..40070
    /note="L2 repeat: matches 2114..2197 of consensus"
repeat_region
40217..41560
    /note="L2 repeat: matches 963..2332 of consensus"
repeat_region
41566..42604
    /note="L1PA7 repeat: matches 5099..6136 of consensus"
repeat_region
42636..42925
    /note="L2 repeat: matches 685..977 of consensus"
repeat_region
43503..43884
    /note="MIRH repeat: matches 164..547 of consensus"
repeat_region
47044..47091
    /note="24 copies 2 mer ac 87% conserved"
repeat_region
48849..49072
    /note="112 copies 2 mer tt 55% conserved"
repeat_region
49159..49299
    /note="MIR repeat: matches 114..262 of consensus"
repeat_region
49388..49539

```



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repeat_region /note="L2 repeat: matches 2264. .2405 of consensus"
51927..52472
repeat_region /note="L1 repeat: matches 3473. .4016 of consensus"
52438..53721
repeat_region /note="LIP5 repeat: matches 4862. .6143 of consensus"
53734..54794
repeat_region /note="LIM1 repeat: matches 4453. .5403 of consensus"
54795..55168
repeat_region /note="THE1C repeat: matches 1. .371 of consensus"
55169..55420
repeat_region /note="LIPB3 repeat: matches 5537. .5791 of consensus"
55446..55795
repeat_region /note="LIPB3 repeat: matches 5776. .6127 of consensus"
55810..55847
repeat_region /note="19 copies 2 mer aa 81% conserved"
56194..56486
repeat_region /note="ALuX repeat: matches 1. .298 of consensus"
56520..56875
repeat_region /note="L2 repeat: matches 2179. .2320 of consensus"
56912..57251
repeat_region /note="L2 repeat: matches 1691. .2016 of consensus"
59460..59607
repeat_region /note="LIME2 repeat: matches 5836. .5985 of consensus"
60584..60886
repeat_region /note="LIM4 repeat: matches 3020. .3317 of consensus"
60931..62103
repeat_region /note="LIP16 repeat: matches 1708. .2863 of consensus"
62104..62395
repeat_region /note="ALuY repeat: matches 1. .290 of consensus"
62396..62687
repeat_region /note="LIP16 repeat: matches 2863. .3157 of consensus"
62750..65798
repeat_region /note="LIP16 repeat: matches 3178. .6155 of consensus"
67132..67331

Query Match 68.0%; Score 17; DB 9; Length 174736;
Best Local Similarity 100.0%; Pred.No. 9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAATTTA 22
|||||
Db 116422 CAGGAACCAAGAAATTTA 116406

RESULT 28
AC097065
LOCUS Homo sapiens chromosome 1 clone RP11-532L16, complete sequence.
DEFINITION AC097065 AL358153
ACCESSION AC097065.2 GI:18855081
VERSION HTG.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 176861)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176861)
AUTHORS Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
REFERENCE 3 (bases 1 to 176861)
AUTHORS Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2002) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
COMMENT On Feb 21, 2002 this sequence version replaced gi:15982508.
----- Genome Center

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Center: University of Washington Genome Center
Center Code: UWGC
Web site: <http://www.genome.washington.edu>
Contact: uwchgts@u.washington.edu
Drafting Center: SC

----- Project Information

Center project name: chr-1
Center clone name: RP11-532L16 (sc0733)
----- Summary Statistics
Sequencing vector: plasmid; 48% of reads
Chemistry: Dye-terminator ET; 58% of reads
Chemistry: Dye-terminator Big Dye; 42% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 176627 bases at least Q40
Consensus quality: 176846 bases at least Q30
Consensus quality: 176861 bases at least Q20
Insert size: 176495; sum-of-contigs
Quality coverage: 7.3x in Q20 bases; sum-of-contigs

----- Overlapping Sequences:

5': Mapping in progress
3': RP11-469A15 (UWGC:sc0718) AC104461

----- Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

EcoRI			BglII			HindIII			
SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
8696	8887	9143	8853	8208					
6	<800	2067	2035	6382					
261	<800	5161	5172	512					
273	<800	10110	9769	449					
10535	10457	730	<800	8459					
532	<800	1480	1435	26					
8513	8887	5215	5369	2487					

3891	3859	455	<800	713	<800
2555	2542	3352	3310	2554	2524
12086	11736	5973	5896	18764	19124
11598	11291	2818	2829	17982	17787
5497	5533	5914	5896	2326	2375
3007	3017	1863	1877	1578	1565
7124	7208	1567	1526	9232	9104
642	<800	10015	9769	3804	3794
6549	6624	5405	5369	1080	1096
1561	1528	351	<800	166	<800
2485	2542	1018	1080	408	<800
1825	1788	22	<800	198	<800
3011	3017	1097	1080	10206	10193
460	<800	6800	6861	5942	5855
4973	4928	3983	3943	4168	4090
2725	2727	3427	3450	668	<800
4143	4099	4604	4590	4942	4844
1195	1183	4503	4403	15668	15466
2093	2068	5451	5369	2085	2079
5142	5207	22243	22372	388	<800
4103	4099	6052	6484	1093	1096
13196	12882	7746	7719	4098	4090
8147	8272	4644	4590	8408	8418
3525	3553	3988	3943	1344	1305
3631	3648	1909	1877	4105	4090
2235	2259	1095	1080	1263	1305
3215	3225	2019	2035	4483	4538
5186	5207	6503	6861	145	<800
30944	31100	7011	6861	392	<800
		652	<800	4589	4538
		663	<800	475	<800
		3627	3642	3456	3449
		815	800	860	854
		2140	2147	2511	2524
		2881	2829	5445	5390
		5472	5896	5792	5855
		786	<800	1343	1305

FEATURES
source

Location/Qualifiers

1. .176861
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-532L16"
/clone_lib="RPC1 human BAC library 11"
BASE COUNT 53647 a 38409 c 35065 g 49740 t
ORIGIN

Query Match 68.0%; Score 17; DB 9; Length 176861;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACACGAA 17
|||||
Db 48753 TGTGCCAGGACACGAA 48769

RESULT 29
AL136090/c

LOCUS

AL136090 185473 bp DNA linear PRI 04-APR-2001
Human DNA sequence from clone RP11-97N19 on chromosome 20. Contains
the 5' end of the SLC24A3 gene for solute carrier family 24
(sodium/potassium/calcium exchanger) member 3, ESTs, STSS, GSSs and
a CpG island, complete sequence.

ACCESSION AL136090
VERSION AL136090.12 GI:9662903
KEYWORDS HTG: CpG island; SLC24A3.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (20-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT

On Aug 2, 2000 this sequence version replaced gi:9621474.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
En: EMBL; Sv: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
IMPORTANT: This sequence is not the entire insert of clone
RP11-97N19 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP11-97N19 is at 1 in this sequence. The
true left end of clone RP5-1027G4 is at 185374 in this sequence.
The true right end of clone RP11-3K6 is at 52986 in this sequence.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. RP11-97N19 is from

the library RPI-11.1 constructed by the group of Pieter de Jong.
For further details see
<http://www.chori.org/bacpac/home.htm>

VECTOR: pBacE3.6.

FEATURES

```

source
1..185473
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP11-97N19"
/clone.lib="RPI-11.1"
15..382
/note="match: STS: Em:G56094
match: GSS: Em:AQ319526"
399..699
/note="AluJo repeat: matches 1..299 of consensus"
1194..1509
/note="AluYb repeat: matches 1..310 of consensus"
complement(2925..3402)
/note="match: GSS: Em:AQ724001"
2961..3345
/note="THE1C repeat: matches 1..371 of consensus"
5053..5366
/note="AluJo repeat: matches 1..306 of consensus"
7059..7212
/note="AluJo repeat: matches 1..306 of consensus"
8415..8872
/note="L1ME repeat: matches 5518..5785 of consensus"
8871..9370
/note="match: GSS: Em:AQ463733"
9598..9731
/note="MER90 repeat: matches 35..563 of consensus"
10480..10614
/note="MIR repeat: matches 89..232 of consensus"
10620..10743
/note="MER5A repeat: matches 1..149 of consensus"
10783..10973
/note="AluY repeat: matches 1..129 of consensus"
10984..11016
/note="AluY repeat: matches 121..311 of consensus"
11857..12446
/note="MER5A repeat: matches 156..189 of consensus"
12452..12487
/note="L1MC/D repeat: matches 4381..4948 of consensus"
12514..12850
/note="19 copies 2 mer aa 100% conserved"
12889..13096
/note="L1MC/D repeat: matches 4978..5313 of consensus"
13104..13300
/note="L1MC/D repeat: matches 5320..5530 of consensus"
13309..13850
/note="L1PBa repeat: matches -1545..-1348 of consensus"
13841..19303
/note="L1PB1 repeat: matches -940..-402 of consensus"
19323..19900
/note="L1PB1 repeat: matches -265..6152 of consensus"
20697..21023
/note="L1MC2 repeat: matches 5525..6139 of consensus"
21024..22593
/note="THE1B repeat: matches 1..355 of consensus"
22594..22972
/note="THE1B-INTERNAL repeat: matches 3..1580 of
consensus"
23075..23384
/note="THE1B repeat: matches 1..364 of consensus"
23460..23804
/note="MER1B repeat: matches 2..331 of consensus"
24745..25098
/note="MLT1A repeat: matches 1..365 of consensus"
25272..25696
/note="MLT1A2 repeat: matches 3..374 of consensus"
25697..25851
/note="LTR33 repeat: matches 41..485 of consensus"
/note="MLT1A1 repeat: matches 1..155 of consensus"

```

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repeat_region
25852..26158
/note="AluSc repeat: matches 1..309 of consensus"
26159..26367
/note="MLT1A1 repeat: matches 155..363 of consensus"
26368..26403
/note="L1R33 repeat: matches 8..41 of consensus"
26706..27162
/note="HERVL repeat: matches 4320..4790 of consensus"
27693..27870
/note="MIR repeat: matches 20..194 of consensus"
complement(29124..29524)
/note="match: GSS: Em:AQ736831"
29206..29277
/note="L2 repeat: matches 2470..2534 of consensus"
30160..30193
/note="HSMAR1 repeat: matches 1..34 of consensus"
30281..30354
/note="L2 repeat: matches 2671..2745 of consensus"
32566..32762
/note="L1ME3 repeat: matches 5881..6082 of consensus"
32764..32853
/note="L1ME3 repeat: matches 5615..5709 of consensus"
33032..33160
/note="MIR repeat: matches 42..169 of consensus"
33171..33294
/note="MER97a repeat: matches 767..880 of consensus"
33295..33584
/note="AluY repeat: matches 1..291 of consensus"
33585..34192
/note="MER97a repeat: matches 89..767 of consensus"
34283..35426
/note="L2 repeat: matches 1543..2744 of consensus"
35427..35779
/note="MLT1A1 repeat: matches 5..365 of consensus"
35780..36007
/note="L2 repeat: matches 1321..1543 of consensus"
36071..36127
/note="19 copies 3 mer tta 70% conserved"
37173..37267
/note="L2 repeat: matches 1693..1780 of consensus"
37268..37477
/note="MLT1A1 repeat: matches 158..365 of consensus"
37478..37781
/note="AluYa5 repeat: matches 1..301 of consensus"
37782..37938
/note="MLT1A1 repeat: matches 1..158 of consensus"
37939..38691
/note="L2 repeat: matches 1780..2592 of consensus"
38715..41361
/note="Charlie3 repeat: matches 1..2710 of consensus"
41401..41486
/note="MIR repeat: matches 81..167 of consensus"
41530..41689
/note="L2 repeat: matches 2590..2749 of consensus"
41860..42248
/note="L1PA7 repeat: matches 5756..6143 of consensus"
42261..42422
/note="FRAM repeat: matches 1..163 of consensus"
42780..43076
/note="AluY repeat: matches 1..299 of consensus"
43560..43875
/note="AluSq repeat: matches 1..307 of consensus"
44282..44374
/note="MIR repeat: matches 101..194 of consensus"
44573..45448
/note="L1PA2 repeat: matches 5262..6146 of consensus"
45448..46162
/note="L1PA2 repeat: matches 4528..5242 of consensus"
48401..48761
/note="THE1B repeat: matches 1..364 of consensus"
complement(48756..49120)
/note="match: GSS: Em:AQ017019"
49501..49791

```

```

repeat_region /note="Alusq repeat: matches 11. .297 of consensus"
49904. .50029
/note="MER5B repeat: matches 47. .176 of consensus"
repeat_region 50069. .50360
/note="Alusx repeat: matches 1. .293 of consensus"
repeat_region 51322. .51752
/note="MER63B repeat: matches 20. .428 of consensus"

Query Match 68.0%; Score 17; DB 9; Length 185473;
Best Local Similarity 100.0%; Pred. No. 9,9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGGACCAAGAAATTT 21
|||||
Db 34147 CCAGGACCAAGAAATTT 34131

RESULT 30
HUAC004382/c 217873 bp DNA linear PRI 23-NOV-1999
LOCUS Homo sapiens Chromosome 16 BAC clone C1987SK-A-152E5, complete
DEFINITION sequence.
ACCESSION AC004382
VERSION AC004382.1 GI:3252819
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lofthus B.J., Kim, U. J., Sneddon V.P., Kalush, F., Brandon, R.,
Fuhrmann, J., Mason, T., Crosby, M.L., Barnstead, M., Cronin, L.,
Deslattes Mays, A., Cao, Y., Xu, R.X., Kang, H.L., Mitchell, S.,
Eichler, E., Harris, P.C., Venter, J.C. and Adams, M.D.
Genome duplications and other features in 12 Mb of DNA sequence
from human chromosome 16p and 16q
Genomics 60 (3), 295-308 (1999)
99425270
MEDLINE 10493829
PUBMED 2 (bases 1 to 217873)
ADAMS, M.D., LOFTUS, B.J., ZHOU, L., CROSBY, M., FUHRMANN, J.,
MASON, T.M., BRANDON, R., KIM, U.J., KERLAVAGE, A.R. and VENTER, J.C.
Homo sapiens Chromosome 16 BAC clone C1987SK-A-152E5
Unpublished
3 (bases 1 to 217873)
ADAMS, M.D. and LOFTUS, B.J.
Direct Submission
Submitted (07-MAR-1998) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, Email:
bjloftus@tigr.org
4 (bases 1 to 217873)
ADAMS, M.D.
Direct Submission
Submitted (24-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
5 (bases 1 to 217873)
ADAMS, M.D.
Direct Submission
Submitted (25-JUN-1998) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
On Jun 24, 1998 this sequence version replaced gi:3172165.
Address all correspondence to: Mark Adams The Institute for Genomic
Research 9712 Medical Center Dr, Rockville, MD 20850, USA e-mail
address: mdamads@tigr.org. The orientation of the sequence is
from SP6 end to 3' end. Genes were identified by a combination of
five methods including: XGRAIL (available by anonymous ftp from
arthur.epm.ornl.gov), Genefinder (Phil Green, University of
Washington), Genscan (Chris Burge,
http://gnomic.stanford.edu/~chris/GENSCANW.html) searches of the
complete sequence against a peptide database, and the Human gene
Index database at TIGR (http://www.tigr.org/tdb/hgi/hgi.html).
Genes without peptide homology having spliced EST hits are termed
'Unknown gene product'. Genes encoding tRNAs are predicted by

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TRNAScan-SE (Sean Eddy, http://genome.wustl.edu/eddy/TrNAScan-SE/).
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/gene="A-152E5.9"
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82255. .82328,83818. .83986,86434. .86510,88960. .89073,
90550. .>90706))
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GKKNFVGSQKLKLSITKKSSPVKPAVDPAAKLMTLSANDMEDDSMLIDSDDEL
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LEEOKLVOLGAQKRTDQFLDAVETLRMLPIYIEHWPRALSILMLPHNPSSLS
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Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TGCCAGGACAGAAAT 19
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Db 215636 TGCCAGGACAGAAAT 215620
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RESULT 31
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LOCUS
DEFINITION Mus musculus chromosome UNK clone RP24-33412, WORKING DRAFT
ACCESSION AC122476
VERSION AC122476.1 GI:21105937
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 220388)
McPherson, J.D. and Waterston, R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 220388)
AUTHORS McPherson, J.D. and Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: M_BB0334102
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 210112 bases at least Q40
Consensus quality: 212638 bases at least Q30
Consensus quality: 214538 bases at least Q20
Insert size: 197000; agarose-fp
Insert size: 220179; sum-of-contigs
Quality coverage: 8.38 in Q20 bases; agarose-fp
Quality coverage: 6.32 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1209: contig of 1209 bp in length
* 1210: gap of unknown length
* 1310: contig of 1158 bp in length
* 2468 2567: gap of unknown length
* 2568 3567: contig of 1000 bp in length
* 3568 3667: gap of unknown length
* 3668 4840: contig of 1173 bp in length
* 4841 6056: contig of 1116 bp in length
* 6057 6157: contig of unknown length
* 6157 7607: contig of 1451 bp in length
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* 7608 7707: gap of unknown length
* 7708 8868: contig of 1161 bp in length
* 8869 8968: gap of unknown length
* 8969 10168: contig of 1200 bp in length
* 10169 10268: gap of unknown length
* 10269 11426: contig of 1158 bp in length
* 11427 11527: gap of unknown length
* 11527 12871: contig of 1345 bp in length
* 12871 12971: gap of unknown length
* 12971 14451: contig of 1480 bp in length
* 14451 14551: gap of unknown length
* 14552 16718: contig of 2167 bp in length
* 16719 16819: gap of unknown length
* 16819 18827: contig of 2009 bp in length
* 18828 18927: gap of unknown length
* 18928 21908: contig of 2981 bp in length
* 21909 26312: contig of 4304 bp in length
* 26313 26412: gap of unknown length
* 26413 29890: contig of 3478 bp in length
* 29891 36126: contig of 6136 bp in length
* 36127 36227: gap of unknown length
* 36227 41566: contig of 5339 bp in length
* 41566 49129: contig of 7464 bp in length
* 49130 49230: gap of unknown length
* 49230 66133: contig of 16905 bp in length
* 66133 81647: contig of 15413 bp in length
* 81648 88332: contig of 16585 bp in length
* 88333 98432: gap of unknown length
* 98433 120029: contig of 21597 bp in length
* 120030 120129: gap of unknown length
* 120130 147463: contig of 27334 bp in length
* 147464 147564: gap of unknown length
* 147564 180750: contig of 33187 bp in length
* 180751 180850: gap of unknown length
* 180851 220388: contig of 39538 bp in length.
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36227..41565
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clone_end:SP6
vector_side:right"
81748..98332
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98433..120029
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCCAGGAACACAGAAATT 20
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Db 130456 GCCAGGAACACAGAAATT 130440
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RESULT 32
AC122295/c
LOCUS AC122295 231923 bp DNA linear HTG 25-MAY-2002
DEFINITION Mus musculus chromosome UNK clone RP23-263E3, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
AC122295
AC122295.2 GI:21206454
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 231923)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 231923)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
REFERENCE 3 (bases 1 to 231923)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
COMMENT On May 25, 2002 this sequence version replaced gi:21105151.
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
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Contact: submissions@watson.wustl.edu

Project Information
Center project name: M_BA0263E03

Summary Statistics

Sequencing vector: M13; 0%
Sequencing method: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 228616 bases at least Q40
Consensus quality: 229657 bases at least Q40
Consensus quality: 230256 bases at least Q20
Insert size: 182000; agarose-fp
Insert size: 231323; sum-of-contigs
Quality coverage: 15.81 in Q20 bases; agarose-fp
Quality coverage: 11.58 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1096: contig of 1096 bp in length
* 1097 1196: gap of unknown length
* 1197 4371: contig of 3175 bp in length
* 4372 4471: gap of unknown length
* 4472 26809: contig of 22338 bp in length
* 26810 26909: gap of unknown length
* 26910 54548: contig of 27639 bp in length
* 54549 54648: gap of unknown length
* 54649 91374: contig of 36726 bp in length
* 91375 91474: gap of unknown length
* 91475 141654: contig of 50180 bp in length
* 141655 141754: gap of unknown length
* 141755 231923: contig of 90169 bp in length.
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* Location/Qualifiers
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* /db_xref="taxon:10090"
* /chromosome="UNK"
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* 141755. .231923
* /note="assembly_name:Contig17"
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* BASE COUNT 70704 a 44374 c 44153 g 72072 t
* ORIGIN
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* Query Match 68.0%; Score 17; DB 2; Length 231923;
* Best Local Similarity 100.0%; Pred. No. 9.7;
* Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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* QY 5 CCAGGACCAAGAAATTT 21
* |||||
* Db 167119 CCAGGACCAAGAAATTT 167103
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* RESULT 33
* CEY111B2A/c

LOCUS CEY111B2A 257703 bp DNA linear INV 13-AUG-2002
DEFINITION Caenorhabditis elegans cosmid Y111B2A, complete sequence.
ACCESSION AL132904 AL132885 AL132886 AL132889 AL132890 AL132906 AL132908
AL132945
VERSION AL132904.4 GI:21615504
KEYWORDS HTG.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida;
Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
1 none.
REFERENCE Genome sequence of the nematode C. elegans: a platform for
AUTHORS investigating biology. The C. elegans Sequencing Consortium
TITLE Science 282 (5396), 2012-2018 (1998)
JOURNAL 99069613
MEDLINE
REMARK The C.elegans Sequencing Consortium.
REFERENCE 2 (bases 1 to 257703)
AUTHORS Sulston, J.E.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-2002) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rwenematode.wustl.edu
On Jun 26, 2002 this sequence version replaced gi:13548453.
COMMENT Coding sequences below are predicted from computer analysis, using
predictions from GeneFINDER (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
For a graphical representation of this sequence and its analysis
see: - http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
name=Y111B2A
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlapping between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone Y111B2A.
It may be shorter because we only sequence overlapping sections
once, or longer because we only sequence overlapping sections
neighbouring submissions.
The true right end of clone Y49E10 is at 105 in this sequence. The
start of this sequence (1. .105) overlaps with the end of sequence
238866.
The end of this sequence (257598. .257703) overlaps with the start
of sequence 293397.
FEATURES
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2477. .2541,2602. .2749))
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complement(join(35. .160,217. .298,1625. .2304,2347. .2427,
2477. .2541,2602. .2749))
/gene="Y111B2A.1"
/note="contains similarity to Pfam domain: PF000069
(Eukaryotic protein kinase domain), Score=131.2,
E-value=6.2e-36, N=1"
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/protein_id="CAC35832.1"
/db_xref="GI:13548455"
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CILSELYTCELLFYGNDEHTEQLOPELMQLILOQAPSYLMRKAENKMKMICIDGN
VYMKRAKSFOPPLIKORRRNDRAALPIFELLERLILFDTRRLTFSSEITFF
K*
join(3199, .3335,3381, .3504)
/gene="Y111B2A.2"
join(3199, .3335,3381, .3504)
/gene="Y111B2A.2"
/codon_start=1
/protein_id="CAC35833.1"
/db_xref="GI:13548456"
/db_xref="SPTREMBL:O9BHL9"
/translation="MATRNLQSYGKGIYVSLAVVSTAAFNAYVPHNKNYEEF
FANDPYTRMKEICAAKNGYWHPCKEZAKLYEKGVAEH"
join(3655, .3738,3783, .3895,3945, .4215,4263, .5507,
5580, .5766,5824, .6045,6099, .6133)
/gene="Y111B2A.3"
join(3655, .3738,3783, .3895,3945, .4215,4263, .5507,
5580, .5766,5824, .6045,6099, .6133)
/gene="Y111B2A.3"
/note="predicted using GeneFinder
CDNA EST YK225a3.3 comes from this gene
CDNA EST YK398f12.3 comes from this gene
CDNA EST YK408f6.3 comes from this gene
CDNA EST YK491d12.3 comes from this gene
CDNA EST YK225a3.5 comes from this gene
CDNA EST YK398f12.5 comes from this gene
CDNA EST YK408f6.5 comes from this gene
CDNA EST YK491d12.5 comes from this gene
CDNA EST YK598b11.3 comes from this gene
CDNA EST YK598b11.5 comes from this gene
CDNA EST YK615g12.3 comes from this gene
CDNA EST YK615g12.5 comes from this gene"
/codon_start=1
/protein_id="CAB60972.1"
/db_xref="GI:6434400"
/db_xref="SPTREMBL:O9NEM5"
/translation="MAENKSSSELPDKKTLDMKNKEWQLEALFYSTYNDVSKIRVQ
QFDRSSNELIYDTYNSLSDATQIFQAGITQKQVGLSKYLLMRKLYSMITPSK
QFQOBEVKWQFHEIDITYFTFVLPRFKVASLDEISKNPKEVDVDFQEELEWH
LYSPATLLMEFQCCLKNDAGICVQKVPQFFDRRLKMYHYETEDRVESLM
ALVFRLLINKRWDTYDNEWRNLQELARVICSGKEPALMSAWALLDVLCELYTENR
IPMISVEVLSIAKIVENFDNLEVATYARSKPADKVLTPSIICFLILNTIDIANVSN
TVENCKMLTAKGSMKOPDDEAKSYLTSEVLKRPMPHVPFACSTWFKSLVEARR
IPSAIKVANGAIEETDERESGIFGQSDNGDAERSSFSQSVKTAISIGKSGTA
VDLNKNEINLSPASATVEDKSKSALVAIEFEEIPELTQNLISFEDPLEVITEY
LDIITMGVDVSCANELMCHSSVTFTEQLEKVMKKAFFENFEIAKAGPQIRIEC
AKILEVPSSSESDHRIASSLIEVPTERYEDTGPQDLKKSEITIOPLVLIIPDK
TSMRWPPTEYRKPNEINGSRNSARHEREVKQVALTKSLEMAQLHRLNLAESERN
DHWTRPAGNRPFGGSRMNSSTGRAHGSSTNGFR"
join(6674, .6799,6909, .7097,8145, .8444,11946, .12284,
13244, .13644,16919, .17118,17904, .18232)
/gene="Y111B2A.4"
join(6674, .6799,6909, .7097,8145, .8444,11946, .12284,
13244, .13644,16919, .17118,17904, .18232)
/gene="Y111B2A.4"
/codon_start=1
/protein_id="CAC35834.1"
/db_xref="GI:13548457"
/db_xref="SPTREMBL:O9BHL8"
/translation="MSGWLNRIOGQLDLANEVLNEANDVLAEAATEEVPDPGEIIVA
KKAAEAEKQIAIETSRVLLGNKSHLEOOLYDAHVEMDAIGAKFNGWKQRDDETIK
KLATOMBOLQSEWNSTSDIQICELKQVSHWKSLAEKSGDGGSGKEEEMIK
LSELEKRIEALROOKEHTOSLVESHAENLEMRMEYEEKIAAQVLPYNASSTSINA
DALDAVLEREDLLLOHQKSTNGSDGGERPVVLDGSHDELVDRIKQMEVELQR
CDRMEQCHNSDAQIEDLTONKELANAYTELNEEFEGFEQHTATONANNDLNRRI
DSLKANLIEYERYEYCKESAETASQLIKINDFARKTGVDSVSQRREDCVATVNE
EVDKFRASLETQDRHLRSDVQKQVAVGEIDVELDKLREANRLILNCDLQENL
ANYEDTMKLSISSEQDQIGKEQFQEOENHKOQREAMIAENDALREESAAIKQRD
IVLESALLKAVFKYTIKYNPPIFFPEVNEKLQKSAETEEKIELLQKADLLEQVLE
ERANHQEKDEAVEQKKNLESQIQCDADDDDDDETEQKLNNEIKILAVHRDAGKI
EKL"
join(23999, .24166,24215, .24439)
/gene="Y111B2A.5"

CDS
join(23999, .24166,24215, .24439)
/gene="Y111B2A.5"
/codon_start=1
/protein_id="CAB81956.1"
/db_xref="GI:7320782"
/db_xref="SPTREMBL:O9NEM3"
/translation="MEDQLEAKVKALEAKERSKLEKLEAKERIALEVLQRNR
FLNEKLEKLMKENSQDQASQATAELONSSISQLTEQSVKAENARLASIEKSGI
SNSDELRALQENEOIKVKIIDFSKY"
join(43454, .43465,43514, .43565,43621, .43652)
/gene="Y111B2A.25"
join(43454, .43465,43514, .43565,43621, .43652)
/gene="Y111B2A.25"
/codon_start=1
/protein_id="CAC70118.1"
/db_xref="GI:15718295"
/db_xref="SPTREMBL:Q95Q28"
/translation="METKPPSFGSVWICLRQEKYKYGREGGPG"
complement(join(46115, .46396,47400, .47510,47788, .48063,
49804, .50059,51730, .51923))
/gene="Y111B2A.8"
complement(join(46115, .46396,47400, .47510,47788, .48063,
49804, .50059,51730, .51923))
/gene="Y111B2A.8"
/codon_start=1
/protein_id="CAC35836.1"
/db_xref="GI:13548459"
/db_xref="SPTREMBL:O9BHL6"
/translation="MKAKHCVDLIPSSKLVDFDHLVPVKAFYALVYNGVRAAPLWD
TDNORFTGMLTITDFIKILCKHXKDGNSEIRALEDDQIHSRDOFELDGLTRPFVY
IDPNESLHRAVELLCEESVHRLPYLDKLTGNITYILTHKRMKFLSLYMRDLPFSEM
SCTPRELIGANGDILCCHVDPITPDHAELEFLKNRVSAPLIDENGRVVDIYAKFDVI
SLAAESSYDKLCTQVEALQHRSEWFEQVTCLETSDFQVLEAIKVAEVRHLVTDQ
DKVVGVVSLDILKLVLDPCQKPPPPQSQOAGGCGPFRNASGTSTGCASSDS
PPHSIPGIEWEDDDDDDEAPPSIDCSTPGSSAAT"
complement(54444, .55049)
/gene="Y111B2A.7"
complement(54444, .55049)
/gene="Y111B2A.7"
/note="CDNA EST YK206a4.3 comes from this gene
CDNA EST YK279b12.3 comes from this gene
CDNA EST YK206a4.5 comes from this gene"
/codon_start=1
/protein_id="CAC35835.1"
/db_xref="GI:13548458"
/db_xref="SPTREMBL:O9BHL7"
/translation="VYAKNLTIGPPSNOLNDNSSLPIGELVISYDDEPTAPPVTK
PVKGGHTKAKSKASGTRRLTGRSTKRAKDAEAIHEAGEEEDDYTDQNDIVT
KSLPASHTGKSRVNGTSHTKLDQADEMRLRGGGPPRQSGSEPPIPKPVVIFRVPK
HANSLSLRVSPGAIGPSGVVYKAPLSDPNDFYTWHTSEAG"
complement(join(67074, .67361,68426, .68568,68916, .68990,
79753, .79974,81744, .81935,81988, .82061,82202, .82271,
82321, .82477))
/gene="Y111B2A.9"
Query Match 68.0%; Score 17; DB 3; Length 257703;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGGAACGAGAAATTTA 22
|||||||
Db 129725 CAGGAACGAGAAATTTA 129709
RESULT 34
OMI007725/c
LOCUS 286 bp DNA linear PLN 09-FEB-1999
DEFINITION orobanche minor chloroplast trnf(GAA) gene.
ACCESSION AJ007725
VERSION AJ007725.1 GI:3421348
KEYWORDS transfer RNA-Phe; trnf gene.
SOURCE Orobanche minor.
ORGANISM Chloroplast Orobanche minor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Orobanchaceae; Orobanchae.
1 (bases 1 to 286)
Lohan, A.J.
Direct Submission
Submitted (07-AUG-1998) Lohan A.J., Smurfit Institute of Genetics, Trinity College Dublin, University of Dublin, Trinity College, Dublin 2, IRELAND

2 (bases 1 to 286)
Lohan, A.J. and Wolfe, K.H.
A subset of conserved tRNA genes in plastid DNA of nongreen plants
Genetics 150 (1), 425-433 (1998)
MEDLINE 98393598
PUBMED 9725858

FEATURES

source Location/Qualifiers
1..286
/organism="Orobanchae minor"
/organelle="plastid:chloroplast"
/db_xref="taxon:36748"
27..99
/gene="trnF(GAA)"
27..99
/gene="trnF(GAA)"
/product="tRNA-Phe"
/note="codon recognized: UUC"
/anticodon="(pos:60..62,aa:Phe)
BASE COUNT 94 a 36 c 52 g 104 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 286;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAGA 16
|||||
Db 101 TGTGCCAGGACCCAGA 86

RESULT 35
CH2M05/c
LOCUS
DEFINITION Chloroplast Zea mays gene encoding tRNA specific for Phenylalanine. (tRNA-Phe).
ACCESSION V00174
VERSION V00174.1 GI:12397
KEYWORDS transfer RNA; transfer RNA-Phe.
SOURCE Zea mays.
ORGANISM

Chloroplast Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 320)
Steinmetz, A., Krebbers, E.T., Schwarz, Z., Gubbins, E.J. and Bogorad, L.
Nucleotide sequences of five maize chloroplast transfer RNA genes and their flanking regions
J. Biol. Chem. 258 (9), 5503-5511 (1983)
MEDLINE 83213507
PUBMED 6853530

FEATURES
source Location/Qualifiers
1..320
/organism="Zea mays"
/organelle="plastid:chloroplast"
/db_xref="taxon:4577"
81..153
/product="tRNA-Phe"
BASE COUNT 114 a 43 c 60 g 103 t
ORIGIN

trna
BASE COUNT 114 a 43 c 60 g 103 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 320;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAGA 16
|||||
Db 155 TGTGCCAGGACCCAGA 140

RESULT 36
AX017232/c
LOCUS
DEFINITION Sequence 16 from Patent WO947670. DNA linear PAT 07-SEP-2000
ACCESSION AX017232
VERSION AX017232.1 GI:10042152
KEYWORDS
SOURCE human.
ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 585)
Tate, S.N., Grose, D.T. and Hick, C.A.
Mammalian sodium channel proteins
Patent: WO 9947670-A 16 23-SEP-1999;
TATE SIMON NICHOLAS (GB); GLAXO GROUP LTD (GB); GROSE DAVID THOMAS (GB); HICK CAROLINE ANNE (GB)
JOURNAL

FEATURES
source Location/Qualifiers
1..585
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 181 a 117 c 112 g 175 t
ORIGIN

Query Match 64.0%; Score 16; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCCAGAAATTTAC 23
|||||
Db 471 GGAACCCAGAAATTTAC 456

RESULT 37
SOTRNAPLE/c
LOCUS
DEFINITION S.oleracea chloroplast DNA for phe-tRNA and leu-tRNA.
ACCESSION X87343
VERSION X87343.1 GI:840898
KEYWORDS transfer RNA-Leu; transfer RNA-Phe; tRNA-Leu gene; tRNA-Phe gene.
SOURCE Spinacia oleracea.
ORGANISM

Chloroplast Spinacia oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
1 (bases 1 to 1147)
Lin, C.H., Wu, C.Y. and Chen, L.J.
Characterization of tRNAs maturation of spinach chloroplast
Unpublished
2 (bases 1 to 1147)
Lin, C.H. and Wu, C.Y.
Direct Submission
Submitted (22-MAY-1995) C.H. Lin, Institute of Molecular Biology, National Chung Hsing University, Taichung, 40227 Taiwan, R.O.C.
JOURNAL

FEATURES
source Location/Qualifiers
1..1147
/organism="Spinacia oleracea"
/organelle="plastid:chloroplast"
/db_xref="taxon:3562"
102..151
/gene="tRNA-Leu"
102..151
/gene="tRNA-Leu"
/product="tRNA-Leu"
/note="3' exon"
488..561
/gene="tRNA-Phe"

gene
trna
BASE COUNT 114 a 43 c 60 g 103 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 320;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

trna 488..561
/gene="trna-Phe"
/product="trna-Phe"
BASE COUNT 397 a 172 c 184 g 394 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 1147;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACCAGA 16
|||||
Db 562 TGTGCCAGGAACCAGA 547

RESULT 38
TOBQPLB3/c
LOCUS Tobacco Leu-trna and Phe-trna genes. linear PLN 26-APR-1995
DEFINITION
ACCESSION M16898
VERSION 1 GI:343492
KEYWORDS transfer RNA-Leu; transfer RNA-Phe.
SEGMENT 3 of 3
SOURCE Chloroplast Nicotiana tabacum (variety Bright Yellow 4) DNA.
ORGANISM

REFERENCE
AUTHORS Yamada,K., Shinozaki,K. and Sugiyama,M.
TITLE DNA sequences of tobacco chloroplast genes for trna-Ser (GGA), trna-Thr (UGU), trna-Leu (UAA), trna-Phe (GAA): the trna-Leu gene contains a 503 bp intron
JOURNAL Plant Mol. Biol. 6, 193-199 (1986)
COMMENT The Leu-trna anticodon (TAA) begins with the last bp (119) of exon 1, and ends with the first two bp (623-624) of exon 2.

FEATURES
source
1..1268
/organism="Nicotiana tabacum"
/organelle="plastid:chloroplast"
/variety="Bright Yellow 4"
/db_xref="taxon:4097"
join(85..119,623..673)
/gene="Leu-trna"
join(85..119,623..673)
/gene="Leu-trna"
/product="trna-Leu"
85..119
/gene="Leu-trna"
/note="putative"
/number=1
120..622
/gene="Leu-trna"
/note="putative: does not fit consensus"
/cons_splice=(5'site:no, 3'site:no)
623..673
/gene="Leu-trna"
/note="putative"
/number=2
1029..1101
/gene="Phe-trna"
1029..1101
/gene="Phe-trna"
/product="trna-Phe"
/note="codon recognized: UUC"
anticodon=(pos:1062..1064,aa:Phe)
223 c 226 g 376 t
BASE COUNT 443 a 223 c 226 g 376 t
ORIGIN About 0.7 kb after segment 2.

gene
trna
exon

intron

exon

gene

trna

Query Match 64.0%; Score 16; DB 8; Length 1268;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACCAGA 16
|||||
Db 1103 TGTGCCAGGAACCAGA 1088

RESULT 39
PVTRPHE/c
LOCUS P.vulgaris trna-Phe gene and trna-Leu gene-3'end. linear PLN 08-MAY-1992
DEFINITION
ACCESSION X58537
VERSION X58537.1 GI:14209
KEYWORDS transfer RNA-Leu; transfer RNA-Phe.
SOURCE Phaseolus vulgaris.
ORGANISM

REFERENCE
AUTHORS Mubumbila,M.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-1991) M. Mubumbila, Biochemistry Department, University of Zimbabwe, PO BOX MP, 167 Mount Pleasant, Harare, Zimbabwe
2. (bases 1 to 1358)
Mubumbila,M. and Mubumbila,M.
TITLE DNA heterogeneity in common bean chloroplasts
JOURNAL Unpublished
COMMENT for overlapping sequences see: X02444.

FEATURES
source
1..1358
/organism="Phaseolus vulgaris"
/organelle="plastid:chloroplast"
/strain="Saxa"
/db_xref="taxon:3885"
/tissue_type="leaves"
1..607
/number=1
608..657
/gene="trna-Leu"
608..657
/partial
/gene="trna-Leu"
608..657
/gene="trna-Leu"
/number=2
1015..1020
-35_signal
1039..1044
-10_signal
1077..1140
gene
1077..1140
trna
1077..1140
misc_feature
1141..1358
/note="intergenic spacer"

BASE COUNT 478 a 199 c 202 g 479 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 1358;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

intron

gene

trna

exon

-35_signal

-10_signal

gene

trna

misc_feature

BASE COUNT 478 a 199 c 202 g 479 t
ORIGIN

Query Match 64.0%; Score 16; DB 8; Length 1358;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACCAGA 16
|||||
Db 1142 TGTGCCAGGAACCAGA 1127

Query Match 64.0%; Score 16; DB 8; Length 1268;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGAACCAGA 16
|||||
Db 1142 TGTGCCAGGAACCAGA 1127

RESULT 40
MITATRSF/c
LOCUS MITATRSF 1608 bp DNA linear PLN 31-MAR-1992
DEFINITION Wheat mitochondrial DNA for transfer RNA-Ser (GGA) and -Phe (GAA).
ACCESSION X15118
VERSION X15118.1 GI:13735
KEYWORDS pseudogene; transfer RNA; transfer RNA-Phe; transfer RNA-Ser; trnf

gene; trns gene.
 SOURCE Triticum aestivum.
 ORGANISM Mitochondrion Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Poales; Poaceae; Triticeae; Triticeae; Triticeae.
 REFERENCE 1 (bases 1 to 1608)
 AUTHORS Gray, M.W.
 TITLE Direct Submission
 JOURNAL Submitted (26-APR-1989) Gray M.W., Dalhousie University, Department
 of Biochemistry, Halifax Nova Scotia B3H 4H7, Canada
 REFERENCE 2 (bases 1 to 1608)
 AUTHORS Joyce, P.B. and Gray, M.W.
 TITLE Chloroplast-like transfer RNA genes expressed in wheat mitochondria
 JOURNAL Nucleic Acids Res. 17 (14), 5461-5476 (1989)
 MEDLINE 89345142
 PUBMED 2762145
 COMMENT Data kindly reviewed (31-aug-1989) by Gray M.W.
 FEATURES Location/Qualifiers
 source
 1. .1608
 /organism="Triticum aestivum"
 /organelle="mitochondrion"
 /db_xref="taxon:4565"
 968..1054
 /product="trna-Ser"
 /note="codon recognized: GGA"
 1107..1155
 /note="trna-Leu pseudogene 3'-exon"
 1470..1542
 /product="trna-Phe"
 /note="codon recognized: GAA"
 522 a 304 c 281 g 501 t
 BASE COUNT
 ORIGIN
 Query Match 64.0%; Score 16; DB 8; Length 1608;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTGCCAGGACACAGA 16
 |||||
 Db 1544 TGTGCCAGGACACAGA 1529
 RESULT 41
 AF232699/c
 LOCUS
 DEFINITION Sus scrofa 3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4
 isomerase (3b-HSD) mRNA, 3b-HSD-1 allele, complete cds.
 ACCESSION AF232699
 VERSION AF232699.2 GI:18846439
 SOURCE Sus scrofa.
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 1700)
 AUTHORS von Teichman A., Joerg, H., Werner, P., Brenig, B. and Stranzinger, G.
 TITLE cDNA cloning and physical mapping of porcine 3 beta-hydroxysteroid
 dehydrogenase/Delta 5-Delta 4 isomerase
 JOURNAL Anim. Genet. 32 (5), 298-302 (2001)
 MEDLINE 21540582
 PUBMED 11683717
 REFERENCE 2 (bases 1 to 1700)
 AUTHORS von Teichman A.F., Joerg, H.W., Werner, P. and Stranzinger, G.F.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-2000) Department of Animal Science, Swiss Federal
 Institute of Technology Zurich, Tannenstrasse 1, Zurich 8092,
 Switzerland
 REFERENCE 3 (bases 1 to 1700)
 AUTHORS von Teichman A.F., Joerg, H.W., Werner, P. and Stranzinger, G.F.
 TITLE Direct Submission
 JOURNAL Submitted (21-FEB-2002) Department of Animal Science, Swiss Federal
 Institute of Technology Zurich, Tannenstrasse 1, Zurich 8092,

Switzerland
 Sequence update by submitter
 On Feb 21, 2002 this sequence version replaced gi:7141331.
 Location/Qualifiers
 source
 1. .1700
 /organism="Sus scrofa"
 /db_xref="taxon:9823"
 /chromosome="4"
 /map="4q16-q21"
 /tissue_type="adipose"
 1. .1700
 /gene="3b-HSD"
 /allele="1"
 173..1294
 /gene="3b-HSD"
 /codon_start=1
 /product="3-beta-hydroxysteroid
 dehydrogenase/delta-5-delta-4 isomerase"
 /protein_id="AAF37295.2"
 /db_xref="GI:18846440"
 /translation="MAGWSCIVTGGGGFLGQRIVHLLLEKDLQEIIVLDKVPKPEVR
 EEFSLQSKIKLTMLEGDILDEQCLKAGCOGASVHTASIIDVNAVGRVTKVNV
 KGTQLLEACVQASVPVFLHTSSIEVAGPNSRVETONACEDELETANSAPYLSKK
 LAEKAVLEANGWALONGTTLHTCALRPMYLYGSGPFIFAHMKALENGVLTNKKF
 SRVNPVYGVNVAHILALRALRDPKALSVOQFYVADDTTPQSDLDNTYTGKWK
 GFLDSRSLPSPSLRWLAFLELVSELSPIYQPPFNRHFVTLCSVFTVSYKKA
 QRDLYEPLFTWEEAKQKTKAWGSLVKQKHEALKTKTH"
 BASE COUNT 376 a 497 c 460 g 367 t
 ORIGIN
 Query Match 64.0%; Score 16; DB 4; Length 1700;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TGCAGGACACAGAAA 18
 |||||
 Db 145 TGCAGGACACAGAAA 130
 RESULT 42
 RICMT16/c
 LOCUS
 DEFINITION Oryza sativa (japonica cultivar-group) mitochondrial gene for
 tRNAs, complete sequences.
 ACCESSION D13112
 VERSION D13112.1 GI:287392
 trna-Leu; trna-Phe; trna-Ser.
 KEYWORDS Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare)
 SOURCE Mitochondrion DNA.
 ORGANISM Mitochondrion Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS Nakazono, M. and Hirai, A.
 TITLE Identification of the entire set of transferred chloroplast DNA
 sequences in the mitochondrial genome of rice
 JOURNAL Mol. Gen. Genet. 236 (2-3), 341-346 (1993)
 MEDLINE 93173110
 REFERENCE 2 (bases 1 to 4894)
 AUTHORS Nakazono, M.
 JOURNAL Unpublished
 COMMENT Submitted (28-Aug-1992) to DBJ by:
 Atsushi Hirai
 Laboratory of Radiation Genetics
 Faculty of Agriculture,
 The University of Tokyo
 1-1-1 Yayoi Bunkyo-ku
 Tokyo 113
 Japan
 Phone: 03-3812-2111
 Fax: 03-3815-9335.
 Location/Qualifiers

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source
1. 4894
/organism="Oryza sativa (japonica cultivar-group)"
/organism="Mitochondrion"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
641. 4727
/feature="homologous to ctDNA"
1145. 1231
/product="trna-Ser"
1458. 2058
/gene="rps4"
1458. 2058
/gene="rps4"
2404. 2458
/product="trna-Leu"
2769. 2841
/product="trna-Phe"
<3398. >3885
/product="ORF159"
3983. 4717
/gene="ndhK"
3983. 4717
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BASE COUNT 1523 a 941 c 864 g 1566 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGGAACCGA 16
|||||
Db 2843 TGTGCCAGGAACCGA 2828

RESULT 43
AF072704
LOCUS
DEFINITION
Zea mays stock Acl069 al::rdt sh2 Y21 (y21) gene, complete cds; and
disruption of al gene by rdt transposon.
ACCESSION
AF072704
VERSION
AF072704.1 GI:20385027
KEYWORDS
Zea mays.
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 12558)
Yao,H., Zhou,Q., Li,J., Smith,H., Yandea,M., Nikolau,B.J. and
Schnable,P.S.
Molecular characterization of meiotic recombination across the
140-kb multigenic al-sh2 interval of maize
Proc. Natl. Acad. Sci. U.S.A. 99 (9), 6157-6162 (2002)
21980573
PUBMED
11959909
REFERENCE
2 (bases 1 to 12558)
Zhou,Q., Yao,H., Nikolau,B.J. and Schnable,P.S.
Direct Submission
TITLE
Submitted (20-JUN-1998) Zoology and Genetics, Iowa State
University, Ames, IA 50011, USA
LOCATION/Qualifiers
1. 12558
/organism="Zea mays"
/db_xref="taxon:4577"
/chromosome="3"
/map="3L; between al and sh2"
/feature="al::rdt sh2 stock; obtained from a 10-kb genomic
clone (pE10) derived from the al::rdt sh2 stock (XU et al.
1995). A 4.3-kb EcoRI/HindIII fragment of pE10 was
subcloned into pMOB (Gold Biotechnology, Inc., St. Louis,
MO) to create pEH4.3. Similarly, a 1.5-kb HindIII/SacI
fragment of pE10 was subcloned into pMOB to generate

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pHSL.5. Clones pEH4.3 and pHSL.5 were used as templates
for sequencing the proximal portion of the interval
between al::rdt and y21 via a transposon-mediated
sequencing procedure (STRATHMANN et al., 1991). The 5'
portion of the y21 that is absent from pE10 was obtained
by cloning and sequencing two PCR fragments (1.8 kb and
1.3 kb) amplified from genomic DNA from the al::rdt sh2
stock. In all cases both strands were sequenced.
484. 3589
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Join(484. 634,775. 944,1142. 1228,1774. 1935,2043. 2125,
2803. 2991,3068. 3589)
/gene="y21"
/product="y21"
Join(484. 634,775. 944,1142. 1228,1774. 1935,2043. 2125,
2803. 2991,3068. 3446)
/gene="y21"
/feature="translation start position is predicted based on
conservation among rice, sorghum and maize"
/codon_start=1
/evidence=not_experimental
/product="Y21"
/protein_id="AAM21160.1"
/db_xref="GI:20385028"
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OPTASPAVEVKLHGSVIGALDAMYSNAAGAVITDVHSSLGKYYVDRIQGVFSSLV
LWALEEGKVESESDTDFLTKHQHQAETKAMLAFLWEFPFVPTHDLFH
AMLLFSKHLNVPVYVESMNSAIGFVTDAMVLLQSSGLEWLDKTAQKLSERF
FANVRKVLVYSDQTLADGLHLSKEKTGAVIDRKSRLIGSLQCSLYFLDDSTL
FSKTTTLEELISLNKTDKSTAESNAPGRNIALRSQSGMVGLPATNLESTL
LKQAMEKLTAALRSQSGSFVDEHGRVQGVVTRDIISVFPSPCSDRIDGATFFSALE
QAGCRVENGOMFQ"
order(1319. 1321,1682. 1684)
/feature="transposon MPF target site duplication"
/rpt_type=direct
1322. 1681
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/transposon="mpif"
order(1322. 1336,1667. 1681)
/feature="MPF terminal inverted repeat"
/rpt_type=inverted
complement(3870. 3928)
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/evidence=not_experimental
9168. >10252
/gene="al"
/feature="nonfunctional NADPH-dependent reductase; disrupted
due to transposon rdt insertion in exon 4"
/allele="al::rdt"
9168. 9390
/gene="al"
/number=1
9486. 9655
/gene="al"
/number=2
9772. 9966
/number=3
/number="al"
10113. >10252
/gene="al"
/feature="disrupted due to transposon rdt insertion"
/number=4
order(10245. 10252,10957. 10964)
/feature="transposon rdt target site duplication"
/rpt_type=direct
10253. 10956
/transposon="rdt"
<10957. 11628
/gene="al"
/feature="nonfunctional NADPH-dependent reductase; disrupted
due to transposon rdt insertion in exon 4"
/allele="al::rdt"
<10957. 11628

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/feature="al"
/feature="disrupted due to transposon rdt insertion"
/number=4
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ORIGIN
Query Match 64.0%; Score 16; DB 8; Length 12558;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGGAACACAGA 16
|||||
Db 3868 TGTGCCAGGAACACAGA 3883

RESULT 44
AF434192
LOCUS
DEFINITION
Zea mays line LH82 transposon Ins2, YZ1 (yz1) gene, YZ1-LH82
allele, complete cds; tRNA-Phe (trnF) gene, complete sequence;
retrotransposon Machiavelli Gag and Pol (gag/pol) gene, complete
cds; and retrotransposon-like Ozymandias and MITE Gnat1, complete
sequence.
ACCESSION
AF434192
VERSION
AF434192.1 GI:20502801
KEYWORDS
SOURCE
Zea mays.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
AUTHORS
Yao H., Zhou Q., Li J., Smith H., Yandeuau M., Nikolau B.J. and
Schnable P.S.
TITLE
Molecular characterization of meiotic recombination across the
140-kb multigenic al-sh2 interval of maize
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (9), 6157-6162 (2002)
MEDLINE
21980573
PUBMED
11959909
REFERENCE
2 (bases 1 to 15783)
Yao H., Zhang Y., Nikolau B.J. and Schnable P.S.
Direct Submission
Submitted (15-OCT-2001) Zoology and Genetics, Iowa State
University, Ames, IA 50011, USA
LOCATION/Qualifiers
1. 15783
/organism="Zea mays"
/isolate="line LH82"
/db_xref="taxon:4577"
/chromosome="3"
/map="between al and sh2"
/notes="obtained from the approximately 28-kb cosmid clone
Cos9-10 derived from YAC ASH-2 (Civardi et al., 1994). A
7.5-kb NotI/HindIII fragment from Cos9-10 that has about a
1.4-kb of overlap with the distal end of the al-mum2
sequence (GenBank Accession Number AF347696) was subcloned
into pMOB (Gold Biotechnology, Inc., St. Louis, MO) to
create phy53. A 4.7-kb HindIII fragment from Cos9-10 was
also subcloned into pMOB, generating phy62. A 2.7-kb
EcoRV fragment of Cos9-10 that overlaps both phy62 and
phy53 was subcloned into pMOB to generate phyEV.
Similarly, a 3.8-kb EcoRI fragment of Cos9-10 that
overlaps phy62 was subcloned into pCOS8-72 (GenBank
Accession Number AF061788) vector to generate PCS-YZ.
Clones phy53, phy62, phyEV, and PCS-YZ were used as
templates for sequencing using a transposon-mediated
sequencing procedure (STRATHMANN et al. 1991). In all
cases both strands were sequenced."
1021..1027
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/notes="target site duplication"
/rpt_type=direct
1028..1395
repeat_region
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1396..1402
/notes="target site duplication"
/rpt_type=direct
1649..4390
/genes="yz1"
/allele="YZ1-LH82"
join(1649..1799,1940..2109,2313..2402,2584..2745,
2853..2935,3604..3792,3869..4390)
/genes="yz1"
/product="YZ1"
join(1649..1799,1940..2109,2313..2402,2584..2745,
2853..2935,3604..3792,3869..4247)
/genes="yz1"
/codon_start=1
/product="YZ1"
/protein_id="AAM22634.1"
/db_xref="GI:20502802"
/translaton="MAREASBATARESGAAGAGCWEALKSFDLHPVSPGAL
OPTASPAVEVKGVLGSDGALDAMSSNAAGAVIIDVHSSGLKGYVDRIQGVFESSIV
LWALLELKVSEPTDSTDSFLSTIKOHIOIAETKIAWLAKLFLWEPFPPVTHDILF
HAMLFSKHHLNVAVPVSEMSNVIGFVQDAMVLELLQSSGLEWLDKIDAKQUSEF
RFANVRKVLVYSDTLDGLHILSKERTGAVIDRKTSRLIGLSQCSLILFLDDST
LFSKTTTLEELISNNKTRDKCSTAENSCAPRNILALRSQSGMVGVPATNLESD
TLQAMKLTLLRSQCSFVDEHGRVGVVTRDIIISVPSPLCMSRIDGATFFSAAL
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4248..4390
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/genes="trnF"
complement(4669..4741)
/product="tRNA-Phe"
5402..5406
/notes="target site duplication"
/rpt_type=direct
5407..11559
/transposon="Tyl/copia-like retrotransposon Machiavelli"
5407..6236
/notes="5' LTR"
6239..6252
/notes="reverse of sequence is identical to a sequence
within the LTR of Machiavelli"
6369..10163
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6369..10163
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/codon_start=1
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/protein_id="AAM22635.1"
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TSGKGGGSHSSANVQKNNHKGKPKSNKPNKTNFKKKKAEITCFACGEAHFA
KCDPADRRGKGNVTATASNEEDKGNLPTFFSVQSPWMLDTGANVHVCSDI
NLFYSQGRSDSVLNGVSHSVHGTVDLFTSGKIVQLKNVHVHPSIHKNLVSG
TLLCRDGFVKVLSNKLVSQSGITGKYGCGGLFRESILLDENKNVHNCANVDDL
ASVHSLRCHINFGSMPLATMSLIPNITVYKSGKCHSCVQSKPKPKHAEERHLA
PLELHSDICENGVLTGKGRFMTLIDDAASFCVYLLKTKDEALDYFKIYKAEVE
VQAMKTLKRSRDRGGEFFRVDFDCAEHGIIHERPPYSPESNGIAERKNRTLIDL
NOLMDTCGLSKAMWGAELTSHVLNRPMPKBEKTPYEKVGKRPGLSVLRWGCM
AKVNPMDIKRKLGPRTVDCVFLGASCSIAVRLVVKSEVVDVYDTIMESRDATFF
EHIPPMKDIHNSRYSSEIIPENTPIESFQPEHIVLEEDNDAPKSKQRQVKSF
GDDFIVLVDDPTTIAFAFASDADDAKAEVHNMDSILNSGTWEITDRPYGCKPVG
GLVHQMDVLELNGELDEEIVMEQDGFVVKQESKVKCLKLYGLKQAKRQHE
KFTDTLSAGFAINEADRCVYRGGGVILQYVDDILIFGTNIDVINKVSLKAS
SFDWKLGEADVILNLIKADGGITLSQSHVVEKVLKRFGECKPSPPTPYPSVTL
RKNKRTGLDQRLAYQIVGSLWYLAGATRPDISFAVSKLSRPSNFGTDHHALEVRNR
YLOGMTSYGIHYSQHAVLEGYSDSNWISDADELYATSGYFTVGGGAVSWRSQKTI
LTSTMEALAAALDAIVEAGVLEWLELLMDLPVVEKPIPALMNCONQTVIAKVTSSKD
NGKSSRHVKRRLKSVYKLRNSGVISVTYISTDKNLADPFTKGLPRNVEIASRMGR
PE"

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misc_feature 10706..10714
LTR          /note="polypurine tract"
10717..11559
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11560..11564
/repeat_region /note="target site duplication"
13761..13768
/rpt_type-direct
/note="target site duplication"
/repeat_region /rpt_type-direct
complement(13769..14767)
/note="incomplete"
/transposon="retrotransposon-like Ozymandias"
complement(13769..14246)
/note="3' LTR"
complement(14253..14290)
complement(14291..14767)
/note="5' LTR"
14768..14775
/repeat_region /note="target site duplication"
/note="target site duplication"
/repeat_region /rpt_type-direct
join(14858..15041,15630..15783)
/note="part of a 1.1-kb tandem duplication interrupted by
the Gnat1 insertion"
15034..15041
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/rpt_type-direct
15042..15629
/transposon="MITE Gnat1"
15042..15053
/note="terminal inverted repeat of Gnat1"
15618..15629
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/note="terminal inverted repeat of Gnat1"
/rpt_type-inverted
15630..15637
/repeat_region /note="target site duplication"
/rpt_type-direct
BASE COUNT 4482 a 3258 c 3686 g 4357 t
ORIGIN
1 TGTCGACGAGAACGAGA 16
|||||
Db 4667 TGTCGACGAGAACGAGA 4682

Query Match 64.0%; Score 16; DB 8; Length 15783;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTCGACGAGAACGAGA 16
|||||
Db 4667 TGTCGACGAGAACGAGA 4682

RESULT 45
HSDJ69001
LOCUS      HSDJ69001      21941 bp      DNA      linear      PRI 19-MAR-2001
DEFINITION Human DNA sequence from clone RP4-69001 on chromosome 20 Contains
STSS and GSSs, complete sequence.
ACCESSION AL118521
VERSION    AL118521.18      GI:11182354
KEYWORDS   HTG.
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 21941)
AUTHORS   Sehra,H.
TITLE     Direct Submission
JOURNAL   Submitted (09-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT   On Nov 16, 2000 this sequence version replaced gi:9795208.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; SW., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>

IMPORTANT: This sequence is not the entire insert of clone RP4-69001. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP5-1123D4 is at 21842 in this sequence. The true right end of clone RP3-409010 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-69001 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2.

```

FEATURES             Location/Qualifiers
     source            1..21941
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="20"
                        /clone="RP4-69001"
                        /clone_lib="RPCI-4"
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                        /note="LIMA2 repeat: matches 3039..6308 of consensus"
     repeat_region     3250..3659
                        /note="LIMA9 repeat: matches 5894..6306 of consensus"
                        complement(3573..3797)
     misc_feature       /note="match: STS: Em:HSPF17G3"
                        4058..4253
     repeat_region     /note="MIR repeat: matches 40..248 of consensus"
                        5838..5939
     repeat_region     /note="L2 repeat: matches 2433..2528 of consensus"
                        6071..6302
     repeat_region     /note="L2 repeat: matches 1965..2200 of consensus"
                        6351..6814
     repeat_region     /note="MT1D repeat: matches 1..505 of consensus"
                        complement(7274..7695)
     misc_feature       /note="match: GSS: Em:AQ432967"
                        complement(7295..7621)
     repeat_region     /note="match: GSS: Em:AQ091580"
                        7442..7661
     repeat_region     /note="MIR repeat: matches 21..235 of consensus"
                        8877..9140
     repeat_region     /note="L2 repeat: matches 2452..2750 of consensus"
                        9385..9444
     repeat_region     /note="30 copies 2 mer ca 83% conserved"
                        9486..9700
     repeat_region     /note="MER20 repeat: matches 3..217 of consensus"
                        9936..10026
     repeat_region     /note="MIR repeat: matches 52..144 of consensus"
                        complement(10112..10352)
     misc_feature       /note="match: GSS: Em:AQ035997"
                        10833..10958
     repeat_region     /note="L2 repeat: matches 2585..2710 of consensus"
                        11379..11600
     repeat_region     /note="Charlie2 repeat: matches 3368..3644 of consensus"
                        11601..11726
     repeat_region     /note="L1P4 repeat: matches 5693..5818 of consensus"
                        11737..11880
     repeat_region     /note="L1PAL3 repeat: matches 6013..6156 of consensus"
                        11881..12269

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repeat_region /note="Charlie2 repeat: matches 2944. .3387 of consensus"
12481. .12595
repeat_region /note="Charlie2 repeat: matches 1. .134 of consensus"
12850. .13137
misc_feature /note="L2 repeat: matches 2128. .2507 of consensus"
14108. .14655
misc_feature /note="match: GSS: Em:AQ759431"
14300. .14704
repeat_region /note="match: GSS: Em:A2024068"
17107. .17134
repeat_region /note="7 copies 4 mer gaag 92% conserved"
17367. .17484
repeat_region /note="L2 repeat: matches 2633. .2750 of consensus"
17520. .17621
repeat_region /note="MER5A repeat: matches 1. .113 of consensus"
18393. .18701
misc_feature /note="AluSp repeat: matches 1. .310 of consensus"
complement(18959. .19398)
repeat_region /note="match: GSS: Em:AQ792207"
19444. .19571
repeat_region /note="MER53 repeat: matches 1. .120 of consensus"
19466. .19654
repeat_region /note="MER53 repeat: matches 17. .177 of consensus"
20090. .20313
repeat_region /note="L2 repeat: matches 2471. .2706 of consensus"
20332. .20375
repeat_region /note="11 copies 4 mer atgg 97% conserved"
20430. .20896
repeat_region /note="L1ME2 repeat: matches 5684. .6152 of consensus"
20937. .21156
repeat_region /note="L1MC4 repeat: matches 7765. .7976 of consensus"
BASE COUNT 7244 a 4202 c 4204 g 6291 t
ORIGIN

```

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Query Match      64.0%; Score 16; DB 9; Length 21941;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  9 GAACGAGAAATTACA 24
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Db  9708 GAACGAGAAATTACA 9723

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Search completed: November 24, 2002, 14:30:46
Job time : 2396.5 secs

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	Matches 1000;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps
QY	1	GGTGTGACCTTATCTCTCTGAACCTCAGTITTCCTCATCCGTAATAATGAAAGAGCTGTAG	60					
Db	1	GGTGTGACCTTATCTCTCTGGAACCTCAGTITTCCTCATCCGTAATAATGAAAGAGCTGTAG	60					
QY	61	ATTGTGCTAAAAAATAAATGAATAGCTTAGCGCGGTGAGCGGTGAGCGCTGTAAATCCCA	120					
Db	61	ATTGTGCTAAAAAATAAATGAATAGCTTAGCGCGGTGAGCGGTGAGCGCTGTAAATCCCA	120					
QY	121	GCACCTTTAGAGGTGCAAGAGGGTGATCATTGAGGTGAGGAGTTTGTAGACACAGCGCTG	180					
Db	121	GCACCTTTAGAGGTGCAAGAGGGTGATCATTGAGGTGAGGAGTTTGTAGACACAGCGCTG	180					
QY	181	CCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAAGCTGGGTGGGTGGCT	240					
Db	181	CCCAACACGGTGAACCCCATCTCTACTAAAAATAAAAAATTAAGCTGGGTGGGTGGCT	240					
QY	241	CACACCTGTAAATCCCAAGCATTCTGGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAG	300					
Db	241	CACACCTGTAAATCCCAAGCATTCTGGGAGGCTGAGACGGGTGATCACTCAAGTCAGGAG	300					
QY	301	TTCAGGCCAGCGCTGGGCAACATGCTGTAACCCAGCTCTACTAAAAATAAAAAATTAAG	360					
Db	301	TTCAGGCCAGCGCTGGGCAACATGCTGTAACCCAGCTCTACTAAAAATAAAAAATTAAG	360					
QY	361	CCAGGTGTGGTGACACAGCGCTTAGTCCAGCTACTCTGGGAGGCTGAGCGGAGAGATC	420					
Db	361	CCAGGTGTGGTGACACAGCGCTTAGTCCAGCTACTCTGGGAGGCTGAGCGGAGAGATC	420					
QY	421	GCTTGAACCCAGTAGGCAGAGGTGCACTGAGCGGAGATAAGAGTCATCGACTCCAGCC	480					
Db	421	GCTTGAACCCAGTAGGCAGAGGTGCACTGAGCGGAGATAAGAGTCATCGACTCCAGCC	480					
QY	481	TGSGGTGACAGCAGAGACTCCCTCTCAGAAAATAAAATAAAATAAAATAAAATAAAATAA	540					
Db	481	TGSGGTGACAGCAGAGACTCCCTCTCAGAAAATAAAATAAAATAAAATAAAATAAAATAA	540					
QY	541	AATAAATAAATAAATAAATCTAAAGGGCTGGCAATTTGCTAGCACTTATATGCCCAATA	600					
Db	541	AATAAATAAATAAATAAATCTAAAGGGCTGGCAATTTGCTAGCACTTATATGCCCAATA	600					
QY	601	AGTAATAGCTATCAATATCCCAACCCCTACCACTGTGCTGAAATTAAGTTCTTTTGTCT	660					
Db	601	AGTAATAGCTATCAATATCCCAACCCCTACCACTGTGCTGAAATTAAGTTCTTTTGTCT	660					
QY	661	ACCCCCCATATAGACTTAAGCAGAAATTCACCCGCTACTCTCTGTAATTTCTGGTTCCT	720					
Db	661	ACCCCCCATATAGACTTAAGCAGAAATTCACCCGCTACTCTCTGTAATTTCTGGTTCCT	720					
QY	721	GGCACATAGTGGGTCTCAGTGAACATGGTGTAGTGAATGAGCAAAATGCAAGGAATCTCC	780					
Db	721	GGCACATAGTGGGTCTCAGTGAACATGGTGTAGTGAATGAGCAAAATGCAAGGAATCTCC	780					
QY	781	AGGCCATCTGGGAGCCCTCCAGGGGGGTGAGTTGCGGAACCTCATAGTCTGCTCTCAAT	840					
Db	781	AGGCCATCTGGGAGCCCTCCAGGGGGGTGAGTTGCGGAACCTCATAGTCTGCTCTCAAT	840					
QY	841	GGCCCCACTGAAAGGTAGAGAGTCTTGGGTCCCACTCCCGACCCCCCATCTCTGACTCAC	900					
Db	841	GGCCCCACTGAAAGGTAGAGAGTCTTGGGTCCCACTCCCGACCCCCCATCTCTGACTCAC	900					
QY	901	TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	960					
Db	901	TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	960					
QY	961	CAGGACTGCAAGGAGCCCAAGCAATGATGACCGCGGTGC	1000					
Db	961	CAGGACTGCAAGGAGCCCAAGCAATGATGACCGCGGTGC	1000					

RESULT 2

US-08-998-416-595/c

```

; Sequence 595, Application US/08998416
; Patent No. 6239284
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgin
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSPYII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 595:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1408RP
; US-08-998-416-595

Query Match 5.1%; Score 51; DB 4; Length 658;
Best Local Similarity 100.0%; Prad. No. 1.5e-15;
Matches 51; Conservative 0; Mismatches 0; Indels 0

QY 508 GAAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAAT 558
Db 655 GAAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAATATAAT 605

RESULT 3
US-09-754-250-3
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0

```


; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 86
; SEQ ID NO 11
; LENGTH: 3609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
; NAME/KEY: unsure
; LOCATION: 92
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 869
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 1385
; OTHER INFORMATION: unknown
US-09-705-299-11

Query Match 4.4%; Score 44; DB 4; Length 3609;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 TCGGFGCTCACACCTGTAACTCCAGCACATTGGGAGGCTGAG 274
|||||
Db 1990 TCGGFGCTCACACCTGTAACTCCAGCACATTGGGAGGCTGAG 2033

RESULT 8

US-09-813-817-3
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match 4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGTGGGCACA 377
|||||
Db 58882 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGTGGGCACA 58925

RESULT 9

US-09-813-817-3/c
; Sequence 3, Application US/09813817
; Patent No. 6340583
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178
; CURRENT APPLICATION NUMBER: US/09/813,817
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065

Query Match 4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TYPE: DNA
; ORGANISM: Human
US-09-813-817-3

Query Match 4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 555
|||||
Db 3447 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 3404

RESULT 10

US-09-978-197-3
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978,197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match 4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGTGGGCACA 377
|||||
Db 58882 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGTGGGCACA 58925

RESULT 11

US-09-978-197-3/c
; Sequence 3, Application US/09978197
; Patent No. 6403353
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001178DIV
; CURRENT APPLICATION NUMBER: US/09/978,197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match 4.4%; Score 44; DB 4; Length 59065;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 555
|||||
Db 3447 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAA 3404

RESULT 12

US-08-781-891-79/c
; Sequence 79, Application US/08781891
; Patent No. 6090620
; GENERAL INFORMATION:
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Yu, Chang-En
; APPLICANT: Oshima, Junko
; APPLICANT: Mulligan, John T.
; APPLICANT: Schellenberg, Gerald D.
; TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
; TITLE OF INVENTION: WERNER'S SYNDROME
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,891
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6090620tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 240052.419
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87350 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-781-891-79

Query Match 4.4%; Score 44; DB 3; Length 87350;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 354 AAATTAGCAGGTGGTGGCACACGCGCTGTAGTCCAGCTACT 397
|||||
DB 67204 AAATTAGCAGGTGGTGGCACACGCGCTGTAGTCCAGCTACT 67161

RESULT 13

US-09-791-211-3/c
; Sequence 3, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 3
; LENGTH: 87543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 7421
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 7427
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 11609
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12605
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 12742
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29370
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29422
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29979
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29980
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 29981
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30136
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 30140
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31205
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31206
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 31592
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33095
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 33160
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34066
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 34072
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 36816
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 39020
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42164
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 42459
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46808
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 46823

OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 46826
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52786
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 52787
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 54684
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 63290
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68660
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79134
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 86336
OTHER INFORMATION: unknown
OTHER INFORMATION:
US-09-791-211-3

Query Match 4.4%; Score 44; DB 4; Length 87543;
Best Local Similarity 100.0%; Pred. No. 3.8e-12;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 AAATTAGCAGGTGTGGTCACAGCGCTGTAGTCCAGCTACT 397
|||||
DB 67397 AAATTAGCAGGTGTGGTCACAGCGCTGTAGTCCAGCTACT 67354

RESULT 14
US-09-593-995-10
; Sequence 10, Application US/09593995
; Patent No. 6406888
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA33
; FILE REFERENCE: 99-38
; CURRENT APPLICATION NUMBER: US/09/593,995
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,121
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-593-995-10

Query Match 4.3%; Score 43; DB 4; Length 20598;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 ATAGGCTAGGCGGTGCTCAGCGCTGTATCCAGCACTTT 127
|||||
DB 3990 ATAGGCTAGGCGGTGCTCAGCGCTGTATCCAGCACTTT 4032

RESULT 15
US-09-810-671-3/c
; Sequence 3, Application US/09810671
; Patent No. 6455291
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO00758
; CURRENT APPLICATION NUMBER: US/09/810,671
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 21234
; TYPE: DNA
; ORGANISM: Human
US-09-810-671-3

Query Match 4.3%; Score 43; DB 4; Length 21234;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGC 270
|||||
DB 15212 GGGTGGGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGC 15170

RESULT 16
US-09-797-906-3
; Sequence 3, Application US/09797906
; Patent No. 6329188
; GENERAL INFORMATION:
; APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001151CIP
; CURRENT APPLICATION NUMBER: US/09/797,906
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3
LENGTH: 84495
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n = A,T,C or G
US-09-797-906-3

Query Match 4.3%; Score 43; DB 4; Length 84495;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 335 GTCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGACACA 377
DB 3963 GTCTCTACTAAAAATACAAAAATAGCCAGGTGTGGTGACACA 4005

RESULT 17
US-08-441-370-1/c
Sequence 1, Application US/08441370
Patent No. 5721138
GENERAL INFORMATION:
APPLICANT: Lawn, Richard M.
TITLE OF INVENTION: Apolipoprotein(A) Promoter and
TITLE OF INVENTION: Regulatory Sequence Constructs and Methods of Use
Patent No. 5721138
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441.370
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,849
FILING DATE: 15-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7627-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 900-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-441-370-1

Query Match 4.2%; Score 42; DB 1; Length 2542;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 511 AATAAATAAATAAATAAATAAATAAATAAATAAATAA 552
DB 73 AATAAATAAATAAATAAATAAATAAATAAATAAATAA 32

RESULT 18
US-08-471-454-1
Sequence 1, Application US/08471454
Patent No. 5731169
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.454
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,642
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: FR 89/13770
FILING DATE: 20-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 960-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4100
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2784 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-471-454-1
Query Match 4.2%; Score 42; DB 1; Length 2784;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 CGGTGGCTCACACCTGTATCCACGACACTTTGGAGGCTGAG 274
DB 1947 CGGTGGCTCACACCTGTATCCACGACACTTTGGAGGCTGAG 1988

RESULT 19
US-08-466-974-1
Sequence 1, Application US/08466974
Patent No. 5861258
GENERAL INFORMATION:
APPLICANT: MOGENSEN, Knud E.
APPLICANT: UZE, Gilles
APPLICANT: LUTFALLA, Georges
APPLICANT: GRESSER, Ion
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN

```
;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,974
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
;
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2784 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-466-974-1
;
; Query Match 4.2%; Score 42; DB 2; Length 2784;
; Best Local Similarity 100.0%; Pred. No. 3.6e-11;
; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 233 CGGTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
; |||||||||||||||||||||||||||||||||||||||||||
; Db 1947 CGGTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 1988
;
; RESULT 20
; US-08-471-453-1
; Sequence 1, Application US/08471453
; Patent No. 5886153
;
; GENERAL INFORMATION:
; APPLICANT: MOGENSEN, Knud E.
; APPLICANT: UZE, Gilles
; APPLICANT: LUTFALLA, Georges
; APPLICANT: GRESSER, Ion
;
; TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR
; TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE
; TITLE OF INVENTION: PREPARATION OF THE CORRESPONDING PROTEIN
;
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,453
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,642
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: FR 89/13770
; FILING DATE: 20-OCT-1989
;
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 960-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2784 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
; US-08-471-453-1
;
; Query Match 4.2%; Score 42; DB 2; Length 2784;
; Best Local Similarity 100.0%; Pred. No. 3.6e-11;
; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 233 CGGTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
; |||||||||||||||||||||||||||||||||||||||||||
; Db 1947 CGGTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 1988
;
; RESULT 21
; US-09-026-033-17/c
; Sequence 17, Application US/09026033
; Patent No. 6368791
;
; GENERAL INFORMATION:
; APPLICANT: Felix, Carolyn A.
; APPLICANT: Jones, Douglas H.
; APPLICANT: Rappaport, Eric
;
; TITLE OF INVENTION: METHOD AND KITS FOR ANALYSIS OF
; TITLE OF INVENTION: CHROMOSOMAL REARRANGEMENTS ASSOCIATED WITH LEUKEMIA
;
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: One Commerce Square, 2005 Market Street, 22nd
; STREET: Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103-7086
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,033
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/038,624
; FILING DATE: 19-FEB-1997
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/056,923
; FILING DATE: 26-AUG-1997
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,911
; FILING DATE: 17-NOV-1997
;
; ATTORNEY/AGENT INFORMATION:
```


NAME: Doyle Leary, Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600-1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3441 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-026-033-17

Query Match 4.2%; Score 42; DB 4; Length 3441;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 234 GTGGCTCACACCTGTAATCCAGCACCTTTGGGAGGCTGAGA 275
|||||
Db 2330 GTGGCTCACACCTGTAATCCAGCACCTTTGGGAGGCTGAGA 2289

RESULT 22

US-09-345-882-1/c
Sequence 1. Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENST-031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.Pm
SEQ ID NO 1
LENGTH: 162450
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 9714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele
LOCATION: 97122
OTHER INFORMATION: 99-1442-224 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5-129-144 : polymorphic base deletion of T
FEATURE:
NAME/KEY: allele
LOCATION: 99098

OTHER INFORMATION: 5-130-257 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 99117
OTHER INFORMATION: 5-130-276 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 103806
OTHER INFORMATION: 5-131-395 : polymorphic base A or T
FEATURE:
NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION: 5-133-375 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5-135-155 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 108149
OTHER INFORMATION: 5-135-198 : polymorphic base insertion of GTTT
FEATURE:
NAME/KEY: allele
LOCATION: 108308
OTHER INFORMATION: 5-135-357 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 108471
OTHER INFORMATION: 5-136-174 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION: 5-140-120 : polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 134362
OTHER INFORMATION: 5-140-348 : polymorphic base insertion of A
FEATURE:
NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION: 5-140-361 : polymorphic base insertion of CA
FEATURE:
NAME/KEY: allele
LOCATION: 146328
OTHER INFORMATION: 5-143-84 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 146345
OTHER INFORMATION: 5-143-101 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 150329
OTHER INFORMATION: 5-145-24 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352 : polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
FEATURE:
NAME/KEY: allele
LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
FEATURE:
NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52

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FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
FEATURE:
NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
FEATURE:
NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
FEATURE:
NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FEATURE:
NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
FEATURE:
NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
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NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
FEATURE:
NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
Query Match 4.2%; Score 42; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 233 CGTGGCTCACACTGTAATCCCGACACTTTGGGAGGCTGAG 274
Db 78684 CGTGGCTCACACTGTAATCCCGACACTTTGGGAGGCTGAG 78643
RESULT 23
US-09-511-625B-43
; Sequence 43, Application US/09511625B
; Patent No. 6368828
; GENERAL INFORMATION:
; APPLICANT: LaRoche, William J.
; APPLICANT: Patel, Bharvin
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT
; TITLE OF INVENTION: CDNAS OF STAT6: STAT6b AND STAT6c
; FILE REFERENCE: 14014.0300u1
; CURRENT APPLICATION NUMBER: US/09/511,625B
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US98/17821
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/070,397
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 60/056,075
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e -
NAME/KEY: misc.feature
LOCATION: (1)..(1110)
; OTHER INFORMATION: No. 6368828e: n = a, t, c, or g
US-09-511-625B-43
Query Match 4.1%; Score 41; DB 4; Length 1110;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 234 GGTGGCTCACACTGTAATCCCGACACTTTGGGAGGCTGAG 274
Db 411 GGTGGCTCACACTGTAATCCCGACACTTTGGGAGGCTGAG 451
RESULT 24
5187077-16/c
; Patent No. 5187077
; APPLICANT: GEARING, DAVID P.; GOUGH, NICHOLAS M.; HILTON,
; DOUGLAS J.; KING, JULIE A.; METCALF, DONALD; NICE, EDOUARD C.
; NICOLA, NICOS A.; SIMPSON, RICHARD J.; WILLSON, TRACY A.
; TITLE OF INVENTION: LEUKEMIA INHIBITORY FACTOR
; NUMBER OF SEQUENCES: 41
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,514
; FILING DATE: 09-DEC-1988
; SEQ ID NO:16:
; LENGTH: 1437
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5187077-16

Query Match 4.1%; Score 41; DB 6; Length 1437;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 552
|||||
Db 1181 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 1141

RESULT 25

5427925-14/c
; Patent No. 5427925
; APPLICANT: GEARING, DAVID P.; GOUGH, NICHOLAS M.; HILTON,
; DOUGLAS J.; KING, JULIE A.; METCALF, DONALD; NICE, EDOUARD C.
; NICOLA, NICOS A.; SIMPSON, RICHARD J.; WILLSON, TRACY A.
; TITLE OF INVENTION: RECOMBINANT METHOD FOR MAKING
; LEUKEMIA INHIBITOR FACTOR
; NUMBER OF SEQUENCES: 38
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/58,979
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 948,614
; FILING DATE: 22-SEP-1992
; APPLICATION NUMBER: 667,159
; FILING DATE: 11-MAR-1991
; SEQ ID NO: 14:
; LENGTH: 1437
5427925-14

Query Match 4.1%; Score 41; DB 6; Length 1437;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 512 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 552
|||||
Db 1181 ATAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 1141

RESULT 26

US-08-370-975B-10/c
; Sequence 10, Application US/08370975B
; Patent No. 5622851
; GENERAL INFORMATION:
; APPLICANT: Maley, Frank
; APPLICANT: Maley, Gladys F.
; APPLICANT: Weiner, Karen X.B.
; TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,975B
; FILING DATE: 10-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/POCKET NUMBER: 20894/80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716)263-1636
; TELEFAX: (716)263-1600

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1554 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 4q35
US-08-370-975B-10

Query Match 4.1%; Score 41; DB 1; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GGTGGCTCACACCTGTATCCACGACTTTGGAGGCTGAG 274
|||||
Db 636 GGTGGCTCACACCTGTATCCACGACTTTGGAGGCTGAG 596

RESULT 27

US-09-078-294-9/c
; Sequence 9, Application US/09078294
; Patent No. 6265211
; GENERAL INFORMATION:
; APPLICANT: Choo, Kong-Hong Andy
; APPLICANT: Du Sart, Desiree
; APPLICANT: Cancilla, Michael R.
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
; FILE REFERENCE: Davies Col
; CURRENT APPLICATION NUMBER: US/09/078,294
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: BAC-F2 contig 5
US-09-078-294-9

Query Match 4.1%; Score 41; DB 4; Length 1701;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GGTGGCTCACACCTGTATCCACGACTTTGGAGGCTGAG 274
|||||
Db 1390 GGTGGCTCACACCTGTATCCACGACTTTGGAGGCTGAG 1350

RESULT 28

US-09-880-427-2/c
; Sequence 2, Application US/09880427
; Patent No. 6358728
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Elliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/880,427
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 09/306,538
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure

; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-880-427-2

Query Match 4.1%; Score 41; DB 4; Length 6330;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
|||||
Db 3624 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 3584

RESULT 29

US-09-306-538B-2/C
; Sequence 2, Application US/09306538B
; Patent No. 6372463
; GENERAL INFORMATION:
; APPLICANT: Simon, Andras
; APPLICANT: Eriksson, Ulf
; APPLICANT: Dryja, Thaddeus P.
; APPLICANT: Berson, Eliot
; APPLICANT: Yamamoto, Hiroyuji
; TITLE OF INVENTION: Mutations in Nucleic Acid Molecules Encoding 11-Cis Retinol
; TITLE OF INVENTION: Dehydrogenase, The Mutated Proteins, and Uses Thereof
; FILE REFERENCE: LUD 5601
; CURRENT APPLICATION NUMBER: US/09/306,538B
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 6330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5357, 5448
; OTHER INFORMATION: nucleotide not determined
US-09-306-538B-2

Query Match 4.1%; Score 41; DB 4; Length 6330;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
|||||
Db 3624 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 3584

RESULT 30

US-08-646-301A-1
; Sequence 1, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-646-301A-1

Query Match 4.1%; Score 41; DB 4; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 133
|||||
Db 540 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 580

RESULT 31

US-08-481-968A-4
; Sequence 4, Application US/08481968A
; Patent No. 6300490
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Comprising a Carcinoembryonic Antigen (C
; TITLE OF INVENTION: Transcriptional Regulatory Region
; FILE REFERENCE: PB1087US4
; CURRENT APPLICATION NUMBER: US/08/481,968A
; CURRENT FILING DATE: 1998-06-07
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-481-968A-4

Query Match 4.1%; Score 41; DB 4; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 133
|||||
Db 540 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 580

RESULT 32

US-08-154-712B-4
; Sequence 4, Application US/08154712B
; Patent No. 6337209
; GENERAL INFORMATION:
; APPLICANT: Huber, Brian
; APPLICANT: Richards, Cynthia
; TITLE OF INVENTION: Molecular Constructs Containing a Carcinoembryonic Antigen R
; TITLE OF INVENTION: Sequence
; FILE REFERENCE: PB1087US3
; CURRENT APPLICATION NUMBER: US/08/154,712B
; CURRENT FILING DATE: 1993-11-19
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 11288
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-154-712B-4

Query Match 4.1%; Score 41; DB 4; Length 11288;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 133
|||||
Db 540 GCGCGGTGGCTCACGCTGTAATCCAGCAGCTTTAGAAGG 580

RESULT 33

US-09-801-052-3
; Sequence 3, Application US/09801052
; Patent No. 6368842
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001045

; CURRENT APPLICATION NUMBER: US/09/801,052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16063
; TYPE: DNA
; ORGANISM: Human
US-09-801-052-3

Query Match 4.1%; Score 41; DB 4; Length 16063;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 10954 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 10994

RESULT 34
US-09-511-625B-5
; Sequence 5, Application US/09511625B
; Patent No. 6368828
; GENERAL INFORMATION:
; APPLICANT: LaRocheville, William J.
; APPLICANT: Patel, Bhavvin
; APPLICANT: Pierce, Jagalyn H.
; TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT
; TITLE OF INVENTION: CDNAS OF STAT6; STAT6B AND STAT6C
; FILE REFERENCE: 14014.0300ul
; CURRENT APPLICATION NUMBER: US/09/511.625B
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US98/17821
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/070,397
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 60/056,075
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 17425
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e -
; NAME/KEY: misc.feature
; LOCATION: (1)...(17425)
; OTHER INFORMATION: n = a, t, c or g
US-09-511-625B-5

Query Match 4.1%; Score 41; DB 4; Length 17425;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
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Db 11733 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 11773

RESULT 35
US-08-370-975B-1/c
; Sequence 1, Application US/08370975B
; Patent No. 5622851
; GENERAL INFORMATION:
; APPLICANT: Maley, Frank
; APPLICANT: Maley, Gladys F.
; APPLICANT: Weiner, Karen X.B.
; TITLE OF INVENTION: Human Deoxycytidylate Deaminase Gene
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle

; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,975B
; FILING DATE: 10-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20894/80
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716)263-1636
; TELEFAX: (716)263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26764 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 4q35
US-08-370-975B-1

Query Match 4.1%; Score 41; DB 1; Length 26764;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
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Db 24473 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 24433

RESULT 36
US-08-965-048-5/c
; Sequence 5, Application US/08965048
; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freimer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45716
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-965-048-5

Query Match 4.1%; Score 41; DB 4; Length 45716;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
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Db 20736 GTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 20696

RESULT 37
US-08-965-048-6/c
; Sequence 6, Application US/08965048

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; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freimer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-965-048-6

Query Match          4.1%; Score 41; DB 4; Length 45989;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
Db 20850 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 20810

RESULT 38
US-09-784-316-3
; Sequence 3, Application US/09784316
; Patent No. 6461843
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001139
; CURRENT APPLICATION NUMBER: US/09/784,316
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 65042
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(65042)
; OTHER INFORMATION: n = A,T,C or G
US-09-784-316-3

Query Match          4.1%; Score 41; DB 4; Length 65042;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 274
Db 13735 GTGGCTCACACCTGTAATCCAGCAGCTTTGGAGGCTGAG 13775

RESULT 39
US-09-268-992-7/c
; Sequence 7, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
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; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7

Query Match          4.1%; Score 41; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 GTGCGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGC 270
Db 2857 GTGCGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGC 2817

RESULT 40
US-09-657-474-7/c
; Sequence 7, Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 72604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: all n positions
; OTHER INFORMATION: n=a, c, g, or t
US-09-657-474-7

Query Match          4.1%; Score 41; DB 4; Length 72604;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 GTGCGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGC 270
Db 2857 GTGCGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGC 2817

RESULT 41
US-09-741-150-3
; Sequence 3, Application US/09741150
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; Patent No. 6436689
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: US9741.150
; FILE REFERENCE: CLO00968
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112132
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

Query Match      4.1%  Score 41;  DB 4;  Length 112132;
Best Local Similarity 100.0%;  Pred. No. 1.1e-10;
Matches 41;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  234  GGTGGCTCACACCTGTATCCAGCACCTTTGGGAGGCTGAG 274
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Db 105191  GGTGGCTCACACCTGTATCCAGCACCTTTGGGAGGCTGAG 105231

RESULT 42
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-OCT-1996
; ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
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; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20

Query Match      4.1%  Score 41;  DB 2;  Length 246240;
Best Local Similarity 100.0%;  Pred. No. 1.1e-10;
Matches 41;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  234  GGTGGCTCACACCTGTATCCAGCACCTTTGGGAGGCTGAG 274
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Db 7967  GGTGGCTCACACCTGTATCCAGCACCTTTGGGAGGCTGAG 8007

RESULT 43
US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

Query Match      4.1%  Score 41;  DB 2;  Length 246240;
Best Local Similarity 100.0%;  Pred. No. 1.1e-10;
Matches 41;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY  234  GGTGGCTCACACCTGTATCCAGCACCTTTGGGAGGCTGAG 274
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Db 7967 GTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAG 8007

RESULT 44
US-08-724-394A-22
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

Query Match 4.1%; Score 41; DB 2; Length 246240;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 GTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAG 274
|||||
Db 7967 GTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAG 8007

RESULT 45
US-08-474-020A-13/c
; Sequence 13, Application US/08474020A
; Patent No. 5840489
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Leppert, Mark F.
; APPLICANT: Morris, Colleen A.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF SUPRAVALVULAR
```

```
; TITLE OF INVENTION: AORTIC STENOSIS AND WILLIAMS SYNDROME
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Ave., N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,020A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,576
; FILING DATE: 05-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 19780-105509
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4800
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1300 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-474-020A-13

Query Match 4.0%; Score 40; DB 2; Length 1300;
Best Local Similarity 100.0%; Pred. No. 3.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 GTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAG 274
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Db 414 GTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCTGAG 375

Search completed: November 24, 2002, 12:19:13
Job time : 1108 secs
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 08:57:23 ; Search time 101 Seconds
(without alignments)
3749.805 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGTGACCTTATCTCTCT.....CAGAAATGATGACGGCGTGC 1000

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 335578 seqs, 189365133 residues
Total number of hits satisfying chosen parameters: 671156

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Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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2	320.2	32.0	7017	10	US-09-764-877-3773	Sequence 3773, Ap
3	320.2	32.0	20522	10	US-09-764-877-3774	Sequence 3774, Ap
4	307	30.7	17424	10	US-09-967-768A-314	Sequence 314, App
5	301.4	30.1	17424	10	US-09-967-768A-314	Sequence 314, App
6	300.6	30.1	32816	10	US-09-729-094-3	Sequence 3, Appli
7	297.2	29.7	24533	9	US-09-764-868-1349	Sequence 1349, Ap
8	296	29.6	15297	9	US-10-003-295-3	Sequence 3, Appli
9	293.8	29.4	30350	9	US-10-118-328-3	Sequence 3, Appli
10	293.8	29.4	99014	10	US-09-880-107-3428	Sequence 3428, Ap
11	291.6	29.2	52216	10	US-09-747-810-1	Sequence 1, Appli
12	291.2	29.1	40645	10	US-09-818-656A-3	Sequence 3, Appli
13	290.8	29.1	465237	10	US-09-933-267A-1	Sequence 1, Appli
14	289.8	29.0	3273	10	US-09-764-878-363	Sequence 363, App
15	289.8	29.0	3276	10	US-09-764-878-362	Sequence 362, App
16	285	28.5	11617	9	US-09-860-670-265	Sequence 265, App
17	284	28.4	2713	10	US-09-967-736-6	Sequence 6, Appli
18	284	28.4	7720	10	US-09-954-456-946	Sequence 946, App
19	284	28.4	7720	10	US-09-954-456-1589	Sequence 1589, Ap

20	282.2	28.2	16086	10	US-09-764-877-2385	Sequence 2385, Ap
21	281.8	28.2	14176	10	US-09-764-864-1644	Sequence 1644, Ap
22	281	28.1	15016	10	US-09-890-107-3783	Sequence 3783, Ap
23	280.4	28.0	33239	10	US-09-814-950-3	Sequence 3, Appli
24	280.2	28.0	32132	10	US-09-764-877-2308	Sequence 2308, Ap
25	279.6	28.0	53332	10	US-09-801-861-3	Sequence 3, Appli
26	279.2	27.9	31168	9	US-09-764-868-1464	Sequence 1464, Ap
27	279.2	27.9	32193	10	US-09-764-877-2623	Sequence 2623, Ap
28	277.8	27.8	22484	10	US-09-875-114-2	Sequence 2, Appli
29	277.8	27.8	22484	10	US-09-880-107-3341	Sequence 3341, Ap
30	276.6	27.7	16086	10	US-09-764-877-2385	Sequence 2385, Ap
31	276.4	27.6	56737	10	US-09-782-378A-17	Sequence 17, Appl
32	276.4	27.6	84539	10	US-09-962-436-36	Sequence 36, Appl
33	276.2	27.6	145831	10	US-09-969-708-79	Sequence 79, Appl
34	276.2	27.6	145831	10	US-09-954-456-2116	Sequence 2116, Ap
35	275.2	27.5	8701	10	US-09-764-847-1976	Sequence 1976, Ap
36	275.2	27.5	11821	10	US-09-764-877-2857	Sequence 2857, Ap
37	274.6	27.5	63000	10	US-09-780-172-18	Sequence 18, Appl
38	274.4	27.4	32193	10	US-09-764-877-2147	Sequence 2147, Ap
39	274	27.4	4963	10	US-09-764-877-2903	Sequence 2903, Ap
40	273.8	27.4	27359	10	US-09-822-863-3	Sequence 3, Appli
41	272.6	27.3	29629	12	US-10-135-689-3	Sequence 3, Appli
42	272.4	27.2	2892	10	US-09-764-878-197	Sequence 197, App
43	272.4	27.2	15275	10	US-09-764-869-1475	Sequence 1475, Ap
44	272.2	27.2	29695	10	US-09-752-820A-3	Sequence 3, Appli
45	272.2	27.2	29695	10	US-09-813-319A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double

TOPOLOGY: Circular
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: no
IMMEDIATE SOURCE:
CLONE: SL32
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 22
SEQUENCE DESCRIPTION: SEQ ID NO: 32

US-09-784-423-32

Query Match 99.9%; Score 999; DB 10; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.7e-173;
Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTGACCTTATCTCTGACCTCAGTTTCCATCCGTAATAAAGAAAGCTGTAG 60
DB 1 GGTGTGACCTTATCTCTGACCTCAGTTTCCATCCGTAATAAAGAAAGCTGTAG 60

QY 61 ATTGTGTAAAAAATAAATGGAATAGGCTAGGCGGGTGGCTCACGCTGTATATCCCA 120
DB 61 ATTGTGTAAAAAATAAATGGAATAGGCTAGGCGGGTGGCTCACGCTGTATATCCCA 120

QY 121 GCACCTTAGAGTGAAGAGGTGGATCACTGAGGTGAGGAGTTTGAGACACAGCTG 180
DB 121 GCACCTTAGAGTGAAGAGGTGGATCACTGAGGTGAGGAGTTTGAGACACAGCTG 180

QY 181 GCACACGGTGAACCCCATCTCTACTAAAAATAAAAAATAGCTNGGTGCGGTGGCT 240
DB 181 GCACACGGTGAACCCCATCTCTACTAAAAATAAAAAATAGCTNGGTGCGGTGGCT 240

QY 241 CACACCTGTATATCCAGCACCTTTGGAGGCTGAGACGGTGGATCACCCTGAAGTCAGGAG 300
DB 241 CACACCTGTATATCCAGCACCTTTGGAGGCTGAGACGGTGGATCACCCTGAAGTCAGGAG 300

QY 301 TTCAGGCGAGCTGGGCAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATAG 360
DB 301 TTCAGGCGAGCTGGGCAACATGGTGAACACACCTCTCTACTAAAAATAAAAAATAG 360

QY 361 CCAGTGTGGTGGCACACGCTCTAGTCCAGCTACTTGGAGGCTGAGCGGGAAGATC 420
DB 361 CCAGTGTGGTGGCACACGCTCTAGTCCAGCTACTTGGAGGCTGAGCGGGAAGATC 420

QY 421 GCTTGAACCCAGTAGGACAGGTTGCAGTGAAGCGAGATGAGATCAGTCCAGCC 480
DB 421 GCTTGAACCCAGTAGGACAGGTTGCAGTGAAGCGAGATGAGATCAGTCCAGCC 480

QY 481 TGGGTGACAGACAGACCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540
DB 481 TGGGTGACAGACAGACCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540

QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
DB 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600

QY 601 AGTAATAGCTATCAATATCCACCCCTACCTGCTGCTGAAATTTAGTTCTTTTGTG 660
DB 601 AGTAATAGCTATCAATATCCACCCCTACCTGCTGCTGAAATTTAGTTCTTTTGTG 660

QY 661 ACCCCCAATAGCTTAAGCAGAAATTCACCGCTACTCTCTGTAATTTCTGTTCT 720
DB 661 ACCCCCAATAGCTTAAGCAGAAATTCACCGCTACTCTCTGTAATTTCTGTTCT 720

QY 721 GGCACATAGTTGGTCTCAGTGAACATGTTGAGTGAATGAGCAAAATGCAAGGAATCTCC 780
DB 721 GGCACATAGTTGGTCTCAGTGAACATGTTGAGTGAATGAGCAAAATGCAAGGAATCTCC 780

QY 781 AGCCCATCTGGAGCCCTCCAGCGGGTGAGTTGCGGAACTCATAGTCTGTCTCAAT 840
DB 781 AGCCCATCTGGAGCCCTCCAGCGGGTGAGTTGCGGAACTCATAGTCTGTCTCAAT 840

QY 841 GGCACCTGAAGCTAGAGATTTCTGGTCCACCTCCACCCCTCCCTCCCTGACTCAC 900
DB 841 GGCACCTGAAGCTAGAGATTTCTGGTCCACCTCCACCCCTCCCTCCCTGACTCAC 900

QY 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
DB 901 TGCTGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960

QY 961 CAGGACTCAGAGGAGCCGACGAGATGATGACCGGGCTGC 1000
DB 961 CAGGACTCAGAGGAGCCGACGAGATGATGACCGGGCTGC 1000

RESULT 2

US-09-764-877-3773/c
; Sequence 3773, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 3773
; LENGTH: 7017
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3773

Query Match 32.0%; Score 320.2; DB 10; Length 7017;

Best Local Similarity 84.6%; Pred. No. 4.1e-50;
Matches 406; Conservative 0; Mismatches 69; Indels 5; Gaps 4;

QY 86 TAGGCTAGGCGGGTGGCTCACGCTGTAAATCCGACGACCTTTAGAGGTCCGAAGGGGTG 145
DB 4509 TGGGCCAGACGGGTGGCTCACACCTGTATCCGACGACCTTTGGAAGCGCGGGGTG 4450

QY 146 GATCAGCTTGTAGGTGAGGAGTTTGTGACCCAGCTGGCCACACGGTGAACCCCATCTCT 205
DB 4449 GATCAGCTGAGACAGAGAG-TTCGAGACCGCTGGCCACATGGTGAACCTCGTCTCT 4391

QY 206 ACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 265
DB 4390 ACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4331

QY 266 GAGGCTGAGACGGGTGGATCACCTGAAGTTCAGAGGAGTTCAAGGCCAGCTGGGCAACATGG 325
DB 4330 GAGGCCAAGCGCGGACAGATCA--TGAGGTGAGAGATGGAGACCATCTCTGCTTAACATGG 4273

QY 326 TGAACACCGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 385
DB 4272 TGAACACCGCTCTCTACTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4213

QY 386 GTCCAGCTACTTGGAGGCTGAGCGGGAAGATCGCTTGAACCCAGTAGGACAGAGGTG 445
DB 4212 GTCCAGCTACTTGGAGGCTGAGCGGAGAGATAGCTTGAACCCAGTAGGAGGTG 4153

QY 446 CAGTGAAGCGGAGATGAAGTCACTGCACCTCCAGCTGGGTGACAGAGCAAGACTCCCTCT 505
DB 4152 CAGTGAAGCGGAGATCA-CGACACTGCACCTCCAGCTGGGCAACAGAGGAGAAATCCGTCT 4094

QY 506 CAGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 565
DB 4093 CA-AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 4035

RESULT 3

US-09-764-877-3774/c
; Sequence 3774, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

Db 69715 AAAACAAAAAATTTTCAGCGCGGCATGGTGGCTCAGCGCTGTAATCCCAAGCACTTTGG 69774
QY 130 AAGCTCGAGAGGGTGGATCACTTTGAGGTCAGGAGCTTTGAGCAGCAGCTGGCCAAACAG 189
Db 69775 GAGGCTGAGGCAAGCAGATCACTGAAGTCAGGAG-TTCGAGACAAGCCTGGCCACATG 69833
QY 190 GTGAACCCCATCTCTACTAAAAATAAAAAATTA---GCTNGGGTGCGGTGGCTCAACC 246
Db 69834 GTGAACCCCTGTCTCTACTAAAAATAAAAAATAAAGGGTCGGCCACGCTGGCCACACC 69893
QY 247 TGTATATCCAGCACTTTGGGAGGCTGAGACGGGTGGATCACTCACTGAAGTCAGGAGTTCAAG 306
Db 69894 TGTATATCCAGCACTTTGGGAGGCGGAGGAGGATCACTTGAGTCAAGAGTTCAAG 69953
QY 307 GTCAGCTGGGCAACATGTCGAACCACTGCTCTACTAAAAATAAAAAATAAATTAAGCAGGT 366
Db 69954 ACCAGCTGGACAAATGATGTAACCCCTGTCTCTACTTAATAATCAAAAAATCAGCAGGC 70013
QY 367 GTGGTGGCACACGCCCTGTAGTCCAGCTACTTTGGAGGCTGAGCGGGAAGATCGCTTGA 426
Db 70014 GTGGTGGCGGCACCTGTAGTCCAGCTACTTCAGGAGGCTGAGCAGAGAAATGCTTGA 70073
QY 427 ACCAGTAGCAGAGTTGCACTGAGCGGAGATAGAGTCACTGCACCTCCAGCCTGGGTG 486
Db 70074 ACCTGGAGGAGCAGAGTTGCACTGAGCGGAGCAT-TGCGCCACTGCACCTAGCCTGGGCG 70132
QY 487 ACAGAGCAAGACTCCCTCTCTCAGAAAAATAAAAAATAAAAAATAAAAAATAAAAA 546
Db 70133 ACAGAGAAAGTCTCTCAGAAAAATAA---TAATAATAATAATAATAATAATAATA 70190
QY 547 ATAAAA 552
Db 70191 TAAAAA 70196

RESULT 6
US-09-729-094-3
; Sequence 3, Application US/09729094
; Patent No. US2002019028A1
; GENERAL INFORMATION:
; APPLICANT: CHATURVEDI, Kabir et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL000662
; CURRENT APPLICATION NUMBER: US/09/729,094
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 32816
; TYPE: DNA
; ORGANISM: Human
US-09-729-094-3

Query Match 30.1%; Score 300.6; DB 10; Length 32816;
Best Local Similarity 80.3%; Pred. No. 1.7e-46;
Matches 376; Conservative 0; Mismatches 90; Indels 2; Gaps 2;
QY 85 ATAGCTAGGCGGTGGCTCAGCGCTGTAATCCAGCACTTTAGAGGTCGAAGAGGT 144
Db 16124 ACAGCGCGGCGGCTGAGCTCAGCTGTAATCCCAACATTTTGGAGGCGGAGTGGGC 16183
QY 145 GATCACTTTAGGTCAGGAGTTTTCAGACCAAGCCTGGCCAAACAGGTCGAACCCCATCTC 204
Db 16184 AGATCCCTGAGTCAGGAG-TTTTGAACCAAGCCTGGCCAAACAGTGTGAACCCCATCTC 16242
QY 205 TACTAAAAATAAAAAATAGCTNGGGTGGCTGGCTCAACCTGTAAATCCAGCACTTTG 264
Db 16243 TACTAAAAATAAAAAATAGCGGGCGTGGTAGCCCAAGCCTGAAATCCAGCACTTTG 16302
QY 265 GGAGGCTGAGCGGTGGATCACTGAGTCAGGAGTTCAAGCGCAGCCTGGGCAACATG 324

Db 16303 GGAGGCCAAGAGGGCGGATCCCTGAGGTCAGAGCTCGAGACCAGCCTGGCCACATG 16362
QY 325 GTCAAAACCACTCTCTACTAAAAATAACAAAAATAGCAGAGTGGTGGCACAACGCTGT 384
Db 16363 GTGAACCCCATCTCTACTAAAAATAACAAAAATAGTGGCATGTGGCACAATGCTGT 16422
QY 385 AOTCCCACTACTTTGGAGGCTGAGCGGAGGAATCGCTTGAACCCAGTAGCAGAGTT 444
Db 16423 AACCCCACTACTTTGGAGGCTGAGCGAGGAAATTTGCTTGAAGCCGGGAGGTAGAGTT 16482
QY 445 GCAGTAGCCGATAGAGTCACTTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCCTC 504
Db 16483 GCAGTAACCAAGTCA-TGCCACTGCACTCCAGCCTGGCGCAGCAGCAAGACTCTGC 16541
QY 505 TCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 552
Db 16542 TCAAAACAAAAAAGTTGCTATACATATTCAAAACAATCAATAA 16589

RESULT 7
US-09-764-868-1349/c
; Sequence 1349, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ32
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1349
; LENGTH: 24533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1349

Query Match 29.7%; Score 297.2; DB 9; Length 24533;
Best Local Similarity 80.0%; Pred. No. 6.9e-46;
Matches 399; Conservative 0; Mismatches 94; Indels 6; Gaps 4;
QY 56 TGTAAAAAATAAATGATAGGTAGCGGTGGCTCAGCGCTGTAATCCAGCACT 125
Db 6364 TGTCTCAAAATAAATAAATAGCGCGGTGGTGGCGGTGCTGTATCCAGCACT 6305
QY 126 TTAGAAGGTCGAAGAGGTTGGATCACTTGAGGTCAGGAGTTTGAACCAAGCCTGGCCAA 185
Db 6304 TTGAGAGCGCGAGGCGGTGGATCACTGAGGTCGGAG-TTAGAGACCAAGCCTGACCAA 6246
QY 186 CAGCGTGAACCCCATCTCTACTAAAAATAAATAAATAAATAGCTNGGTCGGTGCACAC 245
Db 6245 CATGGAGAACCCCGTCTCTACTAAAAATAAACAATTAGCCAGCGCT--GGTGGCAGATGC 6186
QY 246 CTGTAATCCAGCACTTTGGAGGCTGAGACGGGTGGATCACTGAGTCAGGAGTCAAGTCAAG 305
Db 6187 CTGTAATCCAGCACTTTGAGAGCGCGGCGGTGGATCACTGAGTCGGAGTTAGA 6128
QY 306 GGCCAGCCTGGCCACATGTTGAACCAAGCTCTCTACTAAAAATAAATAAATAAATAGCCAG 365
Db 6127 GACCAGCCTGACCAACATGAGAGAACCCCGTCTCTACTAAAA--TACAACATAGCCAGG 6070
QY 366 TGTGTGGCAGACGCGCTGTAGTCCAGCTACTTTGGAGGCTGAGCGCAAGAAATCGCTTG 425
Db 6069 CGTGTGGCGGTCGCTGTATCCAGCTACTCCAGAGGCTGAGCAGATGATTCGCTTG 6010
QY 426 AACCCAGTAGGAGGTTGCACTGAGCGGAGATAAGAGTCACTGCACTCCAGCCTGGT 485
Db 6009 AACCCGGAGCGGAGGTTGCACTGAGCGGAGAT-TCCGCCATTCGACTCCAGCCTAGGC 5951
QY 486 GACAGCAAGACTCCCTCTCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAA 545
Db 5950 AAGAGTGAGACTCCGTTTCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5891

```
QY 546 AATAAAATAAAATCTAAA 564
|||||
Db 5890 AATAAAATAAAATAAAAA 5872

RESULT 8
US-10-003-295-3
; Sequence 3, Application US/10003295
; Patent No. US20020168741A1
; GENERAL INFORMATION:
; APPLICANT: GAN, Weinliu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001183D1V
; CURRENT APPLICATION NUMBER: US/10/003,295
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Homo sapiens
us-10-003-295-3

Query Match 29.6%; Score 296; DB 9; Length 15297;
Best Local Similarity 83.4%; Pred. No. 1,1e-45;
Matches 371; Conservative 0; Mismatches 71; Indels 3; Gaps 3;

QY 97 CGGTGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTGTCAGAGGGTGGATCATTGAG 156
|||||
Db 11700 CAGTTGCTCAGCGCTGTCATCCCGACACTTTGGGAGGCTGAGCTGGGTGATCATTGAG 11759
|||||

QY 157 GTCAGAGTTTGTAGACCGAGCTGCCAACACGGTGAACCCCATCTCTACTAAAAATAA 216
|||||
Db 11760 CCAGGAG-TTCAAGATFCAGCTTGGACAACACAGACTGAACTCTGTACAAAAATAC 11818
|||||

QY 217 AAAATTAGTNGGTGGGTGGCTCAGACCTGTAAATCCCGACACTTTGGGAGGCTCAGAC 276
|||||
Db 11819 AAAATAGACTGGCAGCGTGGCTCAGACCTGTAAATCCCGACACTTTGGGAGGCTCAGAC 11878
|||||

QY 277 GGTGGTCACTGAGTCAAGGAGTTCAAGCCAGCTTGGGCAACATGGTGAACCAAGT 336
|||||
Db 11879 AGTGGATCAGCTGTGTCAGGAGTTTGAGACCAGCAGCAACATGGTGAACCCCAT 11938
|||||

QY 337 CTTCTACTAAATAACAAAAATTAGCCAGGTTGGTGGCAGCGCTGTAGTCCAGCTAC 396
|||||
Db 11939 CTTCTACTAAATAACAAAAATTAGCCAGGCTGTGGCAGCTGTAGTCCAGCTAC 11998
|||||

QY 397 TTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCAGTAGGCGAGAGTTGCGAGTGAGCCGA 456
|||||
Db 11999 TTGGGAGGCTGAGGTGGAGAAATTCCTTGAACCCAGTAGGCGAGGCTGCGAGTGAGCCGA 12058
|||||

QY 457 GATAAGACTACTGCTCCAGCTGGGTGAC-AGAGCAAGACTCCCTCTCAGAAAAATAA 515
|||||
Db 12059 GAT-TGTGCCACTGCTCCAGCTGGGCGACAGAGTGAACCTCCATCTCAAAAAAATC 12117
|||||

QY 516 AATAAAATAAAATAAAATAA 540
|||||
Db 12118 CAAAAACAAAAATACAAAAATTA 12142

RESULT 9
US-10-118-328-3
; Sequence 3, Application US/10118328
; Patent No. US20020169289A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001220
```

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; CURRENT APPLICATION NUMBER: US/10/118,328
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 30350
; TYPE: DNA
; ORGANISM: Homo sapiens
us-10-118-328-3

Query Match 29.4%; Score 293.8; DB 9; Length 30350;
Best Local Similarity 79.0%; Pred. No. 2.9e-45;
Matches 411; Conservative 0; Mismatches 103; Indels 6; Gaps 5;

QY 40 CGTAAATGAAAGCTGCTAGATTGTTGTAATAAAATTAATGAATGAGCTAGGCTAGCGCGG 99
|||||
Db 25097 CGGACAAAGTGACAGAAGGAGTGTCTGACCTCAATTTGTAGGATGGCTGGGCATGG 25156
|||||

QY 100 TGGCTCAGCGCTGTAATCCCGACACTTTAGAGGTGCAAGAGGGTGGATCATTGAGGTC 159
|||||
Db 25157 TGGCTCAGAACTGTAATCCCGACACTTTGGGAGGTCAAGGTGGTGGATTTGCTGAGCTC 25216
|||||

QY 160 AGGAGTTTGGAGACCGAGCTGGCCAAACCGGTGAACCCCATCTCTACTAAAAATAAAAA 219
|||||
Db 25217 AGGAG-TTTGAGACCGAGCTGGGCAACATGAGAGACCCCATCTATACAAAAATAGAGA 25275
|||||

QY 220 ATTAGTNGGTGGGTGGCTGCTC-ACACCTGTAAATCCCGACACTTTGGGAGGCTGAGACGG 278
|||||
Db 25276 AATTGGTGGGTGGCTGCTCAACGCTGTAAATCCCGGACACTTTGGGAGGCCAAAGCGG 25335
|||||

QY 279 GTGATCACTCAAGTCAAGGAGTTCAGGCCAGCTGGGCAACATGGTGAACCAACCGCTCT 338
|||||
Db 25336 GTGATCACTTGAAGTTCAGGAGTTCGAGACCGCTGGCCAAACATGGTGAACCCCGCTCT 25395
|||||

QY 339 CTACTAAAAATAC--AAAAATTAGCCAGGTGTGGTGGCAGACCCCTGTAGTCCAGCTAC 396
|||||
Db 25396 CTACTAAAAATACAAAAAATTAGCTGGCATGGTGGCAGCATGCCGTAGTCTCAGCTAC 25455
|||||

QY 397 TTGGGAGGCTGAGCGGGAAGAAATCGCTTGAACCCAGTAGGCGAGGTTGCGAGTGAGCCGA 456
|||||
Db 25456 TCGGAGGCTGAGGCGAGAAGAAATCGCTTGAACCCAGGAGCGGAGTTGCGAGTGAGCCGA 25515
|||||

QY 457 GATAAGACTCACTGACCTCCAGCTGGGTGACAGAGCAAGCACTCCCTCTCAGAAAAATAA 516
|||||
Db 25516 GAT-CGACCACTGACCTCCAGCT-GGCGACTGAGCAAGCACTCTCTCAAAAAAATAA 25573
|||||

QY 517 AATAAAATAAAATAAAATAAAATAAAATAAAATAAA 556
|||||
Db 25574 AAAAAAATAAAAAAATAAAATAAAATAAAATAAAATAA 25613
|||||

RESULT 10
US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherif, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3428
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; LENGTH: 99014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match      29.4%; Score 293.8; DB 10; Length 99014;
Best Local Similarity 83.8%; Pred. No. 3.3e-45;
Matches 367; Conservative 0; Mismatches 68; Indels 3; Gaps 3;

QY 87 AGGCTAGGCGCGGTGCTCAGCGCTGTAAATCCAGCACTTTAGAAAGTCGAGAGGGTGG 146
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68994 AGGCTGGCTGGTGTGATGCTCTTAATCCAGCACTTTGGAGGCGGAGGTGGCGG 68935
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 147 ATCACTTAGGTCAGAGTTTGGAGCCAGCGCTGGCCAAACACAGCGTGAAACCCCATCTCTA 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68934 ATCACTTAGGCGCAGGAG-TTCGAGATCAGCGCTGTCAACATGGCGAATGCCATCTCTA 68876
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 207 CTAAAAATAAAATTAAGCTNGGTGGTGGCTCACACCTGTAAATCCAGCACTTTGGG 266
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68875 CTAAAAATAAAATTTGCCAGGCT-CAGTGGCTCAGCGCTGTAAATCCAGCACTTTGGG 68817
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 267 AGGCTGAGAGCGGTGATCACTCAAGTCAGGAGTCAAGGCCAGCGCTGGGCAACATGGT 326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68816 AGGCCGAGGTGGTGGATCACTTGAAGTCAAGGAGTCAAGCGCTGGGCAACATGGT 68757
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 327 GAAACCACTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGGCACACGCTGTAG 386
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68756 GAAATGCTGCTCTACTAAATGCAAAATTAAGCTGGCACGCTGGCATGTGCTGTAG 68697
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 387 TCCAGCTACTTGGAGCTGAGCGGGAAGAAATCGCTTGAACCCAGTAGGAGAGGTGTC 446
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68696 TCCAGCTACTCGGAGGCTAAGCCAGGAGAAATCACTTGAACCCAGTAGGAGAGGTGTC 68637
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 447 AGTGAGCGAGATAAGTCACTCACTCCAGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 506
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68636 AGTGAGCGAAAT-CGTCCACTGCACTCCAGCGCTGGTGGTGGTGGTGGTGGTGGTGG 68578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 507 AGAAAAATAAAATA 524
    ||||| ||||| |||||
Db 68577 CAAAAAATAAAAAA 68560
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RESULT 11
US-09-747-810-1
; Sequence 1, Application US/09747810
; Patent No. US20020012903A1
; GENERAL INFORMATION:
; APPLICANT: Goldman, Steven A.
; APPLICANT: Okano, Hideyuki
; TITLE OF INVENTION: A METHOD FOR ISOLATING AND PURIFYING MULTIPOTENTIAL NEURAL PROGEN
; TITLE OF INVENTION: CELLS AND MULTIPOTENTIAL NEURAL PROGENITOR CELLS
; FILE REFERENCE: 19603/3580
; CURRENT APPLICATION NUMBER: US/09/747,810
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/173,003
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 52216
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-747-810-1

Query Match      29.2%; Score 291.6; DB 10; Length 52216;
Best Local Similarity 81.8%; Pred. No. 7.7e-45;
Matches 372; Conservative 0; Mismatches 80; Indels 3; Gaps 3;

QY 74 AATTAATGAATAGGCTAGCGCGTGGCTCAGCGCTGTAAATCCAGCACTTTAGAAGG 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35542 AAAAAATGAATAGGCTGGGCACAGTGTCTCATGCTGTAAATCCAGCACTTTAGAAGG 35601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 134 TCAGAGAGGGTGGATCACTTGAGTCAAGAGTTTTCAGACACAGCCTGCCAACACGGTGA 193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35602 CTGAGTGGTGGATCACTTGAGGCGAGGAG-TTCAGGCCAGCCTGGCCAATACGGTGA 35660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 194 AACCCCATCTCTACTAAAAATA-AAAAATTAGCTNGGTGGTGGTGGTGGTGGTGGTGGT 252
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35661 AGCCAGCTCTCTCTAAAAATAACAAAAATTAGCCGGGAGCAGTAGTGGCACGCACTGCAAT 35720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 253 CCAGCACTTTGGGAGGCTGAGACGGGTGGATCACTGAAGTCAGGAGTTCAAGGCCAGC 312
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35721 CCAGCACTTTGGGAGTCTGAGCGGCGGAATCACTGAGGTGAGGATTCGAGGCCAGC 35780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 313 CTGGGCAACATGCTGCAACACAGCTCTCTACTAAAAATAACAAAAATTAGCCAGGTGGTG 372
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35781 CTGGGCAACATGCTGCAACACAGCTCTCTACTAAAAATAACAAAAATTAGCTGGCATGGTG 35840
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 373 GCACAGCGCTCTAGTCCAGCTACTTTGGGAGGCTGAGGCGGGAAGAAATCGTTGAACCCAG 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35841 GCGTGTGCTCTAATCCAGCTACTTTGGGAGGCTGGGCGAGGAGAAATCTCTTGAACCCAG 35900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 433 TAGGCAGAGGTGTCAGTGAAGCGGAGATAAGAGTCACTGCTCACTGCCAGCTGGGTGACAGAG 492
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35901 GAGGCAGAGGTGTCAGTGAAGCGGAGAT-TGCACCACTGCGCTTCCAACTGGGCCACAGAG 35959
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 493 CAAGACTCCCTCTCAGAAAAATAAAATAAAAA 527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35960 TGAGACTCCATCTCAAAAAAATAAAAAA 35994
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-818-656A-3/c
; Sequence 3, Application US/09818656A
; Patent No. US20020142381A1
; GENERAL INFORMATION:
; APPLICANT: GONG, Pangcheng et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: CL001191
; CURRENT APPLICATION NUMBER: US/09/818,656A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 40645
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-818-656A-3

Query Match      29.1%; Score 291.2; DB 10; Length 40645;
Best Local Similarity 80.6%; Pred. No. 8.9e-45;
Matches 402; Conservative 0; Mismatches 89; Indels 8; Gaps 5;

QY 69 AAAAAAATAAATTAAGTAAGCTAGGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16379 AAAAAAATAAAGTAAGTAAGCTAGGCGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 16320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 129 GAAGTCGAGAGGGTGGATCACTTGAGGTCAAGGATTTTGAGACACAGCTGGCCAAACAC 188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16319 GGAGGCCAAGCGCAGATAC--GAGGTCAAGAG-ATCAGAGACCATCTCTGGCCAAAT 16263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 189 GGTGAACCCCATCTCTACTAAAAATAAAAAATTAGCTNGGTGGTGGTGGTGGTGGTGGT 248
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16262 GGTGAACCCCATCTCTAGTAAAAATAACAAAAATTAGCTGGGCGGTGGTCAAGCCTG 16203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 249 TAATCCAGCACTTTGGGAGGCTGAGACGGGTGGATCACTTGAAGTCAGAGTTCAGAGC 308
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16202 TAATCCAGCACTTTGGGAGGCTGAGGCGGTGGATCA--TCAGGTCAAGATTCAGAGC 16145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 309 CAGCTGGGCAACATGGTGAACACCACTCTCTACTAAAAATACAAAAAATAGC--AAAAATTAGCCAGGT 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16144 CATCTGGCTAACACAGTGAACCCCATCTCTACTAAAAAATACAAAAAATTAGCCGGGT 16085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 367 GTGGTGGACACGCGCTGTAGTCCAGCTACTTGGGAGGCTGAGCGGAGAAATCGCTTGA 426
Db 16084 GTGGTGGTGGTGGCTTATAGTCCAGCTACTTGGGAGGCTGAGGAGGAGATGCGGTGA 16025
QY 427 ACCAGTAGGACAGAGGTTGCACTGAGCGGAGATAGAGTCACTCCAGCTCCAGCTGGGTG 486
Db 16024 ACCAGTAGGCGGAGGTTGCACTGAGCGGAGAT-TGTGCCACTCAATCCAGCTGGGTG 15966
QY 487 ACAGAGCAAGACTCCCTCTCAGAAAAATAAAATAAAATAAAATAAAATAAAATAAA 546
Db 15965 ACAGAGCAAGACTCCATCTCAAAAAATAAAAGTAAATAAAATAAAATAAAATAAA 15906
QY 547 ATAAAAATAAAATCTTAAAA 565
Db 15905 AATAAAATAAAATAAAATAAA 15887
RESULT 13
US-09-933-267A-1/c
; Sequence 1, Application US/09933267A
; Patent No. US20020123095A1
; GENERAL INFORMATION:
; APPLICANT: Kalush, Francis et al.
; TITLE OF INVENTION: Estrogen receptor alpha variants and
; TITLE OF INVENTION: methods of detection thereof
; FILE REFERENCE: CL000258C14
; CURRENT APPLICATION NUMBER: US/09/933,267A
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/160626
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 60/183756
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/692414
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/768184
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 09/804076
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: 09/826314
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 465237
; TYPE: DNA
; ORGANISM: human
US-09-933-267A-1

Query Match 29.1%; Score 290.8; DB 10; Length 465237;
Best Local Similarity 81.3%; Pred. No. 1.3e-44;
Matches 373; Conservative 0; Mismatches 83; Indels 3; Gaps 3;
QY 78 AATGGAATAGGTAGCGGGTGGCTCAGCGCTGTATCCAGCACTTTAGAGGTGCA 137
Db 35056 AAAAGGTTTAGGGGGGATGGTGGCTCAGCGCTGTATCCAGCACTCTCGGAGGCCGA 34997
QY 138 AGAGGTGATCACTTGAGTCAAGAGTTTGAGACACAGCGCTGGCCACACAGGTGAACCC 197
Db 34996 GGTGGTGGATCACTGAGGTCAAGAGT-TCAAGACACAGGATGGCCACATGTTGAACCC 34938
QY 198 GCATCTCTACTAAAAATA-AAAAATTAGTCTGGGTGGCTCACACCTGTAATCCCA 256
Db 34937 TCGTCTCTATTAAAAATACAAAAAATGACCTGGCGAGTGGCTCACGCTGTATCCCA 34878
QY 257 GCATTTGGAGGCTGAGACGGGTGGATCACTGAAGTCAAGGATTCAGGCCAGCGCTGG 316
Db 34877 GCATTTGGAGGCGGAGGAGTGGATCACTGAGTCAAGAGTTTGAACACGCTGG 34818
QY 317 GCACATGTTGAACACGCTCTCTACTAAAAATAACAAAAATTAGCCAGGTGTGTGGCAC 376
Db 34817 CCAACATGCGAAACCCCGACTCTCTAACATAACAAAAATTAGTGGCACGCTGGAT 34758
QY 377 ACCGCTGTAGTCCCGAGTCTTGGAGGCTGAGCGCGGAGAAATCGCTTGAACCCAGTAGG 436

Db 34757 GTGCTGTATCCAGCTACTAGGAGGCTGAGCGAGGAAATCGCTGGAACCTTGAAGG 34698
QY 437 CAGAGTTCCAGTGGAGCGGAGATAGAGTCACTCCAGCTCCAGCTGGGTGACAGAGCAAG 496
Db 34697 CAGAGTCACTAGTGGAGCAAGAT-GGTGCCACTCACTCCAGCTGGGCAACAGAGCAAG 34639
QY 497 ACTCCCTCTCAGAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 535
Db 34638 ACTCCCTCTCAAAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 34600

RESULT 14
US-09-764-878-363
; Sequence 363, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA121
; CURRENT APPLICATION NUMBER: US/09/764,878
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 363
; LENGTH: 3273
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-363

Query Match 29.0%; Score 289.8; DB 10; Length 3273;
Best Local Similarity 84.5%; Pred. No. 1.3e-44;
Matches 372; Conservative 0; Mismatches 63; Indels 5; Gaps 4;
QY 88 GGCTAGGCGCGGTGGCTCAGCGCTGTATCCAGCACTTTAGAGGTGCAAGAGGTGGA 147
Db 2686 GGCCAGGCGCGGTAGTCTACGCGCTGTATCCAGCACTTTGGAGGCTGAGAGGCGCGGA 2745
QY 148 TCACTTGAGTCAAGAGTTTTCAGACAGCGCTGGCCACACAGCGTGAACCCACTCTAC 207
Db 2746 TCACTTGAGTCAAGAGTTT-GAGACAGCGCTGGCCACACATGGTGAACCTCTCTAT 2804
QY 208 TAAAAATAAAAAATTAGCTNGGTCGGTGGCTCAGCTGTATATCCAGCACTTTGGGA 267
Db 2805 TAAAAATAAAAAATAAGCGCGCGGTGGCTCAAGCTGTATATCCAGCACTTTGGGA 2864
QY 268 GGCTGAGACGGGTGGATCACTGAAGTCAAGGAGTTCAGGGCAGCGCTGGGCAACATGTG 327
Db 2865 GGCCAGGCGCGCGGATCAC--GAGGTCAAGAGATCGAGACCTTCCTGGCTAACAGGTG 2922
QY 328 AAACCACTCTCTACTAAAAATAC-AAAAATTAGCAGGTGTGGTGGCACAGCGCTGTAG 386
Db 2923 AAACCCATCTCTACTAAAAATAACAAAAATTAGCGGCGGTGGTGGCGGCGCTGTAA 2982
QY 387 TCCCAAGTCTCTGGAGGCTGAGCGGAGAAATTCGCTTGAACCCAGTTCAGAGAGGTTC 446
Db 2983 TCCCAAGTCTCTGGAGGCTGAGCGGAGAAATGGCGTGAACCCAGGAGGCGGAGTTCG 3042
QY 447 AGTGAGCGGAGATAGAGTCACTGCATCCAGCGTGGGTGACAGAGAGAGAGTCCCTCTC 506
Db 3043 AGTGAGCGGAGAT-AGCGCACTGCATCCAGCGTGGCGGAGAGAGTGGAGACTCCCTCTC 3101
QY 507 AGAAAAATAAAATAAAATAAA 526
Db 3102 CAAAAATAAAATAAAATAAA 3121

RESULT 15
US-09-764-878-362
; Sequence 362, Application US/09764878
; Patent No. US20020090615A1
; GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 07:40:52 ; Search time 71 Seconds
(without alignments)
4319.391 Million cell updates/sec

Title: US-09-784-423-32
Perfect score: 1000
Sequence: 1 GGTGACCTTACCTCTCT.....CAGATGATGACGGCGTGC 1000

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	999	99.9	1000	US-09-018-584A-32	Sequence 32, Appl
2	296	29.6	15297	US-09-817-180-3	Sequence 3, Appl
3	284	28.4	2713	US-08-916-901-6	Sequence 6, Appl
4	284	28.4	2713	US-09-154-602-6	Sequence 6, Appl
5	284	28.4	7720	US-09-318-448-5	Sequence 5, Appl
6	277.8	27.8	7210	US-08-257-963B-10	Sequence 10, Appl
7	277.8	27.8	7210	US-08-367-841A-10	Sequence 10, Appl
8	277.8	27.8	7210	US-08-367-841A-10	Sequence 10, Appl
9	277.8	27.8	14581	PCT-US95-07201-10	Sequence 10, Appl
10	277.8	27.8	22481	US-08-520-373D-4	Sequence 4, Appl
11	277.8	27.8	22481	US-08-367-841A-43	Sequence 43, Appl
12	277.8	27.8	22484	US-09-875-223-2	Sequence 43, Appl
13	275.6	27.6	112132	US-09-875-223-2	Sequence 2, Appl
14	272.6	27.3	29629	US-09-729-995-3	Sequence 3, Appl
15	271.4	27.1	62804	US-09-800-960-3	Sequence 3, Appl
16	269.6	27.0	59065	US-09-813-817-3	Sequence 3, Appl
17	269.6	27.0	59065	US-09-978-197-3	Sequence 3, Appl
18	267.4	26.7	14581	US-08-520-373D-4	Sequence 4, Appl
19	266.6	26.7	17327	US-07-906-871-15	Sequence 15, Appl
20	265.8	26.6	7210	US-08-257-963B-10	Sequence 10, Appl
21	265.8	26.6	7210	US-08-367-841A-10	Sequence 10, Appl
22	265.8	26.6	7210	US-08-367-841A-10	Sequence 10, Appl
23	265.8	26.6	22481	PCT-US95-07201-10	Sequence 10, Appl
24	265.8	26.6	22481	US-08-367-841A-43	Sequence 43, Appl
25	265.8	26.6	22484	US-09-875-223-2	Sequence 43, Appl
26	263.8	26.4	3267	US-08-257-963B-12	Sequence 12, Appl
27	263.8	26.4	3267	US-08-367-841A-12	Sequence 12, Appl

c 28 263.8 26.4 3267 5 PCT-US95-07201-12
c 29 263.8 26.4 5282 4 US-08-520-373D-5
c 30 262.8 26.3 10380 4 US-09-077-354B-3
c 31 261 26.1 16389 4 US-09-741-154-3
c 32 258.6 25.9 162450 4 US-09-345-882-1
c 33 258.6 25.9 246240 2 US-08-724-394A-20
c 34 258.6 25.9 246240 2 US-08-724-394A-21
c 35 258.6 25.9 246240 2 US-08-724-394A-22
c 36 257 25.7 10684 3 US-08-618-100B-3
c 37 256.6 25.7 1363 1 US-08-776-088-21
c 38 256.6 25.7 1363 5 PCT-US95-09145A-21
c 39 256.2 25.6 53526 3 US-08-658-136-2
c 40 256.2 25.6 53577 3 US-08-658-136-1
c 41 253.6 25.4 4192 4 US-09-122-128B-1
c 42 253.2 25.3 162450 4 US-09-345-882-1
c 43 249.4 24.9 11811 4 US-09-078-294-7
c 44 248.4 24.8 59065 4 US-09-813-817-3
c 45 248.4 24.8 59065 4 US-09-978-197-3

ALIGNMENTS

RESULT 1

US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: SI32
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; US-09-018-584A-32

Query Match 99.9%; Score 999; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.4e-217;

Matches 1000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGACCTTATCTCTGAACTCAGTTTCCTCATCCGTAAATGAAAGCTGTAG 60
Db 1 GGTGGACCTTATCTCTGAACTCAGTTTCCTCATCCGTAAATGAAAGCTGTAG 60

QY 61 ATTGTTGTAATAAATAAATGAAATAGGCTAGGCGGGTGGCTCAGCGCTGTAAATCCCA 120
Db 61 ATTGTTGTAATAAATAAATGAAATAGGCTAGGCGGGTGGCTCAGCGCTGTAAATCCCA 120

QY 121 GCATTTAGAGTCCGAGAGGGTGGATCACTTGAGGTGAGGTTTGGAGACCAAGCTG 180
Db 121 GCATTTAGAGTCCGAGAGGGTGGATCACTTGAGGTGAGGTTTGGAGACCAAGCTG 180

QY 181 GCCAACCGGTGAAACCCCATCTCTACTATAAATAAATAAATAGCTNGGTCGGTGCT 240
Db 181 GCCAACCGGTGAAACCCCATCTCTACTATAAATAAATAAATAGCTNGGTCGGTGCT 240

QY 241 CACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTGGATCACTGAAAGTCAGAG 300
Db 241 CACACCTGTATCCAGCAGCTTTGGAGGCTGAGACGGGTGGATCACTGAAAGTCAGAG 300

QY 301 TTCAGGCCAGCTGGGCAACATGGTGAACACACGTCTCTACTATAAATAAATAAATAG 360
Db 301 TTCAGGCCAGCTGGGCAACATGGTGAACACACGTCTCTACTATAAATAAATAAATAG 360

QY 361 CCAGGTGTGGTGGCACAGCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 420
Db 361 CCAGGTGTGGTGGCACAGCTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 420

QY 421 GCTTGAACCCAGTAGGAGAGTTGCGAGTACCGAGATAGAGTCACTGCACTCCAGCC 480
Db 421 GCTTGAACCCAGTAGGAGAGTTGCGAGTACCGAGATAGAGTCACTGCACTCCAGCC 480

QY 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540
Db 481 TGGGTGACAGAGCAAGACTCCCTCTCAGAAATAAATAAATAAATAAATAAATAA 540

QY 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600
Db 541 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 600

QY 601 AGTAAAGTATCAATATCCCAACCTTACACACTGTCTGCTGAAATTTAGTTTCTT 660
Db 601 AGTAAAGTATCAATATCCCAACCTTACACACTGTCTGCTGAAATTTAGTTTCTT 660

QY 661 ACCCCCATTAGACTTAAGGAGAGTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ACCCCCATTAGACTTAAGGAGAGTCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 721 GGCACATAGTTGGTCTCAGTGAACATGTTGAGTGAATGAGCAATGCAAGAAATCTCC 780
Db 721 GGCACATAGTTGGTCTCAGTGAACATGTTGAGTGAATGAGCAATGCAAGAAATCTCC 780

QY 781 AGGCATCTGGAGCCCTCCAGCGGGTGGATTCGGGAACTCATAGTCTGTCTCTCAAT 840
Db 781 AGGCATCTGGAGCCCTCCAGCGGGTGGATTCGGGAACTCATAGTCTGTCTCTCAAT 840

QY 841 GGCCCACTGAAGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTAC 900
Db 841 GGCCCACTGAAGTAGAGAGTTCTGGGTCCCACTCCGACCCCACTCTCTGACTAC 900

QY 901 TGCTGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960
Db 901 TGCTGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 960

QY 961 CAGGACTGCAAGAGCCGACGAGATGATGACCGGCTGC 1000
Db 961 CAGGACTGCAAGAGCCGACGAGATGATGACCGGCTGC 1000

RESULT 2

US-09-817-180-3

; Sequence 3, Application US/09817180
; Patent No. 6340584
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/817.180
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15297
; TYPE: DNA
; ORGANISM: Human
US-09-817-180-3

Query Match 29.6%; Score 296; DB 4; Length 15297;
Best Local Similarity 83.4%; Pred. No. 3.1e-58;
Matches 371; Conservative 0; Mismatches 71; Indels 3; Gaps 3;

QY 97 CGTGGCTCAGCGCTGTATCCAGCAGCTTTAGAGCTGCAAGAGGTGGATCACTTGAG 156
Db 11700 CAGTTGCTCAGCGCTGTATCCAGCAGCTTTGGAGGCTGAGCTGGGTGATCACTTGAG 11759

QY 157 GTGAGAGTTTGGAGCAGCGCTGCCAACACAGCTGAAACCCCATCTCTACTAAAAATAA 216
Db 11760 CCCAGGAG-TTCAAGATCAGCTTGGACACACAGTGAACCTTCACTGTAAAAATAA 11818

QY 217 AAATTAAGTNGGTTGGGTGGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCTGAGAC 276
Db 11819 AAAAATAGACTGCGCAGCGTGGCTCACACCTGTAAATCCAGCAGCTTTGGAGGCGGAGC 11878

QY 277 GGTGGATCACTGAACTCAGGAGTCAAGCCAGCGCTGGGCAACATGTTGAAACCCCAT 11938
Db 11879 AGTGGATCACTGTTGGTGGAGTTGAGACCAAGCAGCAACATGTTGAAACCCCAT 11938

QY 337 CTCTACTAAAAATACAAAAATAGCAGGTGTGGTGGCAGCAGCTGTAGTCCAGCTAC 396
Db 11939 CTCTACTAAAAATACAAAAATAGCAGGCTGTGGCAGCTGTAGTCCAGCTAC 11998

QY 397 TTGGAGGCTCAGCGGAGAGATCGTTGAACCCAGTAGGACAGGTTGCACTGAGCGGA 456
Db 11999 TTGGAGGCTGAGGTGGGAGATTCCTTGAACCCAGGAGCGGAGGCTGCACTGAGCGGA 12058

QY 457 GATAAGACTCACTGCATCCAGCTCCAGCTGGGTGGTGC-AGAGCAAGACTCCCTCTCAGAAATAA 515
Db 12059 GAT-TGTTGCCACTGCACTCCAGCTGGGCGACAGAGTGAACCTCCATCTCAAAAAAAC 12117

QY 516 AATAAATAAATAAATAAATAAATAA 540
Db 12118 CAAAAAATAAATAAATAAATAAATAA 12142

RESULT 3

US-08-916-901-6
; Sequence 6, Application US/08916901
; Patent No. 5892012
; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: RAB PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304


```
; Sequence 5, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stearns, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-5

Query Match      28.4%; Score 284; DB 4; Length 7720;
Best Local Similarity 84.9%; Pred. No. 1.4e-55;
Matches 376; Conservative 0; Mismatches 61; Indels 6; Gaps 5;

QY 87 AGCTAGCGCGGTGGCTCAGCCTGTATCCAGCACTTTAGAGGTGGAAGAGGGTGG 146
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6233 AGCTGGGTGCAGTGGCTTACTTGTATCCAGCACTTTGGAGGCCAGGCAAGTGG 6174
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 147 ATCACTTGAGTCAGGATTTTGAGCAGCCTGGCCACAGCGTGAACCCCATCTCTA 206
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6173 ATCACTTGAGATCAAGAG-TTIGAGACCAGCCTGGCCAAATGTGAACCCCGTCTTA 6115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 207 CTAAAAATA-AAAAATTAGCTNGGTCGGTGGCTCACACCTGTATATCCAGCACTTTGG 265
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6114 CTAAAAATATAAAATTAGCGCGGTGGCTGAGCTGAGCTGTATATCCAGCACTTTGG 6055
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 266 GAGGCTGAGCGGGTGGATCACCTGAAGTCAGAGTTCAAGGCCAGCCTGGGCAACATGG 325
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6054 GAGCGCCAGCGGGTGGATCAC--GAGGCTAAGAGATCAAGACCACCTCTGGCCACATGG 5997
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 326 TGAACACCACTCTCTACTAAAAATAC-AAAAATTAGCAGGTGTGGTGCAACAGCCTGT 384
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5996 TGAACCCCTCTCTACTAAAAATACAAAAAATTAGCGGCGTGGTGGCTGGCACCTGT 5937
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 385 AGTCCAGCTACTTTGGAGGCTGAGCGGAAGATCGCTTGAACCCAGTGGAGAGGTT 444
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5936 AGTCCAGCTACTTTGGAGGCTGAGCGGAAGATGTGTGAACCCAGTGGAGAGCCT 5877
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 445 GCATGAGCGCGAGATAGATCTACTGCTCCAGCCTGGGTGACAGCAAGACTCCCTC 504
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5876 GCATGAGCGCGAGATCA-TGCCACTGCTCCAGCCTGGGCGACAGCAAGACTCCATC 5818
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 505 TCAGAAAAATAAAATAAA 527
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5817 TCAGAAAAATAAACAAAAA 5795
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-08-257-963B-10
; Sequence 10, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, S.
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
; TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
```

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; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,963B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7210 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Human
; IMMEDIATE SOURCE:
; LIBRARY: DASH II
; FEATURE:
; NAME/KEY: JT106
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: 7.2 kb No. 5840686 1 fragments
; US-08-257-963B-10
; US-08-257-963B-10

Query Match      27.8%; Score 277.8; DB 2; Length 7210;
Best Local Similarity 82.3%; Pred. No. 3.5e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GCGTAGGCGCGGTGGCTGATATCCAGCACTTTAGAGGTGCGAGAGGTGGA 147
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3756 GCGCGGACAGGTGGCTGAGCTGAGTCCAGCACTTTGGAGGCCAGGCGGCGAGA 3815
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 148 TCACCTTGAGTTCAGGAGTTTGGAGCAGCCTGGCCACAGCGTGAACCCCATCTCTAC 207
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3816 TCACCTTGAGTTCAGGAG-TTCGAGACCAGCCTGGCTTAACAGATGAACCCGCTCTAC 3874
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 208 TAAAAATA-AAAAATTAGCTNGGTCGGTGGCTCACACCTGTATCCAGCACTTTGGG 266
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3875 TAAAAATACAAAAAATTAGCTGGGCGAGGTGGCTGCTGCTGTAATCCAGCACTTTGGG 3934
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 267 AGGCTGAGCGGGTGGATCACTGAAGTCAGGAGTTCAAGGCCAGCCTGGGCAACATGGT 326
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3935 AGGCGAGAGTGGCGAGATCACTTCAGGTTCAGGAGTTTGGAGCAGCCTAGCCACATGGT 3994
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 327 GAAACCACTCTCTACTAAAAATA-AAAAATTAGCCAGGTGTGTGGCAGACGCTGTAG 386
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3995 GAAACCCCATCTCTACTAAAAATA-AAAAATTAGCCAGGTGTGTGGCAGCTGTAG 4054
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 387 TCCAGCACTCTGGAGGCTGAGCGGGAAGATCCCTTGAAACCCAGTAGGAGGTTCG 446
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4055 TCCAGCCAGTTCAGGAGGTGAGGCGAGAGATCACTGGAATCCTGGAGGTGGAGTGC 4114
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 447 AGTGAGCCGAGATAGAGTCACTGCACTCCAGCCTGGGTGACAGACAGCACTCCCTCTC 506
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4115 AGTGAGCCGAGAT-GGTACCTCTGTACTCCAGCCTGGGCGGAGAGTGAGAGTCCGCTCTC 4173
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 507 AGAAAAATAAA 516
```

Db 4174 AAAAAAAAAA 4183

RESULT 7

US-08-367-841A-10

; Sequence 10, Application US/08367841A

; Patent No. 6319687

; GENERAL INFORMATION:

; APPLICANT: Chader, Gerald J.; Rodriguez,

; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;

; APPLICANT: Tombran-Tink, Joyce

; TITLE OF INVENTION: PIGMENT EPITHELIUM

; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC

; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan

; STREET: 345 Park Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/367,841A

; FILING DATE: 30-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/257,963

; FILING DATE: 07-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/952,796

; FILING DATE: 24-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: DOROTHY R. AUTH

; REGISTRATION NUMBER: 36434

; REFERENCE/DOCKET NUMBER: 20264126US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7210 Base Pairs

; TYPE: Nucleic Acid

; STRANDEDNESS: Double

; TOPOLOGY: Unknown

; MOLECULE TYPE: Genomic DNA

; ORIGINAL SOURCE:

; ORGANISM: Human

; IMMEDIATE SOURCE:

; LIBRARY: DASH II

; FEATURE:

; NAME/KEY: JT6A

; LOCATION:

; IDENTIFICATION METHOD:

; OTHER INFORMATION: 7.0 Kb No. 6319687 1-No. 6319687

; OTHER INFORMATION: fragment; derived from human placental

; OTHER INFORMATION: genomic DNA; also referred to as JT106

US-08-367-841A-10

Query Match 27.8%; Score 277.8; DB 4; Length 7210;

Best Local Similarity 82.3%; Pred. No. 3.5e-54;

Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;

QY 88 GCGTAGCGCGGGTGCACGCTGTATCCAGACATTAGAGGTGCGAAGAGGGTGA 147

Db 3756 GGCGGCGACGGTGGCTACGCGCTGTAGTCCAGCATTGGGAGGCGCGAGCGCAGA 3815

QY 148 TCACCTGAGGTCAGGAGCTTTTGAGACCGCCTGGCCAAACAGGCTGAACCCCATCTCTAC 207

Db 3816 TCACCTGAGGTCAGGAG-TTCGAGACCGCCTGGCTAACACGATGAACCCCGCTCTAC 3874

QY 208 TAAAAATA-AAAAAATTAGCTGGGTGGCTCACACCTGTGAATCCACACACTTTGGG 266

Db 3875 TAAAAATACAAAAAATTAGCTGGGACGGTGGCTGTGCTGTGAATCCACGACTTTGGG 3934

QY 267 AGCGTGAGACGGGTGGATCACCTGAGTCAGAGTTCAGGGCCAGCCTGGGCAACATGGT 326

Db 3935 AGCGAGAGGTGGGAGATCATTGAGGTCAGGAGTTTGAGACCGAGCTAGCCACATGGT 3994

QY 327 GAAACCACTCTCTACTAAAAATACAAAAATAGCCAGGTGGTGGGCACACGCTGTAG 386

Db 3995 GAAACCCATCTCTACTAAAAATACAAAAATAGCCGAGGTGGTGGCACGCTGTAA 4054

QY 387 TCCAGTACTTTGGGAGGCTGAGGGGAGGAATGGCTTGAACCCAGTAGTAGCAGGTTCC 446

Db 4055 TCCAGCGAGTCAGGAGGCTGAGGCGAGGAGATCACTGGAATCCCTGGAGGTGGAGTGGC 4114

QY 447 AGTGAGCGAGATAGAGTCACTGCACCTCCAGCCTGGGTGACAGAGCAAGACTCCCTCTC 506

Db 4115 AGTGAGCGGAGAT-GGTACCTCTGTACTCCAGCCTGGGAGGAGTGGAGTCCGCTCTC 4173

QY 507 AGAAAAATAAA 516

Db 4174 AAAAAAATAAA 4183

RESULT 8

PCT-US95-07201-10

; Sequence 10, Application PC/TUS9507201

; GENERAL INFORMATION:

; APPLICANT: Chader, Gerald J.; Becerra, Sofia

; APPLICANT: Patricia; Schwartz, Joan P.;

; APPLICANT: Taniwaki, Takayuki

; TITLE OF INVENTION: PIGMENT EPITHELIUM

; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC

; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/07201

; FILING DATE: 06-JUN-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/367,841

; FILING DATE: 30-DEC-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/257,963

; FILING DATE: 07-JUN-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/952,796

; FILING DATE: 24-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: DOROTHY R. AUTH

; REGISTRATION NUMBER: 36434

; REFERENCE/DOCKET NUMBER: 20264126PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 758-4800

; TELEFAX: (212) 751-6849

; INFORMATION FOR SEQ ID NO: 10:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7210 Base Pairs
/ TYPE: Nucleic Acid
/ STRANDEDNESS: Double
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Human
/ IMMEDIATE SOURCE:
/ LIBRARY: DASH II
/ FEATURE:
/ NAME/KEY: JT6A
/ LOCATION:
/ IDENTIFICATION METHOD:
/ OTHER INFORMATION: 7.0 kb Not 1-Not
/ OTHER INFORMATION: fragment; Derived from human placental
/ OTHER INFORMATION: genomic DNA; also referred to as JT106
/ PCT-US95-07201-10

Query Match 27.8%; Score 277.8; DB 5; Length 7210;
Best Local Similarity 82.3%; Pred. No. 3.5e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GCCTAGCGCGGTGGCTCAGCCCTGTAAATCCAGCAGCTTTAGAGGTGCGAAGGGTGA 147
DB 3756 GCGCGGCGACGGTGGCTCAGCCCTGTAGTCCAGCAGCTTTGGGAGCGGAGGCGAGA 3815
QY 148 TCACCTGAGGTGAGGAGTTTGAGACCGCCCTGGCCAAACCGGTGAACCCCAATCTCTAC 207
DB 3816 TCACCTGAGGTGAGGAG-TTCGAGACCGCCCTGGCTTAACACGATGAACCCCGTCTCTAC 3874
QY 208 TAAAAATA-AAAAATTAGCTNGGGTGGGTGGCTCAGCCCTGTAAATCCAGCAGCTTTGGG 266
DB 3875 TAAAAATACAAAAATTAGCTGGGCGACGGTGGCTGGCTGTAAATCCAGCAGCTTTGGG 3934
QY 267 AGCTGAGAGCGGTGGATCAGCTGAAGTCAAGAGTTCAGAGCGCCCTGGGCAACATGTT 326
DB 3935 AGCAGAGGTGGGAGATCAGCTTGAAGTTCAGAGCGCCCTGGGCAACATGTT 3994
QY 327 GAAACACAGCTCTACTATAAATAACAAAAATTAGCCAGGTGGTGGGCAACATGTT 386
DB 3995 GAAACCCCAATCTCTACTATAAATAACAAAAATTAGCCAGGTGGTGGGCAACATGTT 4054
QY 387 TCCAGCTACTTGGGAGGTGAGCGGGAAGATCGCTTGAACCCAGTAGGAGGTGC 446
DB 4055 TCCAGCCAGTCAGGAGGTGAGCGGAGATCAGTGAATCCGTGGAGGTGGG 4114
QY 447 AGTGAGCGGAGATAGAGTCACTGACCTCCAGCGTGGGTGACAGCAAGACTCCCTCTC 506
DB 4115 AGTGAGCGGAGAT-GGTACCTCTGTACTCCAGCTGGGGGACAGAGTGAGACTCCGCTC 4173
QY 507 AGAAAAATAA 516
DB 4174 AAAAAATAA 4183

RESULT 9
US-08-520-373D-4
/ Sequence 4, Application US/08520373D
/ Patent No. 6451763
/ GENERAL INFORMATION:
/ APPLICANT: Tombran-Tink, Joyce
/ APPLICANT: Steele, Fintan R
/ APPLICANT: Chader, Gerald J
/ APPLICANT: Becerra, Sofia P
/ APPLICANT: Johnson, Lincoln V
/ APPLICANT: Rodriguez, Ignacio R
/ TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
/ FILE REFERENCE: 2026-4203US1
/ CURRENT FILING DATE: 1995-08-29
/ PRIOR APPLICATION NUMBER: 08/377,710
/ PRIOR FILING DATE: 1995-01-25

/ PRIOR APPLICATION NUMBER: 08/279,979
/ PRIOR FILING DATE: 1994-07-25
/ PRIOR APPLICATION NUMBER: 07/894,215
/ PRIOR FILING DATE: 1992-06-04
/ PRIOR APPLICATION NUMBER: 07/952,796
/ PRIOR FILING DATE: 1992-09-24
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 14581
/ TYPE: DNA
/ ORGANISM: HUMAN
/ FEATURE:
/ OTHER INFORMATION: mRNA: 6683; EXON: 6683-6790; EXON 11584-11675;
/ OTHER INFORMATION: EXON: 14539-14581; INTRON: 6791-11583; INTRON:
/ OTHER INFORMATION: 11676-14538; CDS: 11584-11675; 14539-14580
/ US-08-520-373D-4

Query Match 27.8%; Score 277.8; DB 4; Length 14581;
Best Local Similarity 82.3%; Pred. No. 4e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GCCTAGCGCGGTGGCTCAGCCCTGTAAATCCAGCAGCTTTAGAGGTGCGAAGGGTGA 147
DB 3755 GCGCGGCGACGGTGGCTCAGCCCTGTAGTCCAGCAGCTTTGGGAGCGGAGGCGAGA 3814
QY 148 TCACCTGAGGTGAGGAGTTTGAGACCGCCCTGGCCAAACCGGTGAACCCCAATCTCTAC 207
DB 3815 TCACCTGAGGTGAGGAG-TTCGAGACCGCCCTGGCTTAACACGATGAACCCCGTCTCTAC 3873
QY 208 TAAAAATA-AAAAATTAGCTNGGGTGGGTGGCTCAGCCCTGTAAATCCAGCAGCTTTGGG 266
DB 3874 TAAAAATACAAAAATTAGCTGGGCGACGGTGGCTGGCTGTAAATCCAGCAGCTTTGGG 3933
QY 267 AGCTGAGAGCGGTGGATCAGCTGAAGTCAAGAGTTCAGAGCGCCCTGGGCAACATGTT 326
DB 3934 AGCAGAGGTGGGAGATCAGCTTGAAGTTCAGAGCGCCCTGGGCAACATGTT 3993
QY 327 GAAACACAGCTCTACTATAAATAACAAAAATTAGCCAGGTGGTGGGCAACATGTT 386
DB 3994 GAAACCCCAATCTCTACTATAAATAACAAAAATTAGCCAGGTGGTGGGCAACATGTT 4053
QY 387 TCCAGCTACTTGGGAGGTGAGCGGGAAGATCGCTTGAACCCAGTAGGAGGTGC 446
DB 4054 TCCAGCCAGTCAGGAGGTGAGCGGAGATCAGTGAATCCGTGGAGGTGGG 4113
QY 447 AGTGAGCGGAGATAGAGTCACTGACCTCCAGCGTGGGTGACAGCAAGACTCCCTCTC 506
DB 4114 AGTGAGCGGAGAT-GGTACCTCTGTACTCCAGCTGGGGGACAGAGTGAGACTCCGCTC 4172
QY 507 AGAAAAATAA 516
DB 4173 AAAAAATAA 4182

RESULT 10
US-08-367-841A-43
/ Sequence 43, Application US/08367841A
/ Patent No. 6319687
/ GENERAL INFORMATION:
/ APPLICANT: Chader, Gerald J.; Rodriguez,
/ APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
/ APPLICANT: Tombran-Tink, Joyce
/ TITLE OF INVENTION: PIGMENT EPITHELIUM
/ TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
/ TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
/ NUMBER OF SEQUENCES: 43
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morgan & Finnegan
/ STREET: 345 Park Avenue
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA

```

? ZIP: 10154
?
? COMPUTER REGISTRATION FORM:
? MEDIUM TYPE: Floppy Disk
? COMPUTER: IBM PC Compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: WORDPERFECT 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 08/08/367,841A
? FILING DATE: 30-DEC-1994
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/257,963
? FILING DATE: 07-JUN-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/952,796
? FILING DATE: 24-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: DOROTHY R. AUTH
? REGISTRATION NUMBER: 36434
? REFERENCE/DOCKET NUMBER: 20264126US2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (212) 758-4800
? TELEFAX: (212) 751-6849
? INFORMATION FOR SEQ ID NO: 43:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 22481 Base Pairs
? TYPE: Nucleic Acid
? STRANDEDNESS: Double
? TOPOLOGY: Unknown
? MOLECULE TYPE: Genomic DNA
? FEATURE:
? NAME/KEY: PL-147
? LOCATION:
? IDENTIFICATION METHOD:
? OTHER INFORMATION: full length genomic
? OTHER INFORMATION: sequence for FEDE
US-08-367-841A-43

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RESULT 11
PCT-US95-07201-43
; Sequence 43, Application PC/TUS9507201
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, Sofia
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22481 Base Pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Unknown
; MOLECULE TYPE: Genomic DNA
; FEATURE:
; NAME/KEY: PI-147
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION: full length genomic
; OTHER INFORMATION: sequence for PEDF plus flanking sequences.
PCT-US95-07201-43

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	Best Local Similarity	82.3%;	Pred. No. 4.3e-54;		
	Matches 354;	Conservative 0;	Mismatches 73;	Indels 3;	Gaps
QY	88	GGCTAGCGCGTGGCTCAGCCCTGTAAATCCAGACTTTTGAAGGTCGAAGAGGTTGGA	147		
Db	3748	GGCGGGCAGGTGGCTCAGCCCTGTAGTCCAGCACTTTGGAGCGCGGAGCGGCAGC	3807		
QY	148	TCACTTGAGGTCAGGAGTTTGTAGACACCGCTTGCCACACAGGTCGAACCCCACTCTTAC	207		
Db	3808	TCACTTGAGGTCAGGAG-TTCGAGACCACTGGCTTACACGATGAACCCCGCTCTTAC	3866		
QY	208	TAAATAATAAATTAAGTTCGGTGGCTCACACTGTAAATCCAGCACTTTGGG	266		

Db 3867 TAAAAATACAAAAATAGCTGGCCACGGTGGCTGGTGGCTGTAAATCCAGCAGCTTTGGG 3926
QY 267 AGGTGAGAGCGGTGGATCAGCTTAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGT 326
Db 3927 AGGAGAGGTGGGAGATCAGCTTGAAGTCAGGAGTTGACAGCAGCGCTAGCCACATGGT 3986
QY 327 GAAACACAGCTCTCTACTAAATAACAAAAATAGCAGGTTGGTGGCCACAGCGCTGTAG 386
Db 3987 GAAACCCCAATCTCTACTAAATAACAAAAATAGCGGGAGTGGTGGCACGCTGCTTAA 4046
QY 387 TCCAGCTACTTGGGAGCTGAGCGGAAGATCGCTGAACCCAGTAGGAGGAGGTGGC 446
Db 4047 TCCAGCGAGTCAGGAGCTGAGCGAGAGATCAGTGGARTCTTGGAGGTGGAGTGGC 4106
QY 447 AGTGAGCCAGATAGAGTCAGTGCCTCCAGCGCTGGGTGACAGAGCAAGACTCCCTCTC 506
Db 4107 AGTGAGCCAGAT-GGTACCTCTGTACTCCAGCGTGGGGACAGAGTGAGACTCCGCTC 516
QY 507 AGAAAAATAA 516
Db 4166 AAAAAAATAA 4175

RESULT 12

US-09-875-223-2
; Sequence 2, Application US/09875223
; Patent No. 6391850
; GENERAL INFORMATION:
; APPLICANT: No. 6391850 Western University
; APPLICANT: David Bouck
; APPLICANT: Paul Gillis
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
; FILE REFERENCE: 0290-2303
; CURRENT APPLICATION NUMBER: US/09/875,223
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 22484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 1...22484
; OTHER INFORMATION: "n" means either a, c, t, or g
US-09-875-223-2

Query Match 27.8%; Score 277.8; DB 4; Length 22484;
Best Local Similarity 82.3%; Pred. No. 4.3e-54;
Matches 354; Conservative 0; Mismatches 73; Indels 3; Gaps 3;
QY 88 GGTAGGCGGCTGGCTCAGCGCTGTAAATCCAGCAGCTTTAGAGGTGCAAGAGGGTGA 147
Db 3748 GCGCGGCGGCTGGCTCAGCGCTGTAGTCCAGCAGCTTTGGGAGCGCCAGGAGGAGA 3807
QY 148 TCACCTTGAAGTCAGGAGTTTGAACCCAGCGCTGGCCACACAGCGTGAACCCATCTCTAC 207
Db 3808 TCACCTTGAAGTCAGGAG-TTCGAGACCGCGCTGGCTAAGCAGATGAACCCGCTCTAC 3866
QY 208 TAAAAATA-AAAAATAGCTNGGGTGGCTCAGACCTGTAAATCCAGCAGCTTTGGG 266
Db 3867 TAAAAATACAAAAATAGCTGGGACGCTGGCTGTGCTGTAAATCCAGCAGCTTTGGG 3926
QY 267 AGGCTGAGAGCGGTGGATCAGCTGAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGT 326

Db 3927 AGGAGAGGTGGCAGATCAGTTGAGTCAGGAGTTTGAACCCAGCGCTAGCCAAATGGT 3986
QY 327 GAAACACAGCTCTCTACTAAATAACAAAAATAGCAGGTTGGTGGCCACACAGCTGTAG 386
Db 3987 GAAACCCCAATCTCTACTAAATAACAAAAATAGCGGGAGTGGTGGCACGCTGCTTAA 4046
QY 387 TCCAGCTACTTGGGAGCTGAGCGGAAGATCGCTGAACCCAGTAGGAGGAGGTGGC 446
Db 4047 TCCAGCGAGTCAGGAGCGCTGAGCGAGAGATCAGTGGARTCTTGGAGGTGGAGTGGC 4106
QY 447 AGTGAGCCAGATAGAGTCAGTGCCTCCAGCGCTGGGTGACAGAGCAAGACTCCCTCTC 506
Db 4107 AGTGAGCCAGAT-GGTACCTCTGTACTCCAGCGTGGGGACAGAGTGAGACTCCGCTC 516
QY 507 AGAAAAATAA 516
Db 4166 AAAAAAATAA 4175

RESULT 13

US-09-741-150-3
; Sequence 3, Application US/09741150
; Patent No. 6436689
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000968
; CURRENT APPLICATION NUMBER: US/09/741,150
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112132
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3

Query Match 27.6%; Score 275.6; DB 4; Length 112132;
Best Local Similarity 79.9%; Pred. No. 1.8e-53;
Matches 373; Conservative 0; Mismatches 90; Indels 4; Gaps 4;
QY 89 GCTAGGCGGCTGGCTCAGCGCTGTAAATCCAGCAGCTTTAGAGGTGCAAGAGGGTGGAT 148
Db 90602 GCTGGACGTGGTGGCTCAGCACCTGTAAATCCCAACACTATATGGGAGCTGAGCAGCCAGAT 90661
QY 149 CACTTCAGCTCAGGAGTTTGAACCCAGCGCTGGCCACACAGCGTGAACCCCATCTCTACT 208
Db 90662 CACTTCAGCTCAGGAG-TTCAGACCCAGCGCTGGTCAACATGTGTAACCCCGCTCTACT 90720
QY 209 AAAAAATA-AAAAATAGCTNGGGTGGCTGAGTGGCTCAGACCTGTAAATCCAGCAGCTTTGGA 267
Db 90721 AAAAAATACAAATTTAGCCAGCGCTCAGTGGCTCAGACCTGTAAATCCAGCAGCTTTGGA 90780
QY 268 GGTGAGAGCGGTGGATCAGCTGAAGTCAGGAGTTCAAGGCCAGCGCTGGGCAACATGGTG 327
Db 90781 GGTGAGGTGGGCGGATCAGCTGAGGTTCAGGAGTTGAGAGCCAGCGCTGGCCACATGCTG 90840
QY 328 AAACACAGCTCTCTACTAAATAACAAAAATAGCAGGTTGAGCCAGGTGGTGGCCACAGCGCTGTAGT 387
Db 90841 AAACCCATCTCTACTAAATAACAAAAATTTAGTGGCATGTGGGCAATGCTGTAGT 90900
QY 388 CCCAGCTACTTGGAGCGCTGAGCGGAAGATCGCTTGAACCCAGTAGGAGGAGGTGCA 447
Db 90901 CCCAGCTAC-AGGAGGTTGAGCCAGGAGATCGCTTGAACCCAGGAGGTGGAGGTGCA 90959
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Db 90960 GTGACCCATCAT-TGTGGCACTACAAGCACCSCCTGGTGCACACAGCGACTCCATCTCA 91018

QY   508 GAAATAAAAAAATAAAAATAAAAAATAAAAAATAAAAAATAAATA 554
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RESULT 14
US-09-729-995-3
; Sequence 3, Application US/09729995
; Patent No. 6426206
; GENERAL INFORMATION:
; APPLICANT: WEL, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; CURRENT APPLICATION NUMBER: US/09/729,995
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 29629
; TYPE: DNA
; ORGANISM: Human
US-09-729-995-3

Query Match          27.3%; Score 272.6; DB 4; Length 29629;
Best local Similarity 79.7%; Pred. No. 6.8e-53;
Matches 370; Conservative 0; Mismatches 90; Indels 4; Gaps 4;

QY   85 ATAGGCTAGGCCGGTGCTCAGCGCTCTAATCCCAGCACCTTTAGAAGTCGAAGGGT 144
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QY   145 GGATCACTTAGGTCAGGAGTCTTTCAGACACAGCCTGGCCAACAGCTGGAACCCCACTTC 204
      ||| |||| |
Db 13937 GGATCACTTAGGTCAGGAG-TTTGAGACAGAGCCTGGCCAACTGTGGTGTGAACCCCGTCTC 13995

QY   205 TACTT-AAATAAATAATTTAGCTNGGTGGGTGGCTCACACCTGTAATCCACGACTTT 263
      ||| |||| |
Db 13996 TACTTAAATAAATAACAAAATTTAGCCGGCAGTGTGGCGGCCAACCTGTAAATCCAGCTACTT 14055

QY   264 GGGAGGCTCAGACGGGTGGATCACTCGAAGTCAGAGGTTCAAGGCCACCGCTGGCCAACAT 323
      ||| |||| |
Db 14056 GGGAGSCCGAGCAGGTGGATCACTTGGTCTAGAGGTTTGAGCCACGCGTGGCCAACGT 14115

QY   324 GGTGAACCAAGTCTCTACT-AAAAATACAAAATTTAGCCAGGTGTGGTGGCAGCAGCCT 382
      ||| |||| |
Db 14116 GGTGAACCCCGCTCTCTACTTAAAAAATACAAAATTTAGCCGGCATGTGTGCAGGCACCT 14175

QY   383 GTAGTCCACGCTACTTGGGAGGCTGAGCGGAGAAATCGCTTGAACCCATGATGGCAGAGG 442
      ||| |||| |
Db 14176 GTAATTCACGCTACTTGGAGGCTTGAGGCGAAGAAATCGTTGAACCCAGAGGCGAGG 14235

QY   443 TTCAGTGAAGCGGAGATAGAGTCACTGCACCTCCAGCCTGGGTGACAGAGCAGACTCC 502
      ||| |||| |
Db 14236 TTTCAGTGAAGTGAAGT-CGTGCTATTGCACTTGTAGCTGGCGCAGAGTGAGACTCTG 14294

QY   503 TCPCAGAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 546
      ||| |||| |
Db 14295 TCTGAATAAANAAGACATPATCAATATCCAGAGCCTATTATTA 14338

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RESULT 15
US-09-800-960-3
; Sequence 3, Application US/09800960
; Patent NO. 6387677
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEOTIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF

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; FILE REFERENCE: CL001158
; CURRENT APPLICATION NUMBER: US/09/800,960
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 62804
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(62804)
; OTHER INFORMATION: n = A,T,C or G
US-09-800-960-3

Query Match          27.1%; Score 271.4; DB 4; Length 62804;
Best Local Similarity 80.1%; Pred. No. 1.5e-52;
Matches 367; Conservative 0; Mismatches 87; Indels 4; Gaps

QY 79 AATGGAAATAGGCTAGGCCGGTGGCTCAGGCTCTAATCCACAGCACTTTAGAGTGCAG 138
Db 53984 AAATAAATAGGCGAGGTGGTGACTCAACACTTAATCCCCACACATTTGGGAGGCGAG 54043
QY 139 GAGGTGGATCACTTGGAGTTCAGAGTCTTTGAGACAGAGCTGGCCACACAGCGTGAACCC 198
Db 54044 GCAAGTGGATCACTTGAGTTCAGAG-TTCAAAACCAGAGCTGGCCACATGATGAACCC 54102
QY 199 CATCTCTACTAAATAATAAAATTAGCTNGGTGGCTGGCTCACTCTGTAATCCCAGC 258
Db 54103 CGTCTCTACTAAATAATACAAAAGAGCGCGGCGTAGTGGTCAAGCTGTAATCCCAAC 54162
QY 259 ACTTTGGAGGCTGAGAGCGGTGGATCACTTGAA-GTCAAGAGTTCAAGCCAGCGCTGGG 317
Db 54163 ACTTTGGAGGCCAAGGTGGGTGGATCACTTCAAGGTCAAGGTCAAGAGTCAAGCAGCGCTGC 54222
QY 318 CAACATGGTGAACACCGTCTCTACTATAAATAACAAAATTAGCCAGGTGTGGTGGCACA 377
Db 54223 CAACATGGTGAACCTCCATCTCTACTAAATAATAAAATAGCCAGGTGTGGGCGCG 54282
QY 378 CGCCTGTAGTCCAGCTACTTTGGAGGCTGAGCGCGGAAGATCGCTTGAACCCAGTAGGC 437
Db 54283 TGCCTGTGAATCGTAGCTACTTCGGAGGCGGAGGTGGGGAATCGCTTGAACCTGGGAGGT 54342
QY 438 AGAGGTTGAGTGGAGCGAGATAAGAGTCACTGCATCTCCAGCTGGGTGCAC-AGAGCAAG 496
Db 54343 GGAGGTTGAGTGGAGCGGAGTCA-CCCCATTGCCTTCAGCTTGGGCAACAGAGGCA 54401
QY 497 ACTCCCTCTCAGAAATAAATAAATAAATAAATA 534
Db 54402 ACTTCTCTCAAAAAAATAAAAAAAAAAAAAAAAAATTA 54439

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Job time : 322 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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(without alignments)
3825.558 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 335578 seqs, 189365133 residues

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Total number of hits satisfying chosen parameters: 671156

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	52	5.2	1503841	10	US-09-946-807-1
5	52	5.2	1503841	10	US-09-795-668-1
6	52	5.2	1503841	10	US-09-795-668-1
7	50	5.0	276	10	US-09-764-869-2086
8	50	5.0	545	10	US-09-741-148A-30
9	50	5.0	10503	10	US-09-764-870-579
10	50	5.0	10503	10	US-09-764-853-854
11	50	5.0	13819	10	US-09-764-860-1032
12	50	5.0	23668	10	US-09-764-877-2596
13	50	5.0	26928	10	US-09-741-148A-30
14	50	5.0	111282	12	US-09-880-107-2278
15	50	5.0	143306	10	US-10-09A-989-3
16	49	4.9	401	9	US-09-729-920-3
17	49	4.9	401	9	US-09-946-807-806
18	49	4.9	401	10	US-09-795-668-806
19	49	4.9	24533	9	US-09-795-668-806
20	49	4.9	24533	9	US-09-764-868-1349

20	49	4.9	99014	10	US-09-880-107-3428	Sequence 3428, Ap
21	49	4.9	99014	10	US-09-880-107-3428	Sequence 3428, Ap
22	48	4.8	1514	10	US-09-822-849A-510	Sequence 510, App
23	48	4.8	180216	10	US-09-835-232-6	Sequence 6, Appli
24	47	4.7	337	10	US-09-764-869-1528	Sequence 1528, Ap
25	47	4.7	418	10	US-09-867-701-8320	Sequence 8320, Ap
26	47	4.7	546	10	US-09-998-598-647	Sequence 647, App
27	47	4.7	562	10	US-09-764-877-2628	Sequence 2628, Ap
28	47	4.7	4766	9	US-09-764-868-1443	Sequence 1443, Ap
29	47	4.7	6124	8	US-08-913-322-21	Sequence 21, Appl
30	47	4.7	6124	8	US-09-967-768A-184	Sequence 184, App
31	47	4.7	6133	8	US-08-913-322-2	Sequence 2, Appli
32	47	4.7	6228	8	US-08-913-322-23	Sequence 23, Appl
33	47	4.7	10867	10	US-09-764-869-2113	Sequence 2113, Ap
34	47	4.7	10867	10	US-09-764-877-3970	Sequence 3970, Ap
35	47	4.7	10894	10	US-09-764-869-2111	Sequence 2111, Ap
36	47	4.7	10907	10	US-09-764-869-2112	Sequence 2112, Ap
37	47	4.7	10907	10	US-09-764-877-3968	Sequence 3968, Ap
38	47	4.7	12718	10	US-09-764-877-3972	Sequence 3972, Ap
39	47	4.7	56737	10	US-09-782-378A-17	Sequence 17, Appl
40	47	4.7	68804	10	US-09-740-041-3	Sequence 3, Appli
41	47	4.7	84539	10	US-09-962-436-36	Sequence 36, Appl
42	46	4.6	574	10	US-09-764-847-1713	Sequence 1713, Ap
43	46	4.6	574	10	US-09-764-847-1714	Sequence 1714, Ap
44	46	4.6	2939	9	US-09-764-868-1314	Sequence 1314, Ap
45	46	4.6	2939	9	US-09-764-868-1315	Sequence 1315, Ap

ALIGNMENTS

RESULT 1
US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double


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; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h-a or c or t/u
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v-a or g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n-a or g or c or t/u
;
US-09-946-807-1

```

```

Query Match          5.2%; Score 52; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 1366616
Db 1366667 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 1366616

```

```

RESULT 4
US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y-t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; NAME/KEY: misc_feature

```

```

; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b-g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d-a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h-a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v-a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n-a or g or c or t/u
;
US-09-795-668-1

```

```

Query Match          5.2%; Score 52; DB 10; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 3.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 1366616
Db 1366667 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATTC 1366616

```

```

RESULT 5
US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y-t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u

```

1

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1032
; LENGTH: 10503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1032

Query Match 5.0%; Score 50; DB 10; Length 10503;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 166 TTGTGAGCAGCGTGGCCACACGCGTGAACCCCATCTCTACTAAATA 215
|||||
DB 4291 TTGTGAGCAGCGTGGCCACACGCGTGAACCCCATCTCTACTAAATA 4340
|||||

RESULT 11
US-09-764-877-2596/c
; Sequence 2596, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2596
; LENGTH: 13819
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2596

Query Match 5.0%; Score 50; DB 10; Length 13819;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
DB 3482 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 3433
|||||

RESULT 12
US-09-741-148A-3/c
; Sequence 3, Application US/09741148A
; Patent No. US20020076750A1
; GENERAL INFORMATION:
; APPLICANT: Chunhua YAN et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000566
; CURRENT APPLICATION NUMBER: US/09/741,148A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/206,982
; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23668
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(23668)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-148A-3

Query Match 5.0%; Score 50; DB 10; Length 23668;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
DB 9671 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 9622
|||||

RESULT 13
US-09-880-107-2278
; Sequence 2278, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherif, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2278
; LENGTH: 26928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M17262
US-09-880-107-2278

Query Match 5.0%; Score 50; DB 10; Length 26928;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 TCCTCTACTAAATACAAAATTTAGCCAGGTGTGTGGCACACGCTGTA 385
|||||
DB 5015 TCCTCTACTAAATACAAAATTTAGCCAGGTGTGTGGCACACGCTGTA 5064
|||||

RESULT 14
US-10-094-989-3
; Sequence 3, Application US/10094989
; Patent No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(111282)
; OTHER INFORMATION: n = A,T,C or G

US-10-094-989-3

Query Match 5.0%; Score 50; DB 12; Length 111282;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 37295 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 37344

RESULT 15

US-09-729-920-3
; Sequence 3, Application US/09729920
; Patent No. US20020103115A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CLO00858
; CURRENT APPLICATION NUMBER: US/09/729,920
; CURRENT FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 143306
; TYPE: DNA
; ORGANISM: Human
US-09-729-920-3

Query Match 5.0%; Score 50; DB 10; Length 143306;
Best Local Similarity 100.0%; Pred. No. 3.1e-14;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 509 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 126990 AAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 126939

RESULT 16

US-09-946-807-806
; Sequence 806, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 806
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-806

Query Match 4.9%; Score 49; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 382
|||||
Db 105 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 153

RESULT 17

US-09-795-668-806
; Sequence 806, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 806
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-806

Query Match 4.9%; Score 49; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 382
|||||
Db 105 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 153

RESULT 18

US-09-795-686-806
; Sequence 806, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 806
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-806

Query Match 4.9%; Score 49; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.3e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 334 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 382
|||||
Db 105 CGTCTCTACTAAAAATACAAAAATTAGCCAGGTGTGGTGACACGCCT 153

RESULT 19

US-09-764-868-1349/c
; Sequence 1349, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1349
; LENGTH: 24533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1349

Query Match 4.9%; Score 49; DB 9; Length 24533;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 5926 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 5878

RESULT 20

US-09-880-107-3428
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3428
; LENGTH: 99014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match 4.9%; Score 49; DB 10; Length 99014;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 337 CTTCTACTAAATAACAAAATTAGCCAGGTGTGGTGCACGCGCTGTA 385
|||||
Db 43211 CTTCTACTAAATAACAAAATTAGCCAGGTGTGGTGCACGCGCTGTA 43259

RESULT 21

US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3428

; LENGTH: 99014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match 4.9%; Score 49; DB 10; Length 99014;
Best Local Similarity 100.0%; Pred. No. 9.1e-14;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 558
|||||
Db 98924 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 98876

RESULT 22

US-09-822-849A-510/c
; Sequence 510, Application US/09822849A
; Patent No. US20020045170A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6403
; CURRENT APPLICATION NUMBER: US/09/822,849A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/195,582
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 598
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 510
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-849A-510

Query Match 4.8%; Score 48; DB 10; Length 1514;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 557
|||||
Db 1451 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAAT 1404

RESULT 23

US-09-835-232-6/c
; Sequence 6, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens


```

;
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

Query Match
; Sequence 48; Score 48; DB 10; Length 180216;
; Best Local Similarity 100.0%; Pred. No. 2.7e-13;
; Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 369 GGTGGCACACCTGTAGTCCAGCTACTTGGGAGGCTGAGCGGAAG 416
|||||
DB 9148 GTGGCACACCGCTGTAGTCCAGCTACTTGGGAGGCTGAGCGGAAG 9101

RESULT 24
US-09-764-869-1528
; Sequence 1528, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1528
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1528

Query Match
; Sequence 47; Score 47; DB 10; Length 337;
; Best Local Similarity 100.0%; Pred. No. 8.1e-13;
; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTGTATCCACACCTTTGGGAGGCTGAGACGGGTGGATCACCTGA 291
|||||
DB 76 CCTGTATCCACACCTTTGGGAGGCTGAGACGGGTGGATCACCTGA 122

RESULT 25
US-09-867-701-8320
; Sequence 8320, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 8320
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(418)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-8320

Query Match
; Sequence 47; Score 47; DB 10; Length 418;
; Best Local Similarity 100.0%; Pred. No. 8.1e-13;
; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 274
|||||
```

```

|||||
DB 143 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 189

RESULT 26
US-09-998-598-647/c
; Sequence 647, Application US/09998598
; Patent No. US20020150922A1
; GENERAL INFORMATION:
; APPLICANT: Stolk, John A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Chenault, Ruth A.
; APPLICANT: Meagher, Madelein Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.561
; CURRENT APPLICATION NUMBER: US/09/998,598
; CURRENT FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 2606
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 647
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-647

Query Match
; Sequence 47; Score 47; DB 10; Length 546;
; Best Local Similarity 100.0%; Pred. No. 8.1e-13;
; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 274
|||||
DB 89 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 43

RESULT 27
US-09-764-877-2628
; Sequence 2628, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2628
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2628

Query Match
; Sequence 47; Score 47; DB 10; Length 562;
; Best Local Similarity 100.0%; Pred. No. 8.1e-13;
; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 274
|||||
DB 207 GGGTGGGTGGCTCACACCTGTATATCCAGCACCTTTGGGAGGCTGAG 253

RESULT 28
US-09-764-868-1443
; Sequence 1443, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
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; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1443
; LENGTH: 4766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1443

Query Match          4.7%; Score 47; DB 9; Length 4766;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
      |||||||
Db 2594 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 2640

RESULT 29
US-08-913-322-21
; Sequence 21, Application US/08913322
; Patent No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; EARLIER FILING DATE: 1997-09-12
; EARLIER FILING DATE: 1997-01-17
; EARLIER FILING DATE: 1997-01-17
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-322-21

Query Match          4.7%; Score 47; DB 8; Length 6124;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
      |||||||
Db 5487 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 5533

RESULT 30
US-09-967-768A-184
; Sequence 184, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR FILING DATE: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 184
; LENGTH: 6124
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-184

Query Match          4.7%; Score 47; DB 10; Length 6124;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
      |||||||
Db 5487 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 5533

RESULT 31
US-08-913-322-2
; Sequence 2, Application US/08913322
; Patent No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; CURRENT FILING DATE: 1997-09-12
; EARLIER FILING DATE: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6133
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-322-2

Query Match          4.7%; Score 47; DB 8; Length 6133;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 274
      |||||||
Db 5496 GGGTGGGTGGCTCACACCTGTAATCCAGCAGCTTTGGGAGGCTGAG 5542

RESULT 32
US-08-913-322-23
; Sequence 23, Application US/08913322
; Patent No. US20020137028A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Roy, Natalie
; APPLICANT: Robertson, George
; APPLICANT: Tamai, Katsu
; TITLE OF INVENTION: USER OF NEURONAL APOPTOSIS INHIBITOR
; FILE REFERENCE: 07891/013001
; CURRENT APPLICATION NUMBER: US/08/913,322
; CURRENT FILING DATE: 1997-09-12
; EARLIER FILING DATE: PCT/IB97/00142
; EARLIER FILING DATE: 1997-01-17
; EARLIER FILING DATE: 1996-01-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
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; LENGTH: 6228
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-913-322-23

Query Match
4.7%; Score 47; DB 8; Length 6228;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 5591 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 5637

RESULT 33
US-09-764-869-2113
; Sequence 2113, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2113
; LENGTH: 10867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2113

Query Match
4.7%; Score 47; DB 10; Length 10867;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1100 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 1146

RESULT 34
US-09-764-877-3970
; Sequence 3970, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; LENGTH: 10867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3970

Query Match
4.7%; Score 47; DB 10; Length 10867;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1100 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 1146

RESULT 35
US-09-764-869-2111
; Sequence 2111, Application US/09764869
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; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2111
; LENGTH: 10894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2111

Query Match
4.7%; Score 47; DB 10; Length 10894;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1138 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 1184

RESULT 36
US-09-764-869-2112
; Sequence 2112, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2112
; LENGTH: 10907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2112

Query Match
4.7%; Score 47; DB 10; Length 10907;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1137 GGGTGGGTGGCTCACACCTGTATCCAGCAGCTTTGGGAGGCTGAG 1183

RESULT 37
US-09-764-877-3968
; Sequence 3968, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3968
; LENGTH: 10907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3968

Query Match
4.7%; Score 47; DB 10; Length 10907;
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Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1137 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 1183
|||||

RESULT 38

US-09-764-877-3972
; Sequence 3972, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3972
; LENGTH: 12718
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3972

Query Match 4.7%; Score 47; DB 10; Length 12718;
Best Local Similarity 100.0%; Pred. No. 8e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 1137 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 1183
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RESULT 39

US-09-782-378A-17/c
; Sequence 17, Application US/09782378A
; Patent No. US20020102731A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/09/782,378A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 56737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-378A-17

Query Match 4.7%; Score 47; DB 10; Length 56737;
Best Local Similarity 100.0%; Pred. No. 7.9e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 556
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Db 18486 AAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAAATAAA 18440
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RESULT 40

US-09-740-041-3/c
; Sequence 3, Application US/09740041
; Patent No. US20020082190A1
; GENERAL INFORMATION:

; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 66804
; TYPE: DNA
; ORGANISM: Human
US-09-740-041-3

Query Match 4.7%; Score 47; DB 10; Length 66804;
Best Local Similarity 100.0%; Pred. No. 7.9e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 274
|||||
Db 35282 GGGTGGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGCTGAG 35236
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RESULT 41

US-09-962-436-36/c
; Sequence 36, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 84539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-36

Query Match 4.7%; Score 47; DB 10; Length 84539;
Best Local Similarity 100.0%; Pred. No. 7.9e-13;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 GAGACAGCCTGGCCACACAGCGTGAAACCCCATCTCTACTAAAAATA 215
|||||
Db 10850 GAGACAGCCTGGCCACACAGCGTGAAACCCCATCTCTACTAAAAATA 10804
|||||

RESULT 42

US-09-764-847-1713/c
; Sequence 1713, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1713
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-847-1713

Query Match
Best Local Similarity 100.0%; Score 46; DB 10; Length 574;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 AGACACCTGGCCACACGGTGAACCCCATCTCTACTAAAATA 215
Db 219 AGACACCTGGCCACACGGTGAACCCCATCTCTACTAAAATA 174

RESULT 43
US-09-764-847-1714/c
; Sequence 1714, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1714
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1714

Query Match
Best Local Similarity 100.0%; Score 46; DB 10; Length 574;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 AGACACCTGGCCACACGGTGAACCCCATCTCTACTAAAATA 215
Db 219 AGACACCTGGCCACACGGTGAACCCCATCTCTACTAAAATA 174

RESULT 44
US-09-764-868-1314
; Sequence 1314, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1314
; LENGTH: 2939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1314

Query Match
Best Local Similarity 100.0%; Score 46; DB 9; Length 2939;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 GTGGCGGTGGCTCACACCTGTAATCCAGCAGCACTTTGGAGGCTGAG 274
Db 1942 GTGGCGGTGGCTCACACCTGTAATCCAGCAGCACTTTGGAGGCTGAG 1987

RESULT 45
US-09-764-868-1315/c

; Sequence 1315, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1315
; LENGTH: 2939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-868-1315

Query Match
Best Local Similarity 100.0%; Score 46; DB 9; Length 2939;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 229 GTGGCGGTGGCTCACACCTGTAATCCAGCAGCACTTTGGAGGCTGAG 274
Db 998 GTGGCGGTGGCTCACACCTGTAATCCAGCAGCACTTTGGAGGCTGAG 953

Search completed: November 24, 2002, 13:38:45
Job time : 1912 secs

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 13:30:43 ; Search time 46.5 seconds
 (without alignments)
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Title: US-09-784-423-124
 Perfect score: 25
 Sequence: 1 GGTTCAGTGAGCGGAGATAGAGT 25

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	80.0	764	4	US-09-288-143-57
4	20	80.0	1875	2	US-08-683-743-3
5	20	80.0	4042	4	US-08-406-030A-17
6	20	80.0	4129	2	US-08-370-319C-12
7	20	80.0	4129	4	US-09-224-834-12
8	20	80.0	45716	4	US-08-965-048-5
9	20	80.0	45989	4	US-08-965-048-6
10	19	76.0	21	1	US-08-133-629-2
11	19	76.0	239	2	US-08-687-080-93
12	19	76.0	265	2	US-08-849-701-1
13	19	76.0	294	2	US-08-481-658B-61
14	19	76.0	294	2	US-08-477-504A-61
15	19	76.0	294	2	US-08-486-756A-61
16	19	76.0	294	2	US-08-485-862B-61
17	19	76.0	294	3	US-08-787-739-61
18	19	76.0	294	3	US-08-485-863A-61
19	19	76.0	294	3	US-08-485-863A-61
20	19	76.0	294	4	US-08-485-049D-61
21	19	76.0	294	4	US-09-178-115-61
22	19	76.0	294	4	US-09-177-776-61
23	19	76.0	302	2	US-08-849-701-3
24	19	76.0	336	4	US-09-385-982-17
25	19	76.0	374	4	US-09-385-982-135
26	19	76.0	379	3	US-09-157-177-134
27	19	76.0	577	4	US-09-227-357-92

c 28	19	76.0	609	4	US-09-385-982-291
c 29	19	76.0	618	4	US-09-385-982-218
c 30	19	76.0	649	4	US-09-535-008-49
c 31	19	76.0	689	4	US-09-105-542A-14
c 32	19	76.0	696	4	US-09-740-235-16
c 33	19	76.0	775	4	US-09-227-357-108
c 34	19	76.0	789	2	US-08-394-152A-42
c 35	19	76.0	821	4	US-09-342-681C-7
c 36	19	76.0	825	2	US-08-486-148B-1
c 37	19	76.0	841	5	PCT-US93-06251-80
c 38	19	76.0	841	5	PCT-US93-06251-81
c 39	19	76.0	866	4	US-09-257-179-11
c 40	19	76.0	885	4	US-09-288-143-55
c 41	19	76.0	889	1	US-08-832-883-52
c 42	19	76.0	889	2	US-08-832-877-52
c 43	19	76.0	891	4	US-09-247-155-141
c 44	19	76.0	1000	4	US-09-018-584A-40
c 45	19	76.0	1000	4	US-09-641-638-636

ALIGNMENTS

RESULT 1
 US-09-018-584A-124
 ; Sequence 124, Application US/09018584A
 ; Patent No. 6238863
 ; GENERAL INFORMATION:
 ; APPLICANT: Schumm, James W.
 ; APPLICANT: Bachter, Jeffrey W.
 ; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
 ; TITLE OF INVENTION: REPEAT DNA MARKERS
 ; NUMBER OF SEQUENCES: 147
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Promega Corporation
 ; STREET: 2800 Woods Hollow Road
 ; CITY: Madison
 ; STATE: Wisconsin
 ; COUNTRY: U.S.A.
 ; ZIP: 53711-5399
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
 ; COMPUTER: IBM compatible PC
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: Word 97 (DOS text format)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/018,584A
 ; FILING DATE: 04-Feb-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Grady J. Frenchick
 ; REGISTRATION NUMBER: 29,018
 ; REFERENCE/DOCKET NUMBER: 16026.9180
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (608) 257-3501
 ; TELEFAX: (608) 257-2275
 ; INFORMATION FOR SEQ ID NO: 124:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 25
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: Linear
 ; US-09-018-584A-124

Query Match 100.0%; Score 25; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCGGAGATAGAGT 25
 |||||
 Db 1 GGTTCAGTGAGCGGAGATAGAGT 25

RESULT 2
US-09-018-584A-32
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffrey W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
US-09-018-584A-32

Query Match 100.0%; Score 25; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCGGAGATAAGAGT 25
|||||
Db 441 GGTTCAGTGAGCGGAGATAAGAGT 465

RESULT 3
US-09-288-143-57
; Sequence 57, Application US/09288143
; Patent No. 6433139
; GENERAL INFORMATION:
; APPLICANT: Brewer et al.
; TITLE OF INVENTION: 53 Human Secreted Proteins
; FILE REFERENCE: P2018P1
; CURRENT APPLICATION NUMBER: US/09/288,143
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/US98/21142
; EARLIER FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 60/061,463
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,529

; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/071,498
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,527
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,536
; EARLIER FILING DATE: 1997-10-09
; EARLIER APPLICATION NUMBER: 60/061,532
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 219
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 764
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-288-143-57

Query Match 80.0%; Score 20; DB 4; Length 764;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCGGAGATA 20
|||||
Db 674 GGTTCAGTGAGCGGAGATA 693

RESULT 4
US-08-683-743-3
; Sequence 3, Application US/08683743
; Patent No. 5843697
; GENERAL INFORMATION:
; APPLICANT: Pestka, Sidney
; APPLICANT: Kotenko, Serguei
; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION
; TITLE OF INVENTION: CHAIN
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,743
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 601-1-050
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1875 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
US-08-683-743-3

Query Match 80.0%; Score 20; DB 2; Length 1875;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
Db 1551 GGTTCAGTGCAGCCGAGATA 1570

RESULT 5

US-08-406-030A-17
; Sequence 17, Application US/08406030A
; Patent No. 6270989
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Hauege, Brian M.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Protein Production and Delivery
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,030A
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/243,391
; FILING DATE: 13-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,586
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,533
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,840
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,188
; FILING DATE: 05-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11704
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09627
; FILING DATE: 05-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: TKT95-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4042 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-406-030A-17

Query Match 80.0%; Score 20; DB 4; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
Db 2894 GGTTCAGTGCAGCCGAGATA 2913

RESULT 6

US-08-370-319C-12
; Sequence 12, Application US/08370319C
; Patent No. 5856091
; GENERAL INFORMATION:
; APPLICANT: Blichard, Vincent; Van Pel, Aline;
; APPLICANT: Traversari, Catia; Wlfel, Thomas; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; De Plaen, Etienne
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE
; TITLE OF INVENTION: REJECTION ANTIGEN PRESENTED BY HLA-A2
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,319C
; FILING DATE: 10-JANUARY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/272,351
; FILING DATE: 8-JULY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,978
; FILING DATE: 18-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5856091man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5377.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence is preceded by an
; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
; OTHER INFORMATION: kilobases
US-08-370-319C-12

Query Match 80.0%; Score 20; DB 2; Length 4129;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
|||||
Db 3066 GGTTCAGTGCAGCCGAGATA 3085

RESULT 7

US-09-224-834-12
; Sequence 12, Application US/09224834
; Patent No. 6201111
; GENERAL INFORMATION:


```
; APPLICANT: Brichard, Vincent; Van Pel, Aline;
; APPLICANT: Traversari, Catia; W Ifel, Thomas; Coullie, Pierre;
; APPLICANT: Boon-Failleu, Thierry; De Plaen, Etienne
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID SEQUENCE CODING FOR A
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PERCURSOR PROCESSED TO AT LEAST ONE TU
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/224,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,319
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/032,978
; FILING DATE: 18-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 620111man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: IUD 5377.1
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: The sequence is preceded by an
; OTHER INFORMATION: unsequenced portion of from 4.7 to 5.3
; OTHER INFORMATION: kilobases
; US-09-224-834-12
;
; Query Match
; Best Local Similarity 80.0%; Score 20; DB 4; Length 4129;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGTTCAGTGAGCCGAGATA 20
; Db 3066 GGTTCAGTGAGCCGAGATA 3085
;
; RESULT 8
; US-08-965-048-5
; Sequence 5, Application US/08965048
; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45716
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-965-048-5
;
; Query Match
; Best Local Similarity 80.0%; Score 20; DB 4; Length 45716;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGTTCAGTGAGCCGAGATA 20
; Db 33531 GGTTCAGTGAGCCGAGATA 33550
;
; RESULT 9
; US-08-965-048-6
; Sequence 6, Application US/08965048
; Patent No. 6323244
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong
; APPLICANT: Freilmer, Nelson
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF NEUROPSYCHIATRIC DISORDERS
; FILE REFERENCE: 7853-093
; CURRENT APPLICATION NUMBER: US/08/965,048
; CURRENT FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 45989
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-08-965-048-6
;
; Query Match
; Best Local Similarity 100.0%; Pred. No. 0.0031;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGTTCAGTGAGCCGAGATA 20
; Db 33645 GGTTCAGTGAGCCGAGATA 33664
;
; RESULT 10
; US-08-133-629-2
; Sequence 2, Application US/08133629
; Patent No. 5597694
; GENERAL INFORMATION:
; APPLICANT: Munroe, David J.
; APPLICANT: Housman, David E.
; TITLE OF INVENTION: AMPLIFICATION OF NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,629
; FILING DATE: 07-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Greer, Helen
; REGISTRATION NUMBER: 36,816
; REFERENCE/DOCKET NUMBER: M0828/7001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
```

```

; TELEFAX: 617-720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-133-629-2

Query Match 76.0%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 3 GGTTCAGTGAGCCGAGAT 21
|||||

RESULT 11
US-08-687-080-93/c
; Sequence 93, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 5' END OF INTRON 16 OF RAD50 GENOMIC
; INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-93

Query Match 76.0%; Score 19; DB 2; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
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```

Db 128 GGTTCAGTGAGCCGAGAT 110

RESULT 12
US-08-849-701-1
; Sequence 1, Application US/08849701
; Patent No. 5922544
; GENERAL INFORMATION:
; APPLICANT: Miyai, Kiyoshi
; APPLICANT: Naïtoch, Tsutomu
; APPLICANT: Yonekawa, Toshihiro
; TITLE OF INVENTION: Method of Cell Detection
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,701
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02734
; FILING DATE: 27-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: EIKEN1.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; IMMEDIATE SOURCE:
; CLONE: Alu sequence BLUR8
US-08-849-701-1

Query Match 76.0%; Score 19; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||

Db 194 GGTTCAGTGAGCCGAGAT 212

RESULT 13
US-08-481-658B-61/c
; Sequence 61, Application US/08481658B
; Patent No. 5955075
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
```

; TITLE OF INVENTION: BACTERIUM PRODUCING L-GLUTAMIC ACID AND METHOD FOR PRODUCING L-GI

; FILE REFERENCE: 210213USO
; CURRENT APPLICATION NUMBER: US/09/895,382
; CURRENT FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: JP 2000-204256
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-895-382-6

Query Match 52.0%; Score 13; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCAGGACACAG 15
|||||
Db 15 TGCAGGACACAG 3

RESULT 21
US-09-946-807-1310/c
; Sequence 1310, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345-2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1310
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-1310

Query Match 52.0%; Score 13; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AACAGAAATTTA 22
|||||
Db 52 AACAGAAATTTA 40

RESULT 22
US-09-795-668-1310/c
; Sequence 1310, Application US/09795668
; Patent No. US2002004577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345-2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28

; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1310
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1310

Query Match 52.0%; Score 13; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AACAGAAATTTA 22
|||||
Db 52 AACAGAAATTTA 40

RESULT 23
US-09-795-686-1310/c
; Sequence 1310, Application US/09795686
; Patent No. US2002009454A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345-2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1310
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-686-1310

Query Match 52.0%; Score 13; DB 10; Length 61;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 AACAGAAATTTA 22
|||||
Db 52 AACAGAAATTTA 40

RESULT 24
US-09-878-574-11569/c
; Sequence 11569, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 11569
; LENGTH: 157
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701064613H1
US-09-878-574-11569

Query Match 52.0%; Score 13; DB 10; Length 157;
Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCCAGGACCA 14
Db 71 GTGCCAGGACCA 59

RESULT 25
US-09-960-352-2301/C
; Sequence 2301, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Neungbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2301
; LENGTH: 209
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 10-LIB34-059-Q1-E1-C9
US-09-960-352-2301

Query Match 52.0%; Score 13; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAAT 19
Db 189 AGGAACCAAGAAAT 177

RESULT 26
US-09-878-574-14842/C
; Sequence 14842, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Pyrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 14842
; LENGTH: 212
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701069323H1
US-09-878-574-14842

Query Match 52.0%; Score 13; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAAACC 13
Db 196 TGTGCCAGGAAACC 184

RESULT 27
US-09-864-761-21959
; Sequence 21959, Application US/09864761

; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21959
; LENGTH: 223
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004585.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
; OTHER INFORMATION: SWISSPROT HIT: Q14031, EVALUO 2.70e-01
; OTHER INFORMATION: EST_HUMAN HIT: A1361780.1, EVALUO 5.10e-02
; OTHER INFORMATION: NT HIT: U24393.1, EVALUO 3.40e-02
US-09-864-761-21959

Query Match 52.0%; Score 13; DB 10; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAAACC 13

```
Db      15  TGTGCCAGGAACC 27
|||||
RESULT 28
US-09-878-574-6327/c
; Sequence 6327, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 6327
; LENGTH: 247
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701098192H1
US-09-878-574-6327

Query Match      52.0%; Score 13; DB 10; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GTGCCAGGAACCA 14
|||||
Db      32  GTGCCAGGAACCA 20

RESULT 29
US-09-878-574-10539/c
; Sequence 10539, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10539
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700966787H1
US-09-878-574-10539

Query Match      52.0%; Score 13; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  GTGCCAGGAACCA 14
|||||
Db      187 GTGCCAGGAACCA 175

RESULT 30
US-09-983-965-117
; Sequence 117, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathalagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 37-21(10297)C
; CURRENT APPLICATION NUMBER: US/09/983,965
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 09/465,231
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: US 60/113,678
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 5912
; SEQ ID NO 117
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Clone ID: 14-BOYMS1-012-Q1-E1-D9
US-09-983-965-117

Query Match      52.0%; Score 13; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  CAGGAACCAAGAA 18
|||||
Db      7  CAGGAACCAAGAA 19

RESULT 31
US-09-783-590-11124/c
; Sequence 11124, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11124
; LENGTH: 294
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (65)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (112)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (121)
```

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (134)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (151)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (159)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (166)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (186)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (194)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (205)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (238)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (240)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (242)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (256)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (281)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (290)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11124

Query Match 52.0%; Score 13; DB 10; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AGGAACCCAGAAAT 19
|||||
Db 276 AGGAACCCAGAAAT 264

RESULT 32
US-09-960-352-2711/c
; Sequence 2711, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2711
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 12-LIB34-005-Q1-E1-C7
US-09-960-352-2711

Query Match 52.0%; Score 13; DB 10; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCCAGAAAT 19
|||||
Db 229 AGGAACCCAGAAAT 217

RESULT 33
US-09-960-352-4653/c
; Sequence 4653, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4653
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB34-012-Q1-E1-E7
US-09-960-352-4653

Query Match 52.0%; Score 13; DB 10; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AGGAACCCAGAAAT 19
|||||
Db 349 AGGAACCCAGAAAT 337

RESULT 34
US-09-960-352-7956/c
; Sequence 7956, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7956
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 34-LIB34-005-Q1-E1-A6
US-09-960-352-7956

Query Match 52.0%; Score 13; DB 10; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AGGAACCCAGAAAT 19
|||||
Db 22 AGGAACCCAGAAAT 10

RESULT 35
US-09-864-761-6412/c

LOCATION: (322)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (336)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (339)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (352)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (356)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (370)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (371)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (392)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (396)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (412)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (428)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (454)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (459)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-6944

Query Match 52.0%; Score 13; DB 10; Length 475;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTGCCAGGACC 13
Db 92 TGTGCCAGGACC 104

RESULT 38
US-09-878-574-4307/c
Sequence 4307, Application US/09878574
Patent No. US20020110549A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Thompson, Michael D.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 4307
LENGTH: 479
TYPE: DNA
ORGANISM: Glycine max
FEATURE:

NAME/KEY: unsure
LOCATION: (1)..(479)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB3028-014-01-B1-E10
US-09-878-574-4307

Query Match 52.0%; Score 13; DB 10; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CAGGACCAGAAA 18
Db 289 CAGGACCAGAAA 277

RESULT 39
US-09-864-761-6095
Sequence 6095, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006657
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006654
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6095
LENGTH: 481
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC004585.1


```

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
US-09-864-761-6095

Query Match          52.0%; Score 13; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACC 13
Db 286 TGTGCCAGGAACC 298

RESULT 40
US-09-783-590-11922
; Sequence 11922, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US/09783,590
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11922
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (73)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (88)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (100)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (275)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (305)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (333)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (351)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (397)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (422)

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; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (445)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (454)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (460)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (466)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (473)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11922

Query Match          52.0%; Score 13; DB 10; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATT 20
Db 208 GGAACCAAGAAATT 220

RESULT 41
US-09-833-790-163
; Sequence 163, Application US/09833790
; Patent No. US20020068288A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongtong
; APPLICANT: Secrist, Heather
; APPLICANT: Mohamath, Raedon
; APPLICANT: Indrias, Carol Y.
; APPLICANT: Fan, Ligu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-512
; CURRENT APPLICATION NUMBER: US/09/833,790
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 501
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(501)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-790-163

Query Match          52.0%; Score 13; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAGAAATTACAG 25
Db 257 CAGAAATTACAG 269

RESULT 42
US-09-783-590-5680/c
; Sequence 5680, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.

```

```
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5680
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (109)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (119)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (214)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (282)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (306)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (314)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (320)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (322)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (329)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (334)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (346)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (364)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (394)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (396)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (399)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (406)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (411)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (424)
; OTHER INFORMATION: n equals a,t,g, or c
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; NAME/KEY: misc feature
; LOCATION: (425)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (430)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (434)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (435)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (439)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (441)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (444)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (451)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (453)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (467)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (471)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (474)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (478)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (479)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (481)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (484)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (496)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-783-590-5680
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Query Match 52.0%; Score 13; DB 10; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 TGTGCCAGGACC 13
    |||||
Db 250 TGTGCCAGGACC 238
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RESULT 43
US-09-974-300-7386
; Sequence 7386, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
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; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7386
; LENGTH: 531
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(531)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-7386
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Query Match 52.0%; Score 13; DB 10; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 8 GGAACCGAAGATT 20
Db 305 GGAACCGAAGATT 317
|||||
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RESULT 44

```
US-10-062-254-119
; Sequence 119, Application US/10062254
; Patent No. US20020138882A1
; GENERAL INFORMATION:
; APPLICANT: Caboon, Edgar B
; APPLICANT: Caboon, Rebecca E
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Fang, Yiwen
; APPLICANT: Hantke, Sabine S.
; APPLICANT: Lee, Jian-Ming
; APPLICANT: Li, Zhongsen
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Morgante, Michele
; APPLICANT: Niu, Xiping
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Zheng, Peizhong
; APPLICANT: Zhu, Qun
; TITLE OF INVENTION: Polynucleotides Encoding Proteins Involved in Plant Metabolism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/062,254
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/630,346
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: 60/146511
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/156006
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/156899
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/157287
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/169767
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/171054
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/172958
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/171515
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 60/173535
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 119
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; LENGTH: 531
; TYPE: DNA
; ORGANISM: Vernonia mespilifolia
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (422)
; NAME/KEY: unsure
; LOCATION: (528)
US-10-062-254-119
```

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Query Match 52.0%; Score 13; DB 12; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 CCAGAAATTACA 24
Db 363 CCAGAAATTACA 375
|||||
```

RESULT 45

```
US-09-834-975-60
; Sequence 60, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(535)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-60
```

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Query Match 52.0%; Score 13; DB 10; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 12 CCAGAAATTACA 24
Db 370 CCAGAAATTACA 382
|||||
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Search completed: November 24, 2002, 16:56:07
Job time : 1156.5 secs
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;
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,658B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-481-658B-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 75 GGTTCAGTGAGCCGAGAT 57

RESULT 14
US-08-477-504A-61/c
; Sequence 61, Application US/08/477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:

;
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-477-504A-61

Query Match 76.0%; Score 19; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 75 GGTTCAGTGAGCCGAGAT 57

RESULT 15
US-08-486-756A-61/c
; Sequence 61, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-486-756A-61

Query Match 76.0%; Score 19; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGAT 19
 |||||
 Db 75 GGTTCAGTGCAGCGAGAT 57

RESULT 16

US-08-485-862B-61/c
 ; Sequence 61, Application US/08485862B
 ; Patent No. 5989838
 ; GENERAL INFORMATION:
 ; APPLICANT: Zavada, Jan
 ; APPLICANT: Pastorekova, Silvia
 ; APPLICANT: Pastorek, Jaromir
 ; TITLE OF INVENTION: MN Gene and Protein
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leona L. Lauder
 ; STREET: 6 Mariposa Court
 ; CITY: Tiburon
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94920
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,862B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/477,504
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/260,190
 ; FILING DATE: 15-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lauder, Leona L.
 ; REGISTRATION NUMBER: 30,863
 ; REFERENCE/DOCKET NUMBER: D-0021.3D
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-435-2034
 ; TELEFAX: 415-435-0727
 ; INFORMATION FOR SEQ ID NO: 61:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-485-862B-61

Query Match 76.0%; Score 19; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGAT 19
 |||||
 Db 75 GGTTCAGTGCAGCGAGAT 57

RESULT 17

US-08-787-739-61/c
 ; Sequence 61, Application US/08787739
 ; Patent No. 6027887
 ; GENERAL INFORMATION:
 ; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia
 ; APPLICANT: Pastorek, Jaromir
 ; TITLE OF INVENTION: MN Gene and Protein
 ; NUMBER OF SEQUENCES: 96
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Leona L. Lauder
 ; STREET: 369 Pine Street, Suite 610
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/787,739
 ; FILING DATE: 24-JAN-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,049
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/486,756
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/477,504
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/481,658
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,862
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/485,863
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/487,077
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lauder, Leona L.
 ; REGISTRATION NUMBER: 30,863
 ; REFERENCE/DOCKET NUMBER: D-0021.4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-981-2034
 ; TELEFAX: 415-981-0332
 ; INFORMATION FOR SEQ ID NO: 61:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-787-739-61

Query Match 76.0%; Score 19; DB 3; Length 294;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGCAGCGAGAT 19
 |||||
 Db 75 GGTTCAGTGCAGCGAGAT 57

RESULT 18

US-08-487-077A-61/c
 ; Sequence 61, Application US/08487077A
 ; Patent No. 6069242
 ; GENERAL INFORMATION:
 ; APPLICANT: Zavada, Jan

```

; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION INFORMATION:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-0727
; TELEFAX: 415-435-2034
; INFORMATION FOR SEQ ID NO: 61:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-487-077A-61

Query Match 76.0%; Score 19; DB 3; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 75 GGTTCAGTGAGCCGAGAT 57

RESULT 19
US-08-485-863A-61/c
; Sequence 61, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,077A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION INFORMATION:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 61:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; US-08-487-077A-61

```

```

; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-485-863A-61

Query Match 76.0%; Score 19; DB 3; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 75 GGTTCAGTGAGCCGAGAT 57

RESULT 20
US-08-485-049D-61/c
; Sequence 61, Application US/08485049D
; Patent No. 6204370
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,049D
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-485-049D-61

```

```

Query Match          76.0%; Score 19; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 GGTTCAGTGAGCCGAGAT 19
    |||||||
Db 75 GGTTCAGTGAGCCGAGAT 57

```

RESULT 21

```

US-09-178-115-61/c
; Sequence 61, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 294
; TYPE: DNA
; ORGANISM: HUMAN
US-09-178-115-61

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```

Query Match          76.0%; Score 19; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 1 GGTTCAGTGAGCCGAGAT 19
    |||||||
Db 75 GGTTCAGTGAGCCGAGAT 57

```

RESULT 22

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US-09-177-776-61/c

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; Sequence 61, Application US/09177776A
; Patent No. 6297051
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/177,776A
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 294
; TYPE: DNA
; ORGANISM: HUMAN
US-09-177-776-61

```

```

Query Match          76.0%; Score 19; DB 4; Length 294;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGTTCAGTGAGCCGAGAT 19
    |||||||
Db 75 GGTTCAGTGAGCCGAGAT 57

```

RESULT 23

```

US-08-849-701-3
; Sequence 3, Application US/08849701
; Patent No. 5922544
; GENERAL INFORMATION:
; APPLICANT: Miyai, Kiyoshi
; APPLICANT: Naitoh, Tsutomu
; APPLICANT: Yonekawa, Toshihiro
; TITLE OF INVENTION: Method of Cell Detection
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/849,701
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/JP95/02734
;; FILING DATE: 27-DEC-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Altman, Daniel E
;; REGISTRATION NUMBER: 34,115
;; REFERENCE/DOCKET NUMBER: EIKEN1.001APC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 714-760-0404
;; TELEFAX: 714-760-9502
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 302 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; CLONE: Alu sequence BLUR2
US-08-849-701-3

Query Match 76.0%; Score 19; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 217 GGTTCAGTGAGCCGAGAT 235

RESULT 24

US-09-385-982-17
;; Sequence 17, Application US/09385982
;; Patent No. 6262334
;; GENERAL INFORMATION:
;; APPLICANT: ENDEGE, WILSON O., ET AL.
;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;; FILE REFERENCE: CCNDA-260XX
;; CURRENT APPLICATION NUMBER: US/09/385,982
;; EARLIER FILING DATE: 1999-08-30
;; EARLIER APPLICATION NUMBER: 09/328,111
;; EARLIER FILING DATE: 1999-06-08
;; EARLIER FILING DATE: 1999-01-27
;; EARLIER FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 544
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 17
;; LENGTH: 336
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(336)
;; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-17

Query Match 76.0%; Score 19; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 240 GGTTCAGTGAGCCGAGAT 258

RESULT 25

US-09-385-982-135/c
;; Sequence 135, Application US/09385982
;; Patent No. 6262334
;; GENERAL INFORMATION:
;; APPLICANT: ENDEGE, WILSON O., ET AL.
;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;; FILE REFERENCE: CCNDA-260XX
;; CURRENT APPLICATION NUMBER: US/09/385,982
;; EARLIER FILING DATE: 1999-08-30
;; EARLIER APPLICATION NUMBER: 09/328,111
;; EARLIER FILING DATE: 1999-06-08
;; EARLIER FILING DATE: 1999-01-27
;; EARLIER APPLICATION NUMBER: 60/098,639
;; EARLIER FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 544
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 135
;; LENGTH: 374
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(374)
;; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-135

Query Match 76.0%; Score 19; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 95 GGTTCAGTGAGCCGAGAT 77

RESULT 26

US-09-157-177-134/c
;; Sequence 134, Application US/09157177
;; Patent No. 6090558
;; GENERAL INFORMATION:
;; APPLICANT: Butler, John M.
;; APPLICANT: Li, Jia
;; APPLICANT: Monforte, Joseph A.
;; APPLICANT: Becker, Christopher H.
;; TITLE OF INVENTION: DNA TYPING BY MASS SPECTROMETRY WITH POLYMORPHIC DNA
;; FILE REFERENCE: GSTR:017/GETR017P
;; CURRENT APPLICATION NUMBER: US/09/157,177
;; EARLIER FILING DATE: 1998-09-18
;; EARLIER APPLICATION NUMBER: 60/059,415
;; EARLIER FILING DATE: 1997-09-19
;; NUMBER OF SEQ ID NOS: 135
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 134
;; LENGTH: 379
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-157-177-134

Query Match 76.0%; Score 19; DB 3; Length 379;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 355 GGTTCAGTGAGCCGAGAT 337

RESULT 27

US-09-227-357-92
;; Sequence 92, Application US/09227357

; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-357-92

Query Match 76.0%; Score 19; DB 4; Length 577;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 489 GGTTCAGTGCAGCCGAGAT 507

RESULT 28

US-09-385-982-291/c
; Sequence 291, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 291
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(609)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-291

Query Match 76.0%; Score 19; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 30 GGTTCAGTGCAGCCGAGAT 12

RESULT 29

US-09-385-982-218/c
; Sequence 218, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544

JS-09-105-542A-14

EARLIER APPLICATION NUMBER: 60/051,930

EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 108
LENGTH: 775
TYPE: DNA
ORGANISM: Homo sapiens
US-09-227-357-108

Query Match 76.0%; Score 19; DB 4; Length 775;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTTGCGAGTGAGCCGAGAT 19
Db 679 GGTTGCGAGTGAGCCGAGAT 697

RESULT 34
US-08-394-152A-42/C
Sequence 42, Application US/08394152A
Patent No. 5935818
GENERAL INFORMATION:
APPLICANT: Israeli, Ron S.
APPLICANT: Heston, Warren D.W.
APPLICANT: Fair, William R.
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,152A
FILING DATE: 24-FEB-95
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41426-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo Sapien
TISSUE TYPE: Carcinoma
IMMEDIATE SOURCE:
CLONE: Prostate Specific Membrane Antigen
US-08-394-152A-42

Query Match 76.0%; Score 19; DB 2; Length 789;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTTGCGAGTGAGCCGAGAT 19
Db 487 GGTTGCGAGTGAGCCGAGAT 469

RESULT 35
US-09-342-681C-7
Sequence 7, Application US/09342681C
Patent No. 6355782
GENERAL INFORMATION:
APPLICANT: Zonana et al.
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
FILE REFERENCE: 52978
CURRENT APPLICATION NUMBER: US/09/342,681C
CURRENT FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 60/092,279
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/112,366
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 821
TYPE: DNA
ORGANISM: Homo sapiens
US-09-342-681C-7

Query Match 76.0%; Score 19; DB 4; Length 821;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 192 GGTTCAGTGAGCCGAGAT 210
RESULT 36
US-08-486-148B-1/c
; Sequence 1, Application US/08486148B
; Patent No. 5840555
; GENERAL INFORMATION:
; APPLICANT: Oshima, Robert G.
; APPLICANT: Meznarov, Nikolay S.
; TITLE OF INVENTION: Transcriptional Regulatory Regions
; TITLE OF INVENTION: Derived from the K18 Gene.
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,148B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,486
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1698
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-486-148B-1
Query Match 76.0%; Score 19; DB 2; Length 825;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCCGAGAT 19
Db 522 GGTTCAGTGAGCCGAGAT 504
RESULT 37
PCT-US93-06251-80
; Sequence 80, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City

; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 841 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-80
Query Match 76.0%; Score 19; DB 5; Length 841;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTTCAGTGAGCCGAGAT 19
Db 275 GGTTCAGTGAGCCGAGAT 293
RESULT 38
PCT-US93-06251-81
; Sequence 81, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 841 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-81

Query Match 76.0%; Score 19; DB 5; Length 841;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 275 GGTTCAGTGAGCCGAGAT 293

RESULT 39
US-09-257-179-11
Sequence 11, Application US/09257179
Patent No. 6410709
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
EARLIER FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 866
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (37)
OTHER INFORMATION: n equals a,t,g, or c
US-09-257-179-11

Query Match 76.0%; Score 19; DB 4; Length 866;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 769 GGTTCAGTGAGCCGAGAT 787

RESULT 40
US-09-288-143-55
Sequence 55, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288,143
EARLIER FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,463

EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
NUMBER OF SEQ ID NOS: 219
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 55
LENGTH: 885
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
US-09-288-143-55

Query Match 76.0%; Score 19; DB 4; Length 885;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 799 GGTTCAGTGAGCCGAGAT 817

RESULT 41
US-08-832-883-52/c
Sequence 52, Application US/08832883
Patent No. 5807681
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-13 US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 889 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-883-52

Query Match 76.0%; Score 19; DB 1; Length 889;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 520 GGTTCAGTGAGCCGAGAT 502

RESULT 42

US-08-832-877-52/c
; Sequence 52, Application US/08832877
; Patent No. 5840506
; GENERAL INFORMATION:
; APPLICANT: Giordano, Antonio
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
; STREET: Suite 1800 Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/832,877
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 8321-13 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-832-877-52

Query Match 76.0%; Score 19; DB 2; Length 889;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 520 GGTTCAGTGAGCCGAGAT 502

RESULT 43

US-09-247-155-141
; Sequence 141, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121

; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 141
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4..447
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 4..147
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8999980926514
; OTHER INFORMATION: seq LILFFGKLLVVG/VG
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 858..863
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 880..891
US-09-247-155-141

Query Match 76.0%; Score 19; DB 4; Length 891;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
|||||
Db 769 GGTTCAGTGAGCCGAGAT 787

RESULT 44

US-09-018-584A-40
; Sequence 40, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275

; INFORMATION FOR SEQ ID NO: 40:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1000 bp
 ; TYPE: Nucleic Acid
 ; STRANDEDNESS: Double
 ; TOPOLOGY: Circular
 ; MOLECULE TYPE: Genomic DNA
 ; HYPOTHETICAL: no
 ; IMMEDIATE SOURCE:
 ; LIBRARY:
 ; CLONE: S077
 ; US-09-018-584A-40

Query Match 76.0%; Score 19; DB 4; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGGCCGAGAT 19
 |||||
 Db 664 GGTTCAGTGGCCGAGAT 682

RESULT 45
 US-09-641-638-636
 ; Sequence 636, Application US/09641638
 ; Patent No. 6432648
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Bougueleret, Lydie
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Cohen, Annick
 ; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
 ; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
 ; FILE REFERENCE: GENSET.051CE1
 ; CURRENT APPLICATION NUMBER: US/09/641,638
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: US 09/502,330
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: US 60/133,200
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: US 09/275,267
 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: US 60/119,917
 ; PRIOR FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 1304
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 636
 ; LENGTH: 1000
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 501
 ; OTHER INFORMATION: 10-508-191 : polymorphic base C or T
 ; NAME/KEY: misc_binding
 ; LOCATION: 481..500
 ; OTHER INFORMATION: 10-508-191.mis1, potential
 ; NAME/KEY: misc_binding
 ; LOCATION: 502..521
 ; OTHER INFORMATION: 10-508-191.mis2, potential complement
 ; NAME/KEY: primer_bind
 ; LOCATION: 311..328
 ; OTHER INFORMATION: upstream amplification primer
 ; NAME/KEY: primer_bind
 ; LOCATION: 727..746
 ; OTHER INFORMATION: downstream amplification primer, complement
 ; NAME/KEY: misc_binding
 ; LOCATION: 489..513
 ; OTHER INFORMATION: 10-508-191 potential probe
 ; US-09-641-638-636

Query Match 76.0%; Score 19; DB 4; Length 1000;
 Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTTCAGTGGCCGAGAT 19
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 Db 140 GGTTCAGTGGCCGAGAT 158
 Search completed: November 24, 2002, 15:03:42
 Job time : 63.5 secs

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 14:30:54 ; Search time 52.5 Seconds
 (without alignments)
 180.348 Million cell updates/sec

Title: US-09-784-423-124

Perfect score: 25

Sequence: 1 GGTGCAGTCAGCCGAGATAGAGT 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 335578 seqs, 189365133 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	10	US-09-784-423-124
2	25	100.0	1000	10	US-09-784-423-32
3	20	80.0	384	10	US-09-867-701-2157
4	20	80.0	1875	12	US-10-052-586-389
5	20	80.0	2529	10	US-09-764-847-1859
6	20	80.0	5000	10	US-09-791-105-1
7	20	80.0	5131	10	US-09-764-877-3800
8	20	80.0	5139	10	US-09-764-877-3802
9	20	80.0	5814	10	US-09-764-847-1860
10	20	80.0	8886	10	US-09-764-878-412
11	20	80.0	8887	10	US-09-764-878-414
12	20	80.0	16106	10	US-09-764-877-2332
13	20	80.0	18878	10	US-09-764-877-2326
14	20	80.0	28588	10	US-09-764-877-3806
15	20	80.0	31994	10	US-09-764-887-399
16	20	80.0	32248	10	US-09-764-860-599
17	20	80.0	32248	10	US-09-764-864-1769
18	20	80.0	49984	10	US-09-764-877-3487
19	20	80.0	49984	10	US-09-739-457-5
20	20	80.0	65608	9	US-09-954-531-180
21	20	80.0	65608	10	US-09-962-436-292
22	20	80.0	65608	10	US-09-962-832-119
23	20	80.0	99014	10	US-09-880-107-3428
24	20	80.0	203654	10	US-09-820-905-3
25	20	80.0	302250	10	US-09-962-832-154
26	19	76.0	90	10	US-09-764-887-601
27	19	76.0	95	10	US-09-764-869-2069
28	19	76.0	98	10	US-09-764-869-1767
29	19	76.0	100	10	US-09-764-887-600
30	19	76.0	102	10	US-09-764-877-3352
31	19	76.0	105	10	US-09-764-860-979
32	19	76.0	107	10	US-09-764-869-2068
33	19	76.0	110	9	US-09-764-868-1442
34	19	76.0	114	10	US-09-764-860-792
35	19	76.0	114	10	US-09-764-847-1408
36	19	76.0	114	10	US-09-764-847-1409
37	19	76.0	118	9	US-09-860-670-234
38	19	76.0	120	10	US-09-764-860-659
39	19	76.0	122	10	US-09-764-877-2168
40	19	76.0	123	10	US-09-764-847-1855
41	19	76.0	126	10	US-09-764-869-2373
42	19	76.0	129	10	US-09-783-590-10234
43	19	76.0	129	10	US-09-764-847-1975
44	19	76.0	130	10	US-09-764-877-4006
45	19	76.0	131	10	US-09-764-877-2688

ALIGNMENTS

RESULT 1

US-09-784-423-124

; Sequence 124, Application US/09784423

; Patent No. US20020012924A1

; GENERAL INFORMATION:

; APPLICANT: Schumm, James W.

; Bacher, Jeffery W.

; TITLE OF INVENTION: MATERIALS AND METHODS FOR IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Promega Corporation

; STREET: 2800 Woods Hollow Road

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53711-5399

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

; COMPUTER: IBM compatible PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 97 (DOS text format)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/784,423

; FILING DATE: 15-Feb-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/018,584

; FILING DATE: 04-Feb-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Grady J. Frenchick

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 16025.9180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 257-3501

; TELEFAX: (608) 257-2275

; INFORMATION FOR SEQ ID NO: 124

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

Sequence 292, App
 Sequence 119, App
 Sequence 3428, App
 Sequence 3, Appli
 Sequence 154, App
 Sequence 601, App
 Sequence 2069, App
 Sequence 1767, App
 Sequence 2198, App
 Sequence 600, App
 Sequence 3352, App
 Sequence 979, App
 Sequence 2068, App
 Sequence 1442, App
 Sequence 792, App
 Sequence 1408, App
 Sequence 1409, App
 Sequence 234, App
 Sequence 659, App
 Sequence 2168, App
 Sequence 1855, App
 Sequence 2373, App
 Sequence 10234, A
 Sequence 1975, App
 Sequence 4006, App
 Sequence 2688, App


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; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 124
US-09-784-423-124

Query Match      100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATAAGAGT 25
    |||||||||||||||||||
Db 1 GGTTCAGTGGCGGAGATAAGAGT 25

RESULT 2
US-09-784-423-32
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
; SEQUENCE DESCRIPTION: SEQ ID NO: 32
US-09-784-423-32

Query Match      100.0%; Score 25; DB 10; Length 1000;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATAAGAGT 25
    |||||||||||||||||||
Db 441 GGTTCAGTGGCGGAGATAAGAGT 455

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RESULT 3
US-09-867-701-2157/c
; Sequence 2157, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2157
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(384)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2157

Query Match      80.0%; Score 20; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCGGAGATA 20
    |||||||||||||||
Db 70 GGTTCAGTGGCGGAGATA 51

RESULT 4
US-10-052-586-389
; Sequence 389, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMERANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544

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1	PRIOR FILING DATE:	1997-10-28
2	PRIOR APPLICATION NUMBER:	60/063564
3	PRIOR FILING DATE:	1997-10-28
4	PRIOR APPLICATION NUMBER:	60/063734
5	PRIOR FILING DATE:	1997-10-29
6	PRIOR APPLICATION NUMBER:	60/063870
7	PRIOR FILING DATE:	1997-10-31
8	PRIOR APPLICATION NUMBER:	60/064103
9	PRIOR FILING DATE:	1997-10-31
10	PRIOR APPLICATION NUMBER:	60/065311
11	PRIOR FILING DATE:	1997-11-13
12	PRIOR APPLICATION NUMBER:	60/066120
13	PRIOR FILING DATE:	1997-11-21
14	PRIOR APPLICATION NUMBER:	60/066466
15	PRIOR FILING DATE:	1997-11-24
16	PRIOR APPLICATION NUMBER:	60/066772
17	PRIOR FILING DATE:	1997-11-24
18	PRIOR APPLICATION NUMBER:	60/069335
19	PRIOR FILING DATE:	1997-12-11
20	PRIOR APPLICATION NUMBER:	60/069425
21	PRIOR FILING DATE:	1997-12-12
22	PRIOR APPLICATION NUMBER:	60/069870
23	PRIOR FILING DATE:	1997-12-17
24	PRIOR APPLICATION NUMBER:	60/068017
25	PRIOR FILING DATE:	1997-12-18
26	PRIOR APPLICATION NUMBER:	60/077450
27	PRIOR FILING DATE:	1998-03-10
28	PRIOR APPLICATION NUMBER:	60/077632
29	PRIOR FILING DATE:	1998-03-11
30	PRIOR APPLICATION NUMBER:	60/077649
31	PRIOR FILING DATE:	1998-03-11
32	PRIOR APPLICATION NUMBER:	60/078886
33	PRIOR FILING DATE:	1998-03-20
34	PRIOR APPLICATION NUMBER:	60/078939
35	PRIOR FILING DATE:	1998-03-20
36	PRIOR APPLICATION NUMBER:	60/079664
37	PRIOR FILING DATE:	1998-03-27
38	PRIOR APPLICATION NUMBER:	60/079786
39	PRIOR FILING DATE:	1998-03-27
40	PRIOR APPLICATION NUMBER:	60/080107
41	PRIOR FILING DATE:	1998-03-31
42	PRIOR APPLICATION NUMBER:	60/080194
43	PRIOR FILING DATE:	1998-03-31
44	PRIOR APPLICATION NUMBER:	60/080327
45	PRIOR FILING DATE:	1998-04-01
46	PRIOR APPLICATION NUMBER:	60/080333
47	PRIOR FILING DATE:	1998-04-01
48	PRIOR APPLICATION NUMBER:	60/081049
49	PRIOR FILING DATE:	1998-04-08
50	PRIOR APPLICATION NUMBER:	60/081070
51	PRIOR FILING DATE:	1998-04-08
52	PRIOR APPLICATION NUMBER:	60/081195
53	PRIOR FILING DATE:	1998-04-09
54	PRIOR APPLICATION NUMBER:	60/081838
55	PRIOR FILING DATE:	1998-04-15
56	PRIOR APPLICATION NUMBER:	60/082568
57	PRIOR FILING DATE:	1998-04-21
58	PRIOR APPLICATION NUMBER:	60/082569
59	PRIOR FILING DATE:	1998-04-21
60	PRIOR APPLICATION NUMBER:	60/082704
61	PRIOR FILING DATE:	1998-04-22
62	PRIOR APPLICATION NUMBER:	60/082797
63	PRIOR FILING DATE:	1998-04-22
64	PRIOR APPLICATION NUMBER:	60/083322
65	PRIOR FILING DATE:	1998-04-28
66	PRIOR APPLICATION NUMBER:	60/083495
67	PRIOR FILING DATE:	1998-04-29
68	PRIOR APPLICATION NUMBER:	60/083496
69	PRIOR FILING DATE:	1998-04-29
70	PRIOR APPLICATION NUMBER:	60/083499
71	PRIOR FILING DATE:	1998-04-29
72	PRIOR APPLICATION NUMBER:	60/083559
73	PRIOR FILING DATE:	1998-04-29

1	60/0843636	PRIOR APPLICATION NUMBER: 60/0843636
2	60/0843636	PRIOR FILING DATE: 1998-05-05
3	60/084414	PRIOR APPLICATION NUMBER: 60/084414
4	60/084414	PRIOR FILING DATE: 1998-05-06
5	60/084639	PRIOR APPLICATION NUMBER: 60/084639
6	60/084639	PRIOR FILING DATE: 1998-05-07
7	60/084640	PRIOR APPLICATION NUMBER: 60/084640
8	60/084640	PRIOR FILING DATE: 1998-05-07
9	60/084643	PRIOR APPLICATION NUMBER: 60/084643
10	60/084643	PRIOR FILING DATE: 1998-05-07
11	60/085573	PRIOR APPLICATION NUMBER: 60/085573
12	60/085573	PRIOR FILING DATE: 1998-05-15
13	60/085579	PRIOR APPLICATION NUMBER: 60/085579
14	60/085579	PRIOR FILING DATE: 1998-05-15
15	60/085580	PRIOR APPLICATION NUMBER: 60/085580
16	60/085580	PRIOR FILING DATE: 1998-05-15
17	60/085582	PRIOR APPLICATION NUMBER: 60/085582
18	60/085582	PRIOR FILING DATE: 1998-05-15
19	60/085700	PRIOR APPLICATION NUMBER: 60/085700
20	60/085700	PRIOR FILING DATE: 1998-05-15
21	60/086023	PRIOR APPLICATION NUMBER: 60/086023
22	60/086023	PRIOR FILING DATE: 1998-05-18
23	60/086392	PRIOR APPLICATION NUMBER: 60/086392
24	60/086392	PRIOR FILING DATE: 1998-05-22
25	60/086486	PRIOR APPLICATION NUMBER: 60/086486
26	60/086486	PRIOR FILING DATE: 1998-05-22
27	60/087098	PRIOR APPLICATION NUMBER: 60/087098
28	60/087098	PRIOR FILING DATE: 1998-05-28
29	60/087208	PRIOR APPLICATION NUMBER: 60/087208
30	60/087208	PRIOR FILING DATE: 1998-05-28
31	60/087609	PRIOR APPLICATION NUMBER: 60/087609
32	60/087609	PRIOR FILING DATE: 1998-06-02
33	60/087759	PRIOR APPLICATION NUMBER: 60/087759
34	60/087759	PRIOR FILING DATE: 1998-06-02
35	60/087827	PRIOR APPLICATION NUMBER: 60/087827
36	60/087827	PRIOR FILING DATE: 1998-06-03
37	60/088025	PRIOR APPLICATION NUMBER: 60/088025
38	60/088025	PRIOR FILING DATE: 1998-06-04
39	60/088028	PRIOR APPLICATION NUMBER: 60/088028
40	60/088028	PRIOR FILING DATE: 1998-06-04
41	60/088029	PRIOR APPLICATION NUMBER: 60/088029
42	60/088029	PRIOR FILING DATE: 1998-06-04
43	60/088033	PRIOR APPLICATION NUMBER: 60/088033
44	60/088033	PRIOR FILING DATE: 1998-06-04
45	60/088167	PRIOR APPLICATION NUMBER: 60/088167
46	60/088167	PRIOR FILING DATE: 1998-06-05
47	60/088202	PRIOR APPLICATION NUMBER: 60/088202
48	60/088202	PRIOR FILING DATE: 1998-06-05
49	60/088212	PRIOR APPLICATION NUMBER: 60/088212
50	60/088212	PRIOR FILING DATE: 1998-06-05
51	60/088217	PRIOR APPLICATION NUMBER: 60/088217
52	60/088217	PRIOR FILING DATE: 1998-06-05
53	60/088326	PRIOR APPLICATION NUMBER: 60/088326
54	60/088326	PRIOR FILING DATE: 1998-06-04
55	60/088655	PRIOR APPLICATION NUMBER: 60/088655
56	60/088655	PRIOR FILING DATE: 1998-06-09
57	60/088722	PRIOR APPLICATION NUMBER: 60/088722
58	60/088722	PRIOR FILING DATE: 1998-06-10
59	60/088738	PRIOR APPLICATION NUMBER: 60/088738
60	60/088738	PRIOR FILING DATE: 1998-06-10
61	60/088740	PRIOR APPLICATION NUMBER: 60/088740
62	60/088740	PRIOR FILING DATE: 1998-06-10
63	60/088811	PRIOR APPLICATION NUMBER: 60/088811
64	60/088811	PRIOR FILING DATE: 1998-06-10
65	60/088824	PRIOR APPLICATION NUMBER: 60/088824
66	60/088824	PRIOR FILING DATE: 1998-06-10
67	60/088825	PRIOR APPLICATION NUMBER: 60/088825
68	60/088825	PRIOR FILING DATE: 1998-06-10
69	60/088826	PRIOR APPLICATION NUMBER: 60/088826
70	60/088826	PRIOR FILING DATE: 1998-06-10
71	60/088861	PRIOR APPLICATION NUMBER: 60/088861
72	60/088861	PRIOR FILING DATE: 1998-06-11
73	60/088863	PRIOR APPLICATION NUMBER: 60/088863

; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 80.0%; Score 20; DB 12; Length 1875;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1551 GGTTCAGTGAGCCGAGATA 1570

RESULT 5

US-09-764-847-1859
; Sequence 1859, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764.847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1859
; LENGTH: 2529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1859

Query Match 80.0%; Score 20; DB 10; Length 2529;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 850 GGTTCAGTGAGCCGAGATA 869

RESULT 6

US-09-791-105-1
; Sequence 1, Application US/09791105
; Patent No. US200202225A1
; GENERAL INFORMATION:
; APPLICANT: Epidauros Biotechnologie AG
; TITLE OF INVENTION: Method for detecting the presence of at least one single allele

; FILE REFERENCE: EPI 01/00
; CURRENT APPLICATION NUMBER: US/09/791.105
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: EP 00103844.7
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5000
; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-791-105-1

Query Match 80.0%; Score 20; DB 10; Length 5000;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 3838 GGTTCAGTGAGCCGAGATA 3857

RESULT 7

US-09-764-877-3800/c
; Sequence 3800, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764.877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3800
; LENGTH: 5131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3800

Query Match 80.0%; Score 20; DB 10; Length 5131;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 3049 GGTTCAGTGAGCCGAGATA 3030

RESULT 8

US-09-764-877-3802/c
; Sequence 3802, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764.877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3802
; LENGTH: 5139
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3802

Query Match 80.0%; Score 20; DB 10; Length 5139;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
| | | | | | | | | | | | | | | | | | | | | |
Db 3049 GGTTCAGTGAGCCGAGATA 3030

RESULT 9

US-09-764-847-1860
; Sequence 1860, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC009
 ; CURRENT APPLICATION NUMBER: US/09/764,847
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 2003
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1860
 ; LENGTH: 5814
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-847-1860

Query Match 80.0%; Score 20; DB 10; Length 5814;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
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 Db 4138 GGTTCAGTGAGCCGAGATA 4157

RESULT 10

US-09-764-878-412
 ; Sequence 412, Application US/09764878
 ; Patent No. US20020090615A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA121
 ; CURRENT APPLICATION NUMBER: US/09/764,878
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 428
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 412
 ; LENGTH: 8886
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-878-412

Query Match 80.0%; Score 20; DB 10; Length 8886;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||||
 Db 8094 GGTTCAGTGAGCCGAGATA 8113

RESULT 11

US-09-764-878-414
 ; Sequence 414, Application US/09764878
 ; Patent No. US20020090615A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA121
 ; CURRENT APPLICATION NUMBER: US/09/764,878
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 428
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 414
 ; LENGTH: 8887
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-878-414

Query Match 80.0%; Score 20; DB 10; Length 8887;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||||
 Db 8094 GGTTCAGTGAGCCGAGATA 8113

RESULT 12

US-09-764-877-2322/c
 ; Sequence 2322, Application US/09764877
 ; Patent No. US20020147140A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC005
 ; CURRENT APPLICATION NUMBER: US/09/764,877
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 4031
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2322
 ; LENGTH: 16106
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-877-2322

Query Match 80.0%; Score 20; DB 10; Length 16106;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||||
 Db 12684 GGTTCAGTGAGCCGAGATA 12665

RESULT 13

US-09-764-877-3806/c
 ; Sequence 3806, Application US/09764877
 ; Patent No. US20020147140A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC005
 ; CURRENT APPLICATION NUMBER: US/09/764,877
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - refer to PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 4031
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3806
 ; LENGTH: 18878
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-877-3806

Query Match 80.0%; Score 20; DB 10; Length 18878;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
 |||||
 Db 1960 GGTTCAGTGAGCCGAGATA 1941

RESULT 14

US-09-764-887-399/c
 ; Sequence 399, Application US/09764887
 ; Patent No. US20020042096A1
 ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA113
 ; CURRENT APPLICATION NUMBER: US/09/764,887
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 399
; LENGTH: 28588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-399

Query Match 80.0%; Score 20; DB 10; Length 28588;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCCGAGATA 20
|||||
Db 3891 GGTTCAGTGGCCGAGATA 3872

RESULT 15

US-09-764-860-599/c
; Sequence 599, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 599
; LENGTH: 31994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-599

Query Match 80.0%; Score 20; DB 10; Length 31994;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCCGAGATA 20
|||||
Db 4422 GGTTCAGTGGCCGAGATA 4403

RESULT 16

US-09-764-864-1769
; Sequence 1769, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1769
; LENGTH: 32248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-1769

Query Match 80.0%; Score 20; DB 10; Length 32248;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCCGAGATA 20
|||||
Db 12778 GGTTCAGTGGCCGAGATA 12797

RESULT 17

US-09-764-877-3487/c
; Sequence 3487, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3487
; LENGTH: 32248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3487

Query Match 80.0%; Score 20; DB 10; Length 32248;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCCGAGATA 20
|||||
Db 19471 GGTTCAGTGGCCGAGATA 19452

RESULT 18

US-09-739-457-5/c
; Sequence 5, Application US/09739457
; Patent No. US20020072488A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady V. et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001014
; CURRENT APPLICATION NUMBER: US/09/739,457
; CURRENT FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 49984
; TYPE: DNA
; ORGANISM: Human
US-09-739-457-5

Query Match 80.0%; Score 20; DB 10; Length 49984;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTTCAGTGGCCGAGATA 20
|||||
Db 19071 GGTTCAGTGGCCGAGATA 19052

RESULT 19

US-09-954-531-180/c
; Sequence 180, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 68290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034

; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 180
; LENGTH: 65608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(65608)
; OTHER INFORMATION: n=a,t,g or c
US-09-954-531-180

Query Match 80.0%; Score 20; DB 9; Length 65608;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
Db 62021 GGTTCAGTGAGCCGAGATA 62002

RESULT 20
US-09-962-436-292/c
; Sequence 292, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962,436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 65608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-962-436-292

Query Match 80.0%; Score 20; DB 10; Length 65608;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
Db 62021 GGTTCAGTGAGCCGAGATA 62002

RESULT 21
US-09-962-832-119/c
; Sequence 119, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Eder, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077

; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 119
; LENGTH: 65608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-962-832-119

Query Match 80.0%; Score 20; DB 10; Length 65608;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
Db 62021 GGTTCAGTGAGCCGAGATA 62002

RESULT 22
US-09-880-107-3428/c
; Sequence 3428, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Logic, Inc.
; FILE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3428
; LENGTH: 99014
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U78027
US-09-880-107-3428

Query Match 80.0%; Score 20; DB 10; Length 99014;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGATA 20
|||||
Db 93447 GGTTCAGTGAGCCGAGATA 93428

RESULT 23
US-09-820-905-3/c
; Sequence 3, Application US/09820905
; Patent No. US20020142938A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Chunhua
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001199
; CURRENT APPLICATION NUMBER: US/09/820,905
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 3
; LENGTH: 203654
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(203654)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-905-3

Query Match      80.0%; Score 20; DB 10; Length 203654;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
Db 33496 GGTTCAGTGCAGCCGAGATA 33477

RESULT 24
US-09-962-832-154/c
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Eber, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962.832
; PRIOR APPLICATION NUMBER: US/01-09-25
; PRIOR FILING DATE: 2001-09-25
; PRIOR FILLING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILLING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
; LENGTH: 302250
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-154

Query Match      80.0%; Score 20; DB 10; Length 302250;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGATA 20
Db 295292 GGTTCAGTGCAGCCGAGATA 295273

RESULT 25
US-09-764-887-601/c
; Sequence 601, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413
; CURRENT APPLICATION NUMBER: US/09/764,887
; PRIOR APPLICATION NUMBER: US/01-01-17
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-601

Query Match      76.0%; Score 19; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 75 GGTTCAGTGCAGCCGAGAT 57

RESULT 26
US-09-764-869-2069
; Sequence 2069, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2069
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2069

Query Match      76.0%; Score 19; DB 10; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 20 GGTTCAGTGCAGCCGAGAT 38

RESULT 27
US-09-764-869-1767/c
; Sequence 1767, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1767
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1767

Query Match      76.0%; Score 19; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 75 GGTTCAGTGCAGCCGAGAT 57

RESULT 28
US-09-764-869-2198
; Sequence 2198, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
```

; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2198
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2198

Query Match 76.0%; Score 19; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 24 GGTTCAGTGCAGCCGAGAT 42

RESULT 29

US-09-764-887-600/c
; Sequence 600, Application US/09764887
; Patent No. US20020042096A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4113
; CURRENT APPLICATION NUMBER: US/09/764,887
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 658
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 600
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-887-600

Query Match 76.0%; Score 19; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 80 GGTTCAGTGCAGCCGAGAT 62

RESULT 30

US-09-764-877-3352/c
; Sequence 3352, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3352
; LENGTH: 102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3352

Query Match 76.0%; Score 19; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 40 GGTTCAGTGCAGCCGAGAT 22

RESULT 31

US-09-764-860-979
; Sequence 979, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 979
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-979

Query Match 76.0%; Score 19; DB 10; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCAGTGCAGCCGAGATA 20
|||||
Db 43 GTTCAGTGCAGCCGAGATA 61

RESULT 32

US-09-764-869-2068
; Sequence 2068, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2068
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2068

Query Match 76.0%; Score 19; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
|||||
Db 23 GGTTCAGTGCAGCCGAGAT 41

RESULT 33

US-09-764-868-1442/c
; Sequence 1442, Application US/09764868
; Patent No. US20020188711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT332
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1442
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Homo sapiens

RESULT 36
US-09-764-847-1409/c
; Sequence 1409, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

```

RESULT 38
US-09-764-860-659/c
; Sequence 659, Application US/0764860
; Patent No. US2002009453A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 659
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-659

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Query Match          76.0%; Score 19; DB 10; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels

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```
QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 40 GGTTCAGTGCAGCCGAGAT 22
|||||
RESULT 39
US-09-764-877-2168
; Sequence 2168, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2168
; LENGTH: 122
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2168

Query Match 76.0%; Score 19; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 46 GGTTCAGTGCAGCCGAGAT 64
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RESULT 40
US-09-764-847-1855
; Sequence 1855, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1855
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1855

Query Match 76.0%; Score 19; DB 10; Length 123;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 47 GGTTCAGTGCAGCCGAGAT 65
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RESULT 41
US-09-764-869-2373/c
; Sequence 2373, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2373
; LENGTH: 126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-2373

Query Match 76.0%; Score 19; DB 10; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
Db 64 GGTTCAGTGCAGCCGAGAT 46
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RESULT 42
US-09-783-590-10234
; Sequence 10234, Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16.2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10234
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (100)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (101)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (113)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (115)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (116)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (124)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (128)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10234

Query Match 76.0%; Score 19; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGCAGCCGAGAT 19
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Db 14 GGTTCAGTGAGCCGAGAT 32

RESULT 43
US-09-764-847-1975/c
; Sequence 1975, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1975
; LENGTH: 129
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1975

Query Match 76.0%; Score 19; DB 10; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 81 GGTTCAGTGAGCCGAGAT 63

Search completed: November 24, 2002, 16:37:43
Job time : 203.5 secs

; LENGTH: 131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2688

Query Match 76.0%; Score 19; DB 10; Length 131;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 81 GGTTCAGTGAGCCGAGAT 63

Search completed: November 24, 2002, 16:37:43
Job time : 203.5 secs

Db 14 GGTTCAGTGAGCCGAGAT 32

RESULT 44
US-09-764-877-4006
; Sequence 4006, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4006
; LENGTH: 130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-4006

Query Match 76.0%; Score 19; DB 10; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCAGTGAGCCGAGAT 19
Db 70 GGTTCAGTGAGCCGAGAT 88

RESULT 45
US-09-764-877-2688/c
; Sequence 2688, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2688
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 13:30:43 ; Search time 46.5 Seconds
(without alignments)
164.880 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TGTGCCAGGACCAAGAAATTACAG 25

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	4	US-09-018-584A-125
c	25	100.0	1000	4	US-09-018-584A-32
3	15	60.0	28720	4	US-09-341-587-7
4	14	56.0	627	4	US-08-981-030-2
5	14	56.0	627	4	US-08-981-030-12
6	14	56.0	682	4	US-08-981-030-1
7	14	56.0	1727	1	US-08-289-458-3
8	14	56.0	1727	2	US-08-761-549-3
9	14	56.0	1727	4	US-09-127-646-3
10	14	56.0	4376	1	US-08-119-125A-1
11	14	56.0	6744	1	US-08-119-125A-2
12	14	56.0	9493	2	US-08-639-857-23
13	14	56.0	9493	4	US-08-469-260A-163
c	14	56.0	99500	4	US-09-798-096-10
c	15	13	52.0	22	US-08-332-766A-76
c	16	13	52.0	56	US-08-229-279-6
c	17	13	52.0	56	US-08-701-269-6
c	18	13	52.0	89	US-09-511-625B-57
c	19	13	52.0	91	US-09-084-120-23
c	20	13	52.0	445	US-08-332-766A-16
c	21	13	52.0	611	US-09-328-111-416
c	22	13	52.0	646	US-08-998-416-77
c	23	13	52.0	691	US-08-365-486A-29
c	24	13	52.0	691	US-08-880-342-29
25	13	52.0	700	4	US-08-991-789A-174
26	13	52.0	700	4	US-09-062-451-174
27	13	52.0	700	4	US-09-598-326-174

Sequence 133, App
Sequence 26, Appl
Sequence 20, Appl
Sequence 514, App
Sequence 515, App
Sequence 516, App
Sequence 17, Appl
Sequence 18, App
Sequence 129, App
Sequence 16, Appl
Sequence 2, Appl
Sequence 9, Appl
Sequence 1, Appl
Sequence 120, App
Sequence 3, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 6, Appl

28 13 52.0 829 3 US-08-961-083-133
c 29 13 52.0 836 1 US-08-554-612C-26
c 30 13 52.0 932 1 US-08-554-612C-20
c 31 13 52.0 1001 4 US-09-641-638-514
c 32 13 52.0 1001 4 US-09-641-638-515
c 33 13 52.0 1001 4 US-09-641-638-516
c 34 13 52.0 1007 1 US-08-554-612C-17
c 35 13 52.0 1007 1 US-08-554-612C-18
c 36 13 52.0 1356 4 US-09-276-531-129
c 37 13 52.0 1508 1 US-08-554-612C-16
c 38 13 52.0 1701 3 US-08-599-968-2
c 39 13 52.0 1743 4 US-08-487-596-9
c 40 13 52.0 1758 5 PCT-US92-01015-1
c 41 13 52.0 1782 4 US-09-149-476-120
c 42 13 52.0 1981 3 US-09-017-706-3
c 43 13 52.0 1981 3 US-09-017-706-4
c 44 13 52.0 1981 3 US-09-017-706-5
c 45 13 52.0 1981 3 US-09-017-706-6

ALIGNMENTS

RESULT 1

US-09-018-584A-125

; Sequence 125, Application US/09018584A

; Patent No. 6238863

; GENERAL INFORMATION:

; APPLICANT: Schumm, James W.

; APPLICANT: Bacher, Jeffery W.

; TITLE OF INVENTION: MATERIALS AND METHODS FOR

; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

; TITLE OF INVENTION: REPEAT DNA MARKERS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Promega Corporation

; STREET: 2800 Woods Hollow Road

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53711-5399

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

; COMPUTER: IBM compatible PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 97 (DOS text format)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/018,584A

; FILING DATE: 04-Feb-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Grady J. Frenchick

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 16026.9180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 257-3501

; TELEFAX: (608) 257-2275

; INFORMATION FOR SEQ ID NO: 125:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

; TOPOLOGY: Linear

; US-09-018-584A-125

Query Match 100.0%; Score 25; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 9.3e-06;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25

|||||

Db 1 TGTGCCAGGACCAAGAAATTACAG 25

RESULT 2
US-09-018-584A-32/C
; Sequence 32, Application US/09018584A
; Patent No. 6238863
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; APPLICANT: Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; TITLE OF INVENTION: REPEAT DNA MARKERS
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 MB
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97 (DOS text format)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,584A
; FILING DATE: 04-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 16026.9180
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: S132
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
US-09-018-584A-32
Query Match 100.0%; Score 25; DB 4; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTGCCAGGACCAAGAAATTACAG 25
Db 726 TGTGCCAGGACCAAGAAATTACAG 702
RESULT 3
US-09-341-587-7
; Sequence 7, Application US/09341587
; Patent No. 6346606
; GENERAL INFORMATION:
; APPLICANT: Mollenhauer, Jan
; TITLE OF INVENTION: Protein Containing an SRCR Domain
; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; EARLIER FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
; EARLIER FILING DATE: 1998-01-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

; LENGTH: 28720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7
Query Match 60.0%; Score 15; DB 4; Length 28720;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGGAACACAGAAATT 20
Db 5047 CAGGAACACAGAAATT 5061
RESULT 4
US-08-981-030-2
; Sequence 2, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
; FILING DATE: 12-JUN-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus pahari
US-08-981-030-2
Query Match 56.0%; Score 14; DB 4; Length 627;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 ACCAGAAATTACCA 24
Db 542 ACCAGAAATTACCA 555
RESULT 5
US-08-981-030-12
; Sequence 12, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011

;; FILING DATE: 12-JUN-1996
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 627 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Rattus norvegicus
US-08-981-030-12

Query Match 56.0%; Score 14; DB 4; Length 627;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTACA 24
|||
Db 542 ACCAGAAATTACA 555

RESULT 6

US-08-981-030-1
; Sequence 1, Application US/08981030
; Patent No. 6447783
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: FGF9 AS A SPECIFIC LIGAND FOR FGFR3
; NUMBER OF SEQUENCES: 13
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/981,030
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/IL96/00011
; FILING DATE: 12-JUN-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 682 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-981-030-1

Query Match 56.0%; Score 14; DB 4; Length 682;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCAGAAATTACA 24
|||
Db 597 ACCAGAAATTACA 610

RESULT 7

US-08-289-458-3
; Sequence 3, Application US/08289458
; Patent No. 5608144
; GENERAL INFORMATION:
; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
; APPLICANT: LEE, Kathleen Y.
; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California

;; COUNTRY: US
;; ZIP: 94105-1493
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/289,458
;; FILING DATE:
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dow, Karen B.
;; REGISTRATION NUMBER: 29,684
;; REFERENCE/DOCKET NUMBER: 12176-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1727 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CAAT_signal
;; LOCATION: 1100..1103
;; FEATURE:
;; NAME/KEY: TATA_signal
;; LOCATION: 1139..1146
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1169
;; OTHER INFORMATION: /note= "Transcriptional start site"
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1172
;; OTHER INFORMATION: /note= "pgp50 5' end"
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1234..1236
;; OTHER INFORMATION: /note= "Translation start codon"
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1298
;; OTHER INFORMATION: /note= "Intron start site"
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..1233
;; OTHER INFORMATION: /note= "Gp2 promoter sequence"
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 1..1727
;; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
US-08-289-458-3

Query Match 56.0%; Score 14; DB 1; Length 1727;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATTT 21
|||
Db 1619 GGAACCAAGAAATTT 1632

RESULT 8

US-08-761-549-3
; Sequence 3, Application US/08761549
; Patent No. 5981727
; GENERAL INFORMATION:
; APPLICANT: BADEN, Catherine S., DUNSMUIR, Pamela,
; APPLICANT: LEE, Kathleen Y.

```

; TITLE OF INVENTION: PLANT Gp2 PROMOTERS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: Stuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,549
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/289,458
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12176-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1727 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CAAT_signal
; LOCATION: 1100..1103
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: 1139..1146
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1169
; OTHER INFORMATION: /note= "Transcriptional start site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1172
; OTHER INFORMATION: /note= "pgp50 5' end"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1234..1236
; OTHER INFORMATION: /note= "Translation start codon"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1298
; OTHER INFORMATION: /note= "Intron start site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1233
; OTHER INFORMATION: /note= "Gp2 promoter sequence"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1727
; OTHER INFORMATION: /note= "Gp2 Genomic DNA clone"
; US-08-761-549-3
;
Query Match 56.0%; Score 14; DB 2; Length 1727;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGAACGAGAAATTT 21
|||||

```

```

Db 1619 GGAACGAGAAATTT 1632
;
RESULT 9
US-09-127-646-3
; Sequence 3, Application US/09127646
; Patent No. 6291744
; GENERAL INFORMATION:
; APPLICANT: Baden, Catherine S.
; APPLICANT: Dunsmuir, Pamela
; APPLICANT: Lee, Kathleen Y.
; APPLICANT: DNA Plant Technology Corporation
; TITLE OF INVENTION: Nucleic Acids Encoding Plant Group 2 Proteins and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 012176-00402005
; CURRENT APPLICATION NUMBER: US/09/127,646
; CURRENT FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 08/289,458
; EARLIER FILING DATE: 1994-08-12
; EARLIER APPLICATION NUMBER: US 08/761,549
; EARLIER FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1727
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1727)
; OTHER INFORMATION: pepper plant Group 2 (Gp2) genomic DNA clone
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1233)
; OTHER INFORMATION: Gp2 promoter sequence
; FEATURE:
; NAME/KEY: CAAT_signal
; LOCATION: (1100)..(1103)
; FEATURE:
; NAME/KEY: TATA_signal
; LOCATION: (1139)..(1146)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1169)
; OTHER INFORMATION: transcriptional start site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1172)
; OTHER INFORMATION: pgp50 5' end
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1234)..(1236)
; OTHER INFORMATION: translation start codon
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1298)
; OTHER INFORMATION: Intron start site
; US-09-127-646-3
;
Query Match 56.0%; Score 14; DB 4; Length 1727;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGAACGAGAAATTT 21
|||||
Db 1619 GGAACGAGAAATTT 1632
;
RESULT 10
US-08-119-125A-1
; Sequence 1, Application US/08119125A
; Patent No. 5610011
; GENERAL INFORMATION:

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APPLICANT: SMITH, Hilda Elizabeth
 APPLICANT: VECHT, Uri
 TITLE OF INVENTION: DNA sequences which code for virulence
 TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, polypeptides and antibodies derived therefrom and the use thereof for the diagnosis and protection against infection by S. suis in mammals, including
 TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the diagnosis and protection against infection by S. suis in mammals, including
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Centraal Diergeneeskundig Instituut
 STREET: Edelhertweg 15
 CITY: PH Lelystad
 STATE:
 COUNTRY: The Netherlands
 ZIP: NL-8219
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS v.6.0
 SOFTWARE: Wordperfect v. 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/119,125A
 FILING DATE: 20-SEP-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/NL92/00054
 FILING DATE: 19-MAR-1992
 APPLICATION NUMBER: NL 9100510
 FILING DATE: 21-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Handal, Anthony H.
 REGISTRATION NUMBER: 26275
 REFERENCE/DOCKET NUMBER: SMITHHE119125
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 838-8589
 TELEFAX: (203) 838-8794
 INFORMATION FOR SEQ ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4376 base pairs
 TYPE: Nucleic acid with corresponding amino acids
 STRANDEDNESS: single stranded
 TOPOLOGY: linear
 MOLECULE TYPE: genomic DNA
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus suis type II (pathogenic)
 FEATURE:
 OTHER INFORMATION: Extracellular protein factor (EF) gene
 FEATURE:
 NAME/KEY: promoter -35 region
 LOCATION: bp 66 to 71
 FEATURE:
 NAME/KEY: promoter -10 region
 LOCATION: bp 89 to 94
 FEATURE:
 NAME/KEY: promoter -35 region
 LOCATION: bp 153 to 158
 FEATURE:
 NAME/KEY: promoter -10 region
 LOCATION: bp 176 to 181
 FEATURE:
 NAME/KEY: ribosome binding site
 LOCATION: bp 350 to 356
 FEATURE:
 NAME/KEY: signal peptide
 LOCATION: bp 361 to 498
 FEATURE:
 NAME/KEY: mature peptide
 LOCATION: bp 499 to 2890
 FEATURE:
 NAME/KEY: dyad symmetry regions
 LOCATION: from bp 4186 to 4198 and from bp 4203 to 4215
 NAME/KEY: dyad symmetry regions
 LOCATION: from bp 4243 to 4257 and from bp 4363 to 4276

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US-08-1119-125A-1
Query Match          56.0%; Score 14; DB 1; Length 4376;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 CAGGAACCAAGAAAT 19
      |||||
Db      314 CAGGAACCAAGAAAT 327

RESULT 11
US-08-1119-125A-2
; Sequence 2, Application US/081119125A
; Patent No. 5610011
; GENERAL INFORMATION:
; APPLICANT: SMITH, Hilda Elizabeth
; APPLICANT: VECHE, Uri
; TITLE OF INVENTION: DNA Sequences which code for Virulence
; TITLE OF INVENTION: Characteristics of Streptococcus suis and parts thereof, po
; TITLE OF INVENTION: antibodies derived therefrom and the use thereof for the di
; TITLE OF INVENTION: protection against infection by S. suis in mammals, includi
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Centraal Diergeneeskundig Instituut
; STREET: Edelhertweg 15
; CITY: PH Lelystad
; STATE:
; COUNTRY: The Netherlands
; ZIP: NL-8219
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS v.6.0
; SOFTWARE: WordPerfect v. 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/119,125A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00054
; FILING DATE: 19-MAR-1992
; APPLICATION NUMBER: NL 9100510
; FILING DATE: 21-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Handal, Anthony H.
; REGISTRATION NUMBER: 26275
; REFERENCE/DOCKET NUMBER: SMITHHEL19125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 838-8589
; TELEFAX: (203) 838-8794
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6744 base pairs
; TYPE: Nucleic acid with corresponding amino acids
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus suis type II (pathogenic)
; FEATURE:
; OTHER INFORMATION: Extracellular factor related protein (EF*) gene
; FEATURE:
; NAME/KEY: promoter -35 region
; LOCATION: bp 66 to 71
; FEATURE:
; NAME/KEY: promoter -10 region
; LOCATION: bp 89 to 94
; FEATURE:
; NAME/KEY: promoter -35 region
; LOCATION: bp 153 to 158
; FEATURE:
; NAME/KEY: promoter -10 region

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/ LOCATION: bp 176 to 181
/ FEATURE:
/ NAME/KEY: ribosome binding site
/ LOCATION: bp 350 to 356
/ FEATURE:
/ NAME/KEY: signal peptide
/ LOCATION: bp 361 to 498
/ FEATURE:
/ NAME/KEY: start of repetitive units R1-R11
/ LOCATION: bp 2869, 3097, 3292, 3520, 4087, 4381, 4609, 4837,
/ LOCATION: 5065, 5293, 5521:
/ FEATURE:
/ NAME/KEY: start of repetitive Asp-Pro-Asn-Leu sequences
/ LOCATION: bp 2932, 3160, 3355, 3583, 4150, 4444, 4672, 4900,
/ LOCATION: 5128, 5356, 5584:
/ FEATURE:
/ NAME/KEY: dyad symmetry regions
/ LOCATION: from bp 6554 to 6566 and from bp 6571 to 6583
/ FEATURE:
/ NAME/KEY: dyad symmetry regions
/ LOCATION: from bp 6611 to 6625 and from bp 6631 to 6644
US-08-119-125A-2

Query Match          56.0%; Score 14; DB 1; Length 6744;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGACCCAGAGAAAT 19
Db 314 CAGGACCCAGAGAAAT 327

RESULT 12
US-08-639-857-23
; Sequence 23, Application US/08639857
; Patent No. 595318
; GENERAL INFORMATION:
; APPLICANT: Simons, J. N.
; APPLICANT: Desai, S. M.
; APPLICANT: Mushahwar I. K.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR CONTROLLING THE
; TITLE OF INVENTION: TRANSLATION OF HEPATITIS GB PROTEINS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/639,857
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Foremski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5793.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-0378
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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US-08-639-857-23

Query Match          56.0%; Score 14; DB 2; Length 9493;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
Db 4037 TGTGCCAGGAACCA 4050
|||||

RESULT 13
US-08-469-260A-163
; Sequence 163, Application US/08469260A
; Patent No. 6451578
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAHWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,260A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-260A-163

Query Match          56.0%; Score 14; DB 4; Length 9493;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
Db 4037 TGTGCCAGGAACCA 4050
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RESULT 14
US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 6398378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

Query Match 56.0%; Score 14; DB 4; Length 99500;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACCA 14
|||||
DB 31468 TGTGCCAGGAACCA 31455

RESULT 15
US-08-332-766A-76/c
; Sequence 76, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
; APPLICANT: JEFFREYS, Alec J.
; APPLICANT: ARMOUR, John
; TITLE OF INVENTION: SIMPLE TANDEM REPEATS
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,766A
; FILING DATE: 01-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326052.9
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BIRD, Donald J.
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-332-766A-76

Query Match 52.0%; Score 13; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 ACCAGAAATTTC 23
|||||
DB 21 ACCAGAAATTTC 9
|||||
RESULT 16
US-08-229-279-6/c
; Sequence 6, Application US/08229279
; Patent No. 5648211
; GENERAL INFORMATION:
; APPLICANT: Fraiser, Melinda S.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Walker, George T.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
; TITLE OF INVENTION: THERMOPHILIC ENZYMES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
; ADDRESSEE: Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: NJ
; COUNTRY: US
; ZIP: 07417
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,279
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugitt, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-2961
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-229-279-6

Query Match 52.0%; Score 13; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGGAACAGAA 17
|||||
DB 19 CCAGGAACAGAA 7

RESULT 17
US-08-701-269-6/c
; Sequence 6, Application US/08701269
; Patent No. 5744311
; GENERAL INFORMATION:
; APPLICANT: Fraiser, Melinda S.
; APPLICANT: Spargo, Catherine A.
; APPLICANT: Walker, George T.
; APPLICANT: Van Cleve, Mark
; APPLICANT: Wright, David J.
; TITLE OF INVENTION: STRAND DISPLACEMENT AMPLIFICATION USING
; THERMOPHILIC ENZYMES

```
/
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
/ ADDRESSEE: Company
/ STREET: 1 Becton Drive
/ CITY: Franklin Lakes
/ STATE: NJ
/ COUNTRY: US
/ ZIP: 07417
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/701.269
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/229,279
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fugit, Donna R.
/ REGISTRATION NUMBER: 32,135
/ REFERENCE/DOCKET NUMBER: P-2961
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 56 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-08-701-269-6

Query Match      52.0%; Score 13; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGGACCAGAA 17
   |||||
DB 19 CCAGGACCAGAA 7

RESULT 18
US-09-511-625B-57/c
; Sequence 57, Application US/09511625B
; Patent No. 6368828
; GENERAL INFORMATION:
; APPLICANT: LaRoche, William J.
; APPLICANT: Patel, Bharvin
; APPLICANT: Pierce, Jacalyn H.
; TITLE OF INVENTION: ATTENUATED AND DOMINANT NEGATIVE VARIANT
; TITLE OF INVENTION: CDNAS OF STAT6: STAT6B AND STAT6C
; FILE REFERENCE: 14014.0300u1
; CURRENT APPLICATION NUMBER: US/09/511,625B
; CURRENT FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: PCT/US98/17821
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/070,397
; PRIOR FILING DATE: 1998-01-05
; PRIOR APPLICATION NUMBER: 60/056,075
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial Sequence:/No. 6368828e -
; OTHER INFORMATION: synthetic construct
/
/ US-09-511-625B-57
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Query Match      52.0%; Score 13; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCCCAGGAACACG 15
   |||||
DB 88 TCCCAGGAACACG 76

RESULT 19
US-09-084-120-23/c
; Sequence 23, Application US/09084120
; Patent No. 6251592
; GENERAL INFORMATION:
; APPLICANT: TANG, Jianqing
; APPLICANT: MELANCON, Serge B.
; TITLE OF INVENTION: A NOVEL STR MARKER SYSTEM
; TITLE OF INVENTION: FOR DNA FINGERPRINTING
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SWABEY OGILVY RENAULT
; STREET: Suite 1600, 1981 McGill College Avenue
; CITY: Montreal
; STATE: QC
; COUNTRY: Canada
; ZIP: H3A 2Y3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/084,120
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: COTE, France
; REGISTRATION NUMBER: 37,037
; REFERENCE/DOCKET NUMBER: 13251-40US FC/1d
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 514 845-7126
; TELEFAX: 514 288-8389
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 91 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
/
/ US-09-084-120-23

Query Match      52.0%; Score 13; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGAACACG 16
   |||||
DB 51 GCCAGGAACACG 39

RESULT 20
US-08-332-766A-16/c
; Sequence 16, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
; APPLICANT: JEFFREYS, Alec J.
; APPLICANT: ARMOUR, John
; TITLE OF INVENTION: SIMPLE TANDEM REPEATS
; NUMBER OF SEQUENCES: 125
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CUSHMAN DABBY & CUSHMAN, L.L.P.
;; STREET: 1100 New York Avenue, N.W.
;; CITY: Washington
;; STATE: D. C.
;; COUNTRY: U.S.A.
;; ZIP: 20005-3918
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/332,766A
;; FILING DATE: 01-NOV-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9326052.9
;; FILING DATE: 21-DEC-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BIRD, Donald J.
;; REGISTRATION NUMBER: 25,323
;; REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 861-3000
;; TELEFAX: (202) 822-0944
;; TELEX: 6714627 CUSH
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 445 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-332-766A-16

Query Match 52.0%; Score 13; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ACCGAAATTTAC 23
|||||
DB 235 ACCGAAATTTAC 223

RESULT 21
US-09-328-111-416/c
;; Sequence 416, Application US/09328111
;; Patent No. 6262333
;; GENERAL INFORMATION:
;; APPLICANT: Endege, Wilson O.
;; APPLICANT: Steinmann, Kathleen E.
;; APPLICANT: Astle, Jon H.
;; APPLICANT: Burgess, Christopher C.
;; APPLICANT: Bushnell, Steven E.
;; APPLICANT: Carroll III, Eddie
;; APPLICANT: Catino, Theodore J.
;; APPLICANT: Derti, Adnan
;; APPLICANT: Ford, Donna M.
;; APPLICANT: Lewis, Marcia E.
;; APPLICANT: Monahan, John E.
;; APPLICANT: Schlegel, Robert
;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;; FILE REFERENCE: CCD-257 (US)
;; CURRENT APPLICATION NUMBER: US/09/328,111
;; CURRENT FILING DATE: 1999-06-08
;; EARLIER APPLICATION NUMBER: US 60/088,801
;; EARLIER FILING DATE: 1998-06-10
;; NUMBER OF SEQ ID NOS: 850
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 416
;; LENGTH: 611

;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(611)
;; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-416

Query Match 52.0%; Score 13; DB 4; Length 611;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCCAGGAACCA 14
|||||
DB 267 GTGCCAGGAACCA 255

RESULT 22
US-08-998-416-77
;; Sequence 77, Application US/08998416
;; Patent No. 6239264
;; GENERAL INFORMATION:
;; APPLICANT: Philippsen, Peter
;; APPLICANT: Pohlmann, Rainer
;; APPLICANT: Steiner, Sabine
;; APPLICANT: Mohr, Christine
;; APPLICANT: Wendland, Jurgen
;; APPLICANT: Knechtle, Philipp
;; APPLICANT: Rebeschung, Corinne
;; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPPII
;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 1152
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6239264artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: No. 6239264th Carolina
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/998,416
;; FILING DATE: 24-DEC-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: CH 0016/97
;; FILING DATE: 31-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-541-8587
;; TELEFAX: 919-541-8689
;; INFORMATION FOR SEQ ID NO: 77:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 646 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: PAG1023UP
;; US-08-998-416-77

Query Match 52.0%; Score 13; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAAT 19
 Db 81 AGGAACCAAGAAAT 93

RESULT 23

US-08-365-486A-29/C
 ; Sequence 29, Application US/08365486A
 ; Patent No. 5834306

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/365,486A
 FILING DATE: 23-DEC-1994
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0980
 TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 691 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: human enolase gene (EMBL #X56832)
 INDIVIDUAL ISOLATE: fragment containing nucleotides -628 to +63
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 629..691
 US-08-365-486A-29

Query Match 52.0%; Score 13; DB 2; Length 691;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAAT 19

Db 581 AGGAACCAAGAAAT 569

RESULT 24

US-08-880-342-29/C
 ; Sequence 29, Application US/08880342
 ; Patent No. 6218179

GENERAL INFORMATION:

APPLICANT: Webster, Keith A.
 APPLICANT: Bishopric, Nanette H.
 APPLICANT: Murphy, Brian
 APPLICANT: Laderoute, Keith R.

APPLICANT: Green, Christopher J.
 TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
 TITLE OF INVENTION: Therapeutic Constructs
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/880,342
 FILING DATE: 23-JUN-1997
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/IB95/00996
 FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486
 FILING DATE: 23-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 8255-0018.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0980
 TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
 LENGTH: 691 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: human enolase gene (EMBL #X56832)
 INDIVIDUAL ISOLATE: fragment containing nucleotides -628 to +63
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 629..691
 US-08-880-342-29

Query Match 52.0%; Score 13; DB 4; Length 691;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCAAGAAAT 19

Db 581 AGGAACCAAGAAAT 569

RESULT 25

US-08-991-789A-17A
 ; Sequence 17A, Application US/08991789A
 ; Patent No. 6225054

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
 Smith, John M.
 Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 292

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group
 STREET: 701 Fifth Avenue, Suite 6300

```
;
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
;
; INFORMATION FOR SEQ ID NO: 174:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 174:
US-08-991-789A-174

Query Match 52.0%; Score 13; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCAGGACCAAC 15
Db 203 TGCAGGACCAAC 215
|||||

RESULT 26
US-09-062-451-174
; Sequence 174, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,451
; FILING DATE: 04-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.419C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 174:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-062-451-174
;
; Query Match 52.0%; Score 13; DB 4; Length 700;
; Best Local Similarity 100.0%; Pred. No. 68;
; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 3 TGCAGGACCAAC 15
; Db 203 TGCAGGACCAAC 215
; |||||
;
; RESULT 27
; US-09-598-326-174
; Sequence 174, Application US/09598326
; Patent No. 6423496
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 247
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group PLLC
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,326
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 174:
US-09-598-326-174

Query Match 52.0%; Score 13; DB 4; Length 700;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCAGGACCAAC 15
Db 203 TGCAGGACCAAC 215
|||||

RESULT 28
US-08-961-083-133
; Sequence 133, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
```

APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-083-133

Query Match 52.0%; Score 13; DB 3; Length 829;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GAACACAGAAATTT 21
|||||
DB 47 GAACACAGAAATTT 59

RESULT 29
US-08-554-612C-26/c
Sequence 26, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:
APPLICANT: Orlicky, David
TITLE OF INVENTION: PROTAGLANDIN F2\ RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela

REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 836 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-26

Query Match 52.0%; Score 13; DB 1; Length 836;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGAACACAG 15
|||||
DB 660 TGCCAGGAACACAG 648

RESULT 30
US-08-554-612C-20/c
Sequence 20, Application US/08554612C
Patent No. 5747660
GENERAL INFORMATION:
APPLICANT: Orlicky, David
TITLE OF INVENTION: PROTAGLANDIN F2\ RECEPTOR REGULATORY
TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,612C
FILING DATE: No. 5747660ember 6, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 06519/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-554-612C-20

Query Match 52.0%; Score 13; DB 1; Length 932;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGAACACAG 15
|||||
DB 526 TGCCAGGAACACAG 514

```

RESULT 31
US-09-641-638-514/c
; Sequence 514, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 514
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-568-207 : polymorphic base G or T
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-568-207.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-568-207.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 295..313
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 812..829
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-568-207 potential probe
US-09-641-638-514

Query Match 52.0%; Score 13; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCGAGAAAT 19
Db 327 AGGAACCGAGAAAT 315

RESULT 32
US-09-641-638-515/c
; Sequence 515, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330

```

```

; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 515
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-568-365 : polymorphic base G or T
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-568-365.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-568-365.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 137..155
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 654..671
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-568-365 potential probe
US-09-641-638-515

```

```

Query Match 52.0%; Score 13; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACCGAGAAAT 19
Db 169 AGGAACCGAGAAAT 157

```

```

RESULT 33
US-09-641-638-516/G
; Sequence 516, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 516
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele

```


/ LOCATION: 501
/ OTHER INFORMATION: 12-568-367 : polymorphic base G or T
/ NAME/KEY: misc.binding
/ LOCATION: 481..500
/ OTHER INFORMATION: 12-568-367.mis1, potential
/ NAME/KEY: misc.binding
/ LOCATION: 502..521
/ OTHER INFORMATION: 12-568-367.mis2, potential complement
/ NAME/KEY: primer_bind
/ LOCATION: 135..153
/ OTHER INFORMATION: upstream amplification primer
/ NAME/KEY: primer_bind
/ LOCATION: 652..669
/ OTHER INFORMATION: downstream amplification primer, complement
/ NAME/KEY: misc.binding
/ LOCATION: 489..513
/ OTHER INFORMATION: 12-568-367 potential probe
US-09-641-638-516

Query Match 52.0%; Score 13; DB 4; Length 1001;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACACAGAAAT 19
Db 167 AGGAACACAGAAAT 155

RESULT 34
US-08-554-612C-17/c
; Sequence 17, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orlicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660ember 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-554-612C-17

Query Match 52.0%; Score 13; DB 1; Length 1007;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGAACACAG 15
Db 526 TGCCAGGAACACAG 514

RESULT 35
US-08-554-612C-18/c
; Sequence 18, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orlicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2' RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660ember 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875

; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-554-612C-18

Query Match 52.0%; Score 13; DB 1; Length 1007;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGAACACAG 15
Db 526 TGCCAGGAACACAG 514

RESULT 36
US-09-276-531-129/c
; Sequence 129, Application US/09276531
; Patent No. 6183968
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Reddy, Roopa
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
; TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
; NUMBER OF SEQUENCES: 134
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/276,531
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/079,677
; FILING DATE: March 27, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lynn E. Murry, Ph.D.
; REGISTRATION NUMBER: 42,918
; REFERENCE/DOCKET NUMBER: PA-0008 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HNT2AZS07
; CLONE: 3143858
; US-09-276-531-129

Query Match 52.0%; Score 13; DB 4; Length 1356;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCAGGAGAACG 15
|||||

DB 465 TGCAGGAGAACG 453

RESULT 37
US-08-554-612C-16/c
; Sequence 16, Application US/08554612C
; Patent No. 5747660
; GENERAL INFORMATION:
; APPLICANT: Orlicky, David
; TITLE OF INVENTION: PROSTAGLANDIN F2₃ RECEPTOR REGULATORY
; TITLE OF INVENTION: PROTEIN AND THERAPEUTIC USES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,612C
; FILING DATE: No. 5747660ender 6, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: 06519/004001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 322-5070
; TELEFAX: (415) 854-0875
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1508 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-554-612C-16

Query Match 52.0%; Score 13; DB 1; Length 1508;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCAGGAGAACG 15
|||||

DB 1027 TGCAGGAGAACG 1015

RESULT 38
US-08-599-968-2/c
; Sequence 2, Application US/08599968
; Patent No. 6084153
; GENERAL INFORMATION:
; APPLICANT: Good, Allen G.
; APPLICANT: Stroeher, Virginia L.
; TITLE OF INVENTION: Plants Having Enhanced Nitrogen
; TITLE OF INVENTION: Assimilation/Metabolism
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BENNETT JONES VERCHERE
; STREET: Suite 1800, 350 Albert Street
; CITY: Ottawa
; STATE: Ontario
; COUNTRY: Canada
; ZIP: K1R 1A4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO),
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,968
; FILING DATE: February 14, 1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: CALDWELL, Roseann B.
; REGISTRATION NUMBER: 37077
; REFERENCE/DOCKET NUMBER: 10230-6
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1701 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-599-968-2

Query Match 52.0%; Score 13; DB 3; Length 1701;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACC 13
|||||

DB 1438 TGTGCCAGGAACC 1426

RESULT 39
US-08-487-596-9

; Sequence 9, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1743 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 143..1627
; OTHER INFORMATION: /product= "ALPHA-6 SUBUNIT"
; US-08-487-596-9

Query Match 52.0%; Score 13; DB 4; Length 1743;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 CAGAAATTACAG 25
| | | | | | | | | |
Db 1648 CAGAAATTACAG 1660

RESULT 40
PCT-US92-01015-1
; Sequence 1, Application PC/TUS9201015

; GENERAL INFORMATION:
; APPLICANT: Davis, Geneva R
; APPLICANT: Provow, Sally P
; TITLE OF INVENTION: Production of Human Serum Albumin in
; TITLE OF INVENTION: Methylophic Yeast Cells
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 South LaSalle Street, Suite 900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/01015
; FILING DATE: 19920204
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/650,040
; FILING DATE: 04-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 50857PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1758 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1758
; OTHER INFORMATION:
; PCT-US92-01015-1

Query Match 52.0%; Score 13; DB 5; Length 1758;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACAGAAA 18
| | | | | | | | | |
Db 280 CAGGAACAGAAA 292

RESULT 41
US-09-149-476-120
; Sequence 120, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626


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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          52.0%; Score 13; DB 4; Length 1782;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACACGAAA 18
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Db 707 CAGGAACGAAA 719

RESULT 42
US-09-017-706-3/c
; Sequence 3, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPENTAPOSE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-4

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; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; FEATURE:
; OTHER INFORMATION: PLASMID POS3410F57
US-09-017-706-3

Query Match          52.0%; Score 13; DB 3; Length 1981;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGGAACGAGAA 17
   |||||
Db 730 CCAGGAACGAGAA 718

RESULT 43
US-09-017-706-4/c
; Sequence 4, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPENTAPOSE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; OTHER INFORMATION: PLASMID POS3410H57
US-09-017-706-4

Query Match          52.0%; Score 13; DB 3; Length 1981;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGGAACGAGAA 17
   |||||
Db 730 CCAGGAACGAGAA 718

RESULT 44
US-09-017-706-5/c
; Sequence 5, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPENTAPOSE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; OTHER INFORMATION: METHOD OF DETERMINING CHARACTERISTIC: E
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; FEATURE:
; OTHER INFORMATION: PLASMID pos34100L57
US-09-017-706-5
```

```
Query Match          52.0%; Score 13; DB 3; Length 1981;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 5 CCAGGAACCGAGAA 17
|||||
Db 730 CCAGGAACCGAGAA 718
```

```
RESULT 45
US-09-017-706-6/c
; Sequence 6, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOTENOTAOSE, VECTOR CONTAINING SAID GENE AND
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1981
; TYPE: DNA
; ORGANISM: Pseudomonas sp., Strain KO-8940
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(1848)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (85)..(1848)
; FEATURE:
; OTHER INFORMATION: MUTATED GENOMIC DNA
; FEATURE:
; OTHER INFORMATION: PLASMID: pos3410F139
US-09-017-706-6
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```
Query Match          52.0%; Score 13; DB 3; Length 1981;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 CCAGGAACCGAGAA 17
|||||
Db 730 CCAGGAACCGAGAA 718
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Search completed: November 24, 2002, 15:04:07
Job time : 71.5 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 24, 2002, 14:30:54 ; Search time 52.5 Seconds
(without alignments)
180.348 Million cell updates/sec

Title: US-09-784-423-125

Perfect score: 25

Sequence: 1 TTGCGCAGAACCCAGAAATTACAG 25

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Gapex 60.0 , Gapex 60.0

Searched: 335578 seqs, 189365133 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PublishedApplications_NA.*

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- 2: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubnpa/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubnpa/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubnpa/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubnpa/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubnpa/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubnpa/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	10	US-09-784-423-125
C 2	25	100.0	1000	10	Sequence 125, Appl
C 3	16	64.0	442	10	Sequence 32, Appl
4	15	60.0	569	10	Sequence 11479, A
5	15	60.0	1302	10	Sequence 198, Appl
6	15	60.0	11821	10	Sequence 9647, Ap
7	15	60.0	15535	10	Sequence 2857, Ap
C 8	15	60.0	106323	10	Sequence 2855, Ap
9	14	56.0	193	10	Sequence 3, Appli
C 10	14	56.0	963	10	Sequence 430, App
11	14	56.0	2273	10	Sequence 1948, Ap
12	14	56.0	9493	8	Sequence 110, App
C 13	14	56.0	12989	10	Sequence 163, App
14	14	56.0	21833	10	Sequence 1489, Ap
15	14	56.0	137997	10	Sequence 2275, Ap
16	14	56.0	684973	10	Sequence 3, Appli
C 17	14	56.0	1503841	9	Sequence 1, Appli
C 18	14	56.0	1503841	10	Sequence 1, Appli
C 19	14	56.0	1503841	10	Sequence 1, Appli

Sequence 6, Appli
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 11569, A
Sequence 2301, Ap
Sequence 14842, A
Sequence 6327, Ap
Sequence 21959, A
Sequence 10539, A
Sequence 117, App
Sequence 11124, A
Sequence 2711, Ap
Sequence 4653, Ap
Sequence 7956, Ap
Sequence 6412, Ap
Sequence 2744, Ap
Sequence 6944, Ap
Sequence 4307, Ap
Sequence 6095, Ap
Sequence 11922, A
Sequence 163, App
Sequence 5680, Ap
Sequence 7386, Ap
Sequence 119, App
Sequence 60, Appli

Sequence 6, Appli
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 1310, Ap
Sequence 11569, A
Sequence 2301, Ap
Sequence 14842, A
Sequence 6327, Ap
Sequence 21959, A
Sequence 10539, A
Sequence 117, App
Sequence 11124, A
Sequence 2711, Ap
Sequence 4653, Ap
Sequence 7956, Ap
Sequence 6412, Ap
Sequence 2744, Ap
Sequence 6944, Ap
Sequence 4307, Ap
Sequence 6095, Ap
Sequence 11922, A
Sequence 163, App
Sequence 5680, Ap
Sequence 7386, Ap
Sequence 119, App
Sequence 60, Appli

ALIGNMENTS

RESULT 1

US-09-784-423-125

; Sequence 125, Application US/09784423

; Patent No. US20020012924A1

; GENERAL INFORMATION:

; APPLICANT: Schumm, James W.

; TITLE OF INVENTION: MATERIALS AND METHODS FOR

; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM

; REPEAT DNA MARKERS

; NUMBER OF SEQUENCES: 147

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Promega Corporation

; STREET: 2800 Woods Hollow Road

; CITY: Madison

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53711-5399

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb

; COMPUTER: IBM compatible PC

; OPERATING SYSTEM: Windows 95

; SOFTWARE: Word 97 (DOS text format)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09784,423

; FILING DATE: 15-Feb-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/018,584

; FILING DATE: 04-Feb-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Grady J. Frenchick

; REGISTRATION NUMBER: 29,018

; REFERENCE/DOCKET NUMBER: 16026.9180

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (608) 257-3501

; TELEFAX: (608) 257-2275

; INFORMATION FOR SEQ ID NO: 125

; SEQUENCE CHARACTERISTICS:

; LENGTH: 25

; TYPE: Nucleic Acid

; STRANDEDNESS: Single

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 125
US-09-784-423-125

Query Match 100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
|||||
Db 1 TGTGCCAGGACCAAGAAATTACAG 25

RESULT 2

US-09-784-423-32/c
; Sequence 32, Application US/09784423
; Patent No. US20020012924A1
; GENERAL INFORMATION:
; APPLICANT: Schumm, James W.
; Bacher, Jeffery W.
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
; REPEAT DNA MARKERS

NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Promega Corporation
; STREET: 2800 Woods Hollow Road
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53711-5399
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
; COMPUTER: IBM compatible PC
; OPERATING SYSTEM: Windows 95
SOFTWARE: Word 97 (DOS text format)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,423
; FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/018,584
; FILING DATE: 04-Feb-1998
ATTORNEY/AGENT INFORMATION:
; NAME: Grady J. Frenchick
; REGISTRATION NUMBER: 29,018
REFERENCE/DOCKET NUMBER: 16026.9180
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 257-3501
; TELEFAX: (608) 257-2275
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
; LENGTH: 1000 bp
; TYPE: Nucleic Acid
; STRANDEDNESS: Double
; TOPOLOGY: Circular
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: no
; IMMEDIATE SOURCE:
; CLONE: SL32
POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 22
SEQUENCE DESCRIPTION: SEQ ID NO: 32

Query Match 100.0%; Score 25; DB 10; Length 1000;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAGAAATTACAG 25
|||||
Db 726 TGTGCCAGGACCAAGAAATTACAG 702

RESULT 3
US-09-864-761-11479/c
; Sequence 11479, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 11479
LENGTH: 442
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
; OTHER INFORMATION: MAP TO AC005961.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
US-09-864-761-11479

Query Match 64.0%; Score 16; DB 10; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCAAG 16
|||||

Db 226 TGTGCCAGGAACAGCA 211

RESULT 4

US-09-917-800A-198
; Sequence 198, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA875126
US-09-917-800A-198

Query Match 60.0%; Score 15; DB 10; Length 569;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGAACAGCA 18
|||||
Db 240 GCCAGGAACAGCA 254

RESULT 5

US-09-815-242-9647
; Sequence 9647, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELTRA 011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9647
; LENGTH: 1302
; TYPE: DNA
; ORGANISM: Salmonella typhi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1302)
US-09-815-242-9647

Query Match 60.0%; Score 15; DB 10; Length 1302;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCAAGAAATTTA 22
|||||
Db 735 GGAACCAAGAAATTTA 749

RESULT 6

US-09-764-877-2857
; Sequence 2857, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2857
; LENGTH: 11821
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2857

Query Match 60.0%; Score 15; DB 10; Length 11821;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGAACAG 15
|||||
Db 3694 TGTGCCAGGAACAG 3708

RESULT 7

US-09-764-877-2855
; Sequence 2855, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

```
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2855
; LENGTH: 15535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2855

Query Match      60.0%; Score 15; DB 10; Length 15535;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAG 15
Db 3783 TGTGCCAGGACCCAG 3797

RESULT 8
US-09-803-661-3/c
; Sequence 3; Application US/09803661
; Patent No. US2002013292A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; AND USES THEREOF
; FILE REFERENCE: CLO01162
; CURRENT APPLICATION NUMBER: US/09/803,661
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 106323
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(106323)
; OTHER INFORMATION: n = A,T,C or G
US-09-803-661-3

Query Match      60.0%; Score 15; DB 10; Length 106323;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCCAG 15
Db 42335 TGTGCCAGGACCCAG 42321

RESULT 9
US-09-783-590-430
; Sequence 430; Application US/09783590
; Patent No. US20020110850A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Haseltine, William A.
; APPLICANT: Li, Haodong
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
; FILE REFERENCE: PO-16,2C1
; CURRENT APPLICATION NUMBER: US/09/783,590
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/420,856
; PRIOR FILING DATE: 1995-04-12
; PRIOR APPLICATION NUMBER: 08/346,731
; PRIOR FILING DATE: 1994-11-21
; NUMBER OF SEQ ID NOS: 12485
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 430
; LENGTH: 193
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (81)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (156)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (160)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (170)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-430

Query Match      56.0%; Score 14; DB 10; Length 193;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GGAACCCAGAAATTT 21
Db 67 GGAACCCAGAAATTT 80

RESULT 10
US-09-833-381-1948/c
; Sequence 1948; Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NO. US20020132090A1el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1948
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(963)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1948

Query Match      56.0%; Score 14; DB 10; Length 963;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGACCCAGAAAT 19
Db 22 CAGGACCCAGAAAT 9

RESULT 11
US-09-853-386-110
; Sequence 110; Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnihan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
```

;; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
;; TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
;; FILE REFERENCE: P01972US1
;; CURRENT APPLICATION NUMBER: US/09/853,386
;; CURRENT FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US 60/203645
;; PRIOR FILING DATE: 2000-05-12
;; NUMBER OF SEQ ID NOS: 153
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 110
;; LENGTH: 2273
;; TYPE: DNA
;; ORGANISM: mus musculus
US-09-853-386-110

Query Match 56.0%; Score 14; DB 10; Length 2273;
Best Local Similarity 100.0%; Pred. No. 34; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 3 TGCCAGGACACCA 16
|||||

Db 1998 TGCCAGGACACCA 2011

RESULT 12
US-08-424-550B-163
; Sequence 163, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUERHOFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9493 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-424-550B-163

Query Match 56.0%; Score 14; DB 8; Length 9493;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTGCCAGGACCA 14
|||||

Db 4037 TGTGCCAGGACCA 4050

RESULT 13
US-09-764-847-1489/C
; Sequence 1489, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1489
; LENGTH: 12989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1489

Query Match 56.0%; Score 14; DB 10; Length 12989;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGAACACGAAATT 20
|||||

Db 8716 AGAACACGAAATT 8703

RESULT 14
US-09-764-877-2275
; Sequence 2275, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2275
; LENGTH: 21833
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2275

Query Match 56.0%; Score 14; DB 10; Length 21833;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TGCCAGGACACCA 16
|||||

Db 17007 TGCCAGGACACCA 17020

RESULT 15
US-09-822-246-3
; Sequence 3, Application US/09822246
; Patent No. US20020142383A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

;; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
;; TITLE OF INVENTION: AND USES THEREOF
;; FILE REFERENCE: CLO01149
;; CURRENT APPLICATION NUMBER: US/09/822,246
;; CURRENT FILING DATE: 2001-04-02
;; NUMBER OF SEQ ID NOS: 4
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 197997
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(197997)
;; OTHER INFORMATION: n = A,T,C or G
US-09-822-246-3

Query Match 56.0%; Score 14; DB 10; Length 197997;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AGGAACAGAAATT 20
|||||
DB 142769 AGGAACAGAAATT 142782

RESULT 16
US-09-263-959-1
;; Sequence 1, Application US/09263959
;; Patent No. US20020150891A1
;; GENERAL INFORMATION:
;; APPLICANT: Hood, Leroy E.
;; APPLICANT: Rowen, Lee
;; APPLICANT: Koop, Ben F.
;; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTIL
;; NUMBER OF SEQUENCES: 1279
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/263,959
;; FILING DATE: 05-MAR-1999
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mcmasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 920010.426C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 684973 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-09-263-959-1

Query Match 56.0%; Score 14; DB 10; Length 684973;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGGAACAGAA 17
|||||

DB 300613 GCCAGGAACAGAA 300626

RESULT 17
US-09-946-807-1/c
;; Sequence 1, Application US/09946807
;; Patent No. US20020165144A1
;; GENERAL INFORMATION:
;; APPLICANT: Stefansson, Hreinn
;; APPLICANT: Steinthorsdottir, Valgerdur
;; APPLICANT: Guicher, Jeffrey R.
;; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;; FILE REFERENCE: 2345.2004-001
;; CURRENT APPLICATION NUMBER: US/09/946,807
;; CURRENT FILING DATE: 2001-09-05
;; PRIOR APPLICATION NUMBER: US/09/795,668
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: US 09/515,716
;; PRIOR FILING DATE: 2000-02-28
;; NUMBER OF SEQ ID NOS: 1531
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 1503841
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: r=g or a
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: y=t/u or c
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: m=a or c
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: k=g or t/u
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: s=g or c
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: w=a or t/u
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: b=g or c or t/u
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: d=a or g or t/u
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: h=a or c or t/u
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: v=a or g or c
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)...(1531)
;; OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1

Query Match 56.0%; Score 14; DB 9; Length 1503841;
Best Local Similarity 100.0%; Pred. No. 46;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19
|||||

Db 816791 CAGGAACCAAGAAAT 816778

RESULT 18

US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US2002004557A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345 2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y-t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b-g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d-a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h-a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v-a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n-a or g or c or t/u

US-09-795-668-1

Query Match 56.0%; Score 14; DB 10; Length 1503841;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19
|||||

Db 816791 CAGGAACCAAGAAAT 816778

RESULT 19

US-09-795-686-1/c
; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345 2005-001
; CURRENT APPLICATION NUMBER: US/09/795,686
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,715
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503841
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: r-g or a
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: y-t/u or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: m-a or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: k-g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: s-g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: w-a or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: b-g or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: d-a or g or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: h-a or c or t/u
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: v-a or g or c
; NAME/KEY: misc_feature
; LOCATION: (1)...(1531)
; OTHER INFORMATION: n-a or g or c or t/u

US-09-795-686-1

Query Match 56.0%; Score 14; DB 10; Length 1503841;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGGAACCAAGAAAT 19
|||||

Db 816791 CAGGAACCAAGAAAT 816778

RESULT 20

US-09-895-382-6/c

; Sequence 6, Application US/09895382

; Patent No. US20020137150A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, HIROMI

; APPLICANT: NAKAMURA, JUN

; APPLICANT: IZUI, HIROSHI

; APPLICANT: NAKAMATSU, TSUYOSHI